

Optimization of the total merit index of Austrian dairy cattle

Validation and adaptation of an approximate multitrait two-step procedure

CAS Touch Down

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Outline of the presentation



- General introduction
- Aims of the thesis
- Approximate multitrait two-step procedure
- Paper II
 - A comparison of methods to calculate a total merit index using stochastic simulation study

General introduction (I)



- Total merit index (TMI) introduced in 1998
- Current TMI based on selection index theory

Drawbacks:

- Combination of estimated breeding values (EBV) of different statistical models with heterogeneous reliabilities
- Imprecise definition of **G** matrix
- Off-diagonal elements of **P** discussed controversially
 - Derivation for calculating covariances between traits by Miesenberger (1997)

General introduction (II)



Calculation of covariances (σ_{ii}) between traits

$$\sigma_{ij} = r_{aij}r_i^2r_j^2\sigma_{ai}\sigma_{aj}$$

 \rightarrow Residual covariances are neglected

General introduction (III)



- The currently used approach ...
 - ... ignores residual covariances
 - ... assumes genetic correlations which were estimated approximately, based on literature or set to zero
 - ... combines EBV with heterogeneous reliabilities of correlated traits

→Bias of the TMI for animals with low to moderate reliabilities?

General introduction (VI)



- Mulitrait animal model based on phenotypic data
 - Improves accuracies
 - Lowly heritable traits benefit
 - Considers selection bias
 - Weighting factors economic weights themselves
- Not feasible (20 mio cows, ~30 traits, different statistical models, computing power)

→ Approximations needed

Aims of the thesis – Stochastic SIMULATION

The validation of an approximate multitrait two-step procedure applied to yield deviations (YD) and de-regressed estimated breeding values (drEBV) under the assumption of an Austrian breeding program.

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- The validation of an approximate multitrait two-step procedure applied to yield deviations (YD) and de-regressed estimated breeding values (drEBV) under the assumtion of an Austrian breeding program.
- The comparison between a full multitrait animal model, the currently used index selection method for calculating a TMI as well as an approximate multitrait procedure applied to YD and drEBV.

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- The investigation of consequences of ignoring residual covariances when a TMI is combined.

Aims of the thesis – Field data



 The application of the approximate two-step procedure applied to YD and drEBV based on field data.

Yield deviations (YD) De-regressed estimated breeding values (drEBV) → Pseudo phenotypes



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Yield deviations

$$YD = y - Xb(-Zp) \longrightarrow$$
 Genetic merit + e

YD... Yield deviation

- y... Phenotypic observation
- b... Vector for fixed effects
- p... Vector for permanent environment effects
- X and Z... Incidence matrices
- De-regressed estimated breeding values

$$drEBV = \frac{\hat{a} - PA}{r^2} \implies Genetic merit + e$$

$$drEBV... De-regressed estimated breeding value$$

$$\hat{a}... Estimated breeding value$$

$$PA... Parent average$$

$$r^2... Reliabilitv$$

$$drEBV... De-regressed estimated breeding value$$

$$r^2 = \frac{1 - \left(\frac{1 - h^2}{h^2}\right)}{Z_i Z_i + \left(\frac{1 - h^2}{h^2}\right)}$$

Approximate multitrait two-step procedure







Genetics Selection Evolution 2015, 47:36

Publication II A comparison of methods to calculate a total merit index using stochastic simulation study







- Comparison of different methods
 - Full multitrait animal model
 - The currently used index selection method
 - Approximate multitrait procedure applied to YD and drEBV
- The investigation of consequences of ignoring residual covariances when a TMI is combined

Materials and methods (I)



- Stochastic simulation program ADAM
- Population size: ~50,000 Brown Swiss cows
- 5 traits: fat yield (FY), protein yield (PY), net daily gain (NDG), somatic cell count (SCC), non-return rate cow (NRR)
- h² and r_a

	FY	ΡΥ	NDG	SCC	NRR
FY	0.40	0.85	0.10	0.25	-0.20
PY		0.39	0.10	0.25	-0.20
NDG			0.27	0.00	0.00
SCC				0.12	-0.10
NRR					0.02

Materials and methods (II)



- 3 scenarios regarding residual correlations:
 - S0: r_e = 0
 - [S1: r_e = 0.5 r_a]
 - S2: r_e = r_a = r_p
- Selection over 30 yrs for TMI based on multivariately EBV
- TMI:

5% FY + 54% PY + 4% NDG + 20% SCC + 17% NRR

10 replicates

Materials and methods (III)



TMI methods

- MULTI: Multitrait animal model based on phenotypic data (corrected for herd-year-effect, MiX99) → reference method
- **YD:** Multitrait animal model based on YD
- drEBV: Multitrait animal model based on drEBV
- YD and drEBV from univariate evaluations (MiX99)

$$\mathsf{TMI} = \hat{a}_{FY}\omega_{FY} + \hat{a}_{PY}\omega_{PY} + \hat{a}_{NDG}\omega_{NDG} + \hat{a}_{SCC}\omega_{SCC} + \hat{a}_{NRR}\omega_{NRR}$$

Materials and methods (IV)



- SI: Selection index approach (Miesenberger, 1997)
 - EBV from univariate evaluations (MiX99)
 - TMI: selction index with EBV as ,phenotypes' covariances between EBV:

 $\sigma_{ij} = r_{aij}r_i^2r_j^2\sigma_{ai}\sigma_{aj}$

- Residual correlations are neglected \rightarrow assumed to be 0
- EBV standardized 100/12
- Results for the last 20 years
 - Rank correlations, bias

Results (I) Rank correlations with MULTI



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Years	YD 0	YD 2	drEBV 0	drEBV 2	SI O	SI 2
11-15						
16-20						
21-25						
26-30						
ALL						

Results (I) Rank correlations with MULTI





Years	YD 0	YD 2	drEBV 0	drEBV 2	SI O	SI 2
11-15	1.000	1.000	1.000	1.000		
16-20	1.000	1.000	1.000	1.000		
21-25	1.000	1.000	1.000	1.000		
26-30	1.000	1.000	1.000	1.000		
ALL	1.000	1.000	1.000	1.000		

Results (I) Rank correlations with MULTI



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Years	YD 0	YD 2	drEBV 0	drEBV 2	SI 0	SI 2
11-15	1.000	1.000	1.000	1.000	0.962	0.948
16-20	1.000	1.000	1.000	1.000	0.963	0.943
21-25	1.000	1.000	1.000	1.000	0.945	0.914
26-30	1.000	1.000	1.000	1.000	0.950	0.932
ALL	1.000	1.000	1.000	1.000	0.989	0.983

Results (II) Bias (TMI_{YD,drEBV,SI} – TMI_{MULTI})



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Reliability	YD 0	YD 2	drEBV 0	drEBV 2	SI 0	SI 2
≤39						
40-49						
50-59						
60-69						
70-79						
80-89						
≥90						

Results (II) Bias (TMI_{YD,drEBV,SI} – TMI_{MULTI})



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drEBV 0 drEBV 2 Reliability YD 0 YD 2 **SI 0 SI 2** 0.0 ≤39 0.1 0.1 0.0 40-49 0.0 0.0 0.1 0.1 50-59 0.1 0.1 0.0 0.0 0.0 60-69 0.1 0.1 0.0 0.0 0.0 70-79 -0.1 -0.1 80-89 0.0 0.00 0.0 0.0 0.0 0.0 0.0 0.0 ≥90

Results (II) Bias (TMI_{YD,drEBV,SI} – TMI_{MULTI})



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Reliability	YD 0	YD 2	drEBV 0	drEBV 2	SI O	SI 2
≤39	0.1	0.1	0.0	0.0	1.0	0.2
40-49	0.1	0.1	0.0	0.0	1.3	0.7
50-59	0.1	0.1	0.0	0.0	-0.5	-1.1
60-69	0.1	0.1	0.0	0.0	-0.6	-1.4
70-79	-0.1	-0.1	0.0	0.0	-1.6	-1.6
80-89	0.0	0.00	0.0	0.0	-2.3	-2.6
≥90	0.0	0.0	0.0	0.0	-2.5	-2.8



Results (IV) Time trend of bias (TMI_{SI,0} – TMI_{MULTI}) Scenario 0





Top 10% Bulls with progeny (BP) and bulls without progeny (BNP)

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Summary



Approximate multitrait methods YD and drEBV

- Very close to reference method MULTI
- No relevant bias in all scenarios and animal groups
- Method drEBV even better than YD (e.g. Interbull EBV)
- Practical advantages for drEBV (e.g. random regression test-day model)
- Inclusion of Interbull EBV and genomic information
- \rightarrow Implementation for routine genetic evaluation can be suggested

Selection index method SI

- Mainly upwards bias in all animals and bulls without progeny and downwards bias in proven bulls
- Strong bias in top animals

Thank you for your attention!

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