



UNIVERSITÀ
DEGLI STUDI
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AGRICOLE, ALIMENTARI, AMBIENTALI E FORESTALI



Genetic correlations between productive and reproductive cow-sisters performance and feed efficiency and greenhouse gasses emissions in growing brothers-bulls

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Introduction

1. Anafibj has started **since 2015** to work on feed efficiency and environmental impact traits
2. Currently predicted breeding value for feed efficiency – pFE (**December 2019**)
3. Predicted breeding value for methane emission (**December 2023**)

✓ ANAFIBJ position:

- ✓ Important to implement data collection for new traits (eg. feed intake and GHG data)
- ✓ Difficult to set routine data-collection in commercial dairy farm



“Feed&Gas” important traits for Italy

Livestock Production Science, 32 (1992) 189–202
Elsevier Science Publishers B.V., Amsterdam

189

Genetic relationships between feed intake, efficiency and production traits in growing bulls, growing heifers and lactating heifers

G.J. Nieuwhof, J.A.M. van Arendonk, H. Vos and S. Korver

Department of Animal Breeding, Wageningen Agricultural University, Wageningen, Netherlands

(Accepted 27 January 1992)



AIM current presentation

Investigate how **productive and reproductive performance of Italian Holstein cows** would be affected by selecting for **improved feed efficiency** and **reduced greenhouse gasses emissions** of growing bulls.

Bull's Phenotypic information

Since March 2018 → 221 Young Bulls

- “Morpho” data
 - 928 records on 221 bulls
- “Feed Intake” data
 - 464'977 records on 212 bulls
- “Green” data
 - 11'202 records on 161 bulls



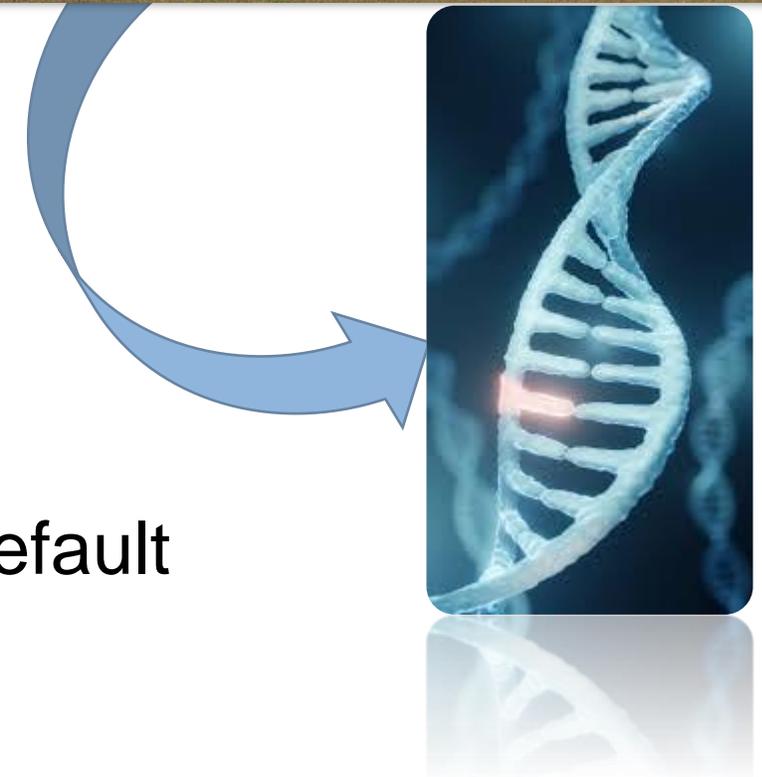
Roughage Intake Control system
(Hokofarm Group, The Netherlands)



GreenFeed system (C-Lock Inc., Rapid City,
SD, USA)

Bull's Genomic information

- 221 individuals genotyped
- 69,127 SNPs over 30 chromosomes
- SNP editing performed using preGSf90 software (Misztal, UGA)
- 61,591 SNPs after editing
- Genomic relationship matrix built using default options



Data Processing and Editing

- Traits included, MORPHO:
 - Weight
 - BCS
 - Heart girth
 - Height

- Each dataset was prepared as showing 1 record per bull-date combination.

Data Processing and Editing

- Traits included, RIC:
 - Number of Visits
 - Number of Meals
 - Intake (Average/Sum)
 - Time (Average/Sum)
 - Adjustment by time of the day at the visit.
 - All traits being adjusted or not.
 - Each dataset was prepared as showing 1 record per bull-date combination.
 - **Records removed if showing negative intake and negative time.**
-

Data Processing and Editing

- Existing Variables

- CO₂ (g/d)
- CH₄ (g/d)
- AirFlow (L/s)
- Duration of Visit



- Traits included, GreenFeed:

- Number of Visits
- CO₂ (Average)
- CH₄ (Average)
- AirFlow (Average)
- Duration of Visit (Average, Sum)

- Each dataset was prepared as showing 1 record per bull-date combination.

Model

$$y = \text{DOB} + \text{AGE} + \text{CG} + \text{ag} + \text{pe} + \text{date} + e$$

y: phenotype

DOB: date of birth (covariate)

AGE: age at phenotyping (covariate)

CG: contemporary group (covariate)

ag: additive genetic (GBLUP)

pe: permanent environmental (bull)

date: date of phenotyping

e: residual

**RESULTS NOT
SHOWN**

Productive Records

- ✓ 123,894 records, on 12,882 cows, from 1,043 herds.
- ✓ Removed records later than 365 days in milk.
- ✓ Removed outliers (by looking at the distribution).
- ✓ Removed cows without genotypes.
 - Genotyped different SNP panels and then imputed to a medium density panel (~69,000 markers) using routine procedures



Productive Records

- Allocated the remaining 9'739 cows in:
 - Full-sib families (55)
 - Paternal half-sib families (77)
 - Maternal half-sib families (84)

- Kept families with at least one bull on trial.
- Kept the 10 cows with most records from each family

656 cows selected



Model



$$y = NOL + SOL + ag + pe + htd + e$$

y: phenotype

NOL: number of lactation (heifer/cow)

SOL: stage of lactation (30-d classes)

ag: additive genetic (GBLUP)

pe: permanent environmental (cow)

htd: herd test-date

e: residual





	MY	FP	PP	FY	PY	SCS	CASp	UREA	LACTp
Weight	0.324	0.343	-0.192	0.336	0.528	-0.443	0.208	-0.400	0.553
BCS	0.527	-0.517	-0.405	0.325	0.808	-0.342	-0.313	-0.181	0.433
Heart Girth	0.353	-0.403	-0.464	-0.641	0.232	-0.108	0.256	-0.519	0.257
Height	0.342	-0.111	-0.236	-0.166	0.579	0.051	0.370	-0.056	0.108
Nvisits.r	0.447	0.742	0.341	0.848	0.638	0.237	0.345	0.215	0.183
Sintake.r	-0.159	0.494	0.330	0.568	0.486	0.080	0.337	-0.050	0.272
Stime.r	0.247	0.458	0.289	0.176	0.166	0.157	0.379	-0.312	0.126
Mintake.r	-0.447	-0.335	-0.327	-0.625	-0.282	-0.166	-0.445	-0.402	-0.067
Mtime.r	0.124	-0.207	-0.459	-0.605	-0.265	-0.449	-0.499	0.002	0.083
Nvisits.g	-0.451	0.640	-0.145	0.133	-0.356	0.143	-0.138	-0.018	0.080
Stime.g	-0.328	0.485	-0.201	0.187	-0.362	0.203	-0.051	0.040	0.261
Mco2.g	0.587	0.028	-0.533	0.296	0.561	-0.237	-0.632	-0.287	0.706
Mch4.g	0.070	0.531	-0.125	0.305	0.177	-0.166	-0.183	0.010	0.303
Mtime.g	0.049	0.368	-0.454	0.276	-0.139	0.417	-0.360	-0.136	0.133



Reproductive Records

Commercial Farms



- 12,207 records, on 12,207 cows, from 966 herds.
- Removed if IFL larger than 250
- Removed if DTFS larger than 200
- Removed if PBW larger than 700

Reproductive Records

- Allocated the 12,207 cows in:

- Full-sib families (55)

- Paternal half-sib families (77)

- Maternal half-sib families (84)

- Kept families with at least one bull on trial.

- Kept the 50 cows with most records from each family

1,686 cows selected

Model

$$y = AGE + SOL + ag + hym + e$$

y: phenotype

AGE: age at scoring/insemination

SOL: stage of lactation at scoring/insemination

ag: additive genetic effect (GBLUP)

hym: herd-year-month of scoring/insemination

e: residual



	BCS (cow)	Predicted Body weight	IFL	DTFS	NRR65
Weight	-0.391	0.323	0.454	0.494	-0.639
BCS (bull)	0.272	-0.374	-0.254	0.368	0.309
Heart Girth	-0.089	-0.038	-0.028	0.367	0.306
Height	-0.504	0.538	-0.822	0.342	0.328
Nvisits.r	-0.239	0.616	0.339	0.541	-0.651
Sintake.r	-0.064	0.375	0.600	0.305	-0.359
Stime.r	-0.157	0.385	0.154	0.690	0.170
Mintake.r	-0.031	0.163	0.204	0.470	-0.006
Mtime.r	-0.351	0.358	0.046	0.943	0.305
Nvisits.g	-0.517	-0.049	0.459	0.280	-0.344
Stime.g	-0.506	0.034	0.466	0.197	-0.381
Mco2.g	-0.162	0.213	0.363	0.360	-0.416
Mch4.g	-0.123	0.386	0.309	0.207	-0.535
Mtime.g	-0.360	0.228	-0.041	0.413	-0.197

Discussion

- ✓ Moderate positive correlations between CH₄ and CO₂ emissions in bulls and milk, fat, protein, and lactose yield in full/half-sisters.
- ✓ Similar correlations were found for feed intake and feeding duration
- ✓ Results suggest the possibility **to increase yield in the cows** while controlling intake and emissions in the growing bulls
- ✓ Fertility traits showed similar correlations → possibility to improve cow fertility while reducing feed intake and emission in dairy bulls

Conclusion

- ✓ Data collection performed on growing candidate bulls seems a valuable option, because the positive genetic correlation found
- ✓ The within-breed across-population genetic correlation estimates, suggest the possibility of improving cow productivity and fertility while also improving efficiency and environmental impact in the bulls.
- ✓ To confirm these results more data on dairy bulls are needed and more data (direct phenotypes) of bull' daughter which is in progress
- ✓ The process is a **LONG PROCESS** but we believe the phenotyping of dairy bulls is a doable approach even though data on commercial dairy farms is needed

Grazie



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