Research status (prediction) and a view (peek) into the future

Mogens Sandø Lund

How to increase genomic reliabilities

- **Increase reference population**
  - Join populations of same breed
  - Cows in reference population
  - Across breeds predictions

- **Increase LD information**
  - Haplotype models
  - Sequence information

- **Statistical models**
  - GBLUP/SNP-BLUP
  - Bayesian VSM
  - Single step BLUP

Reference populations

- **Jersey**
  - Jersey agreement VG America
  - Cows in reference

- **RDC**
  - NRF
 - HF

G-BLUP and Bayesian mixture models

	Reference		GBLUP		Bayes mixture	
	Single	joint	single	joint	single	joint
NRF	2,076	5,717	0%	6%	0%	10%
DR	3,367	5,717	0%	1%	3%	6%
SRB	3.367	5,717	0%	2%	0%	2%
FAY	3,367	5,717	0%	0%	0%	0%

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Joining reference populations

	Nordic HF + Euro HF Lund et al. GSE 2011
REF	3035
Joint REF	10762
Reliability increase	

Low genomic relationships (<0.05)	'High' genomic relationships (>0.05)
<+1%	+8%
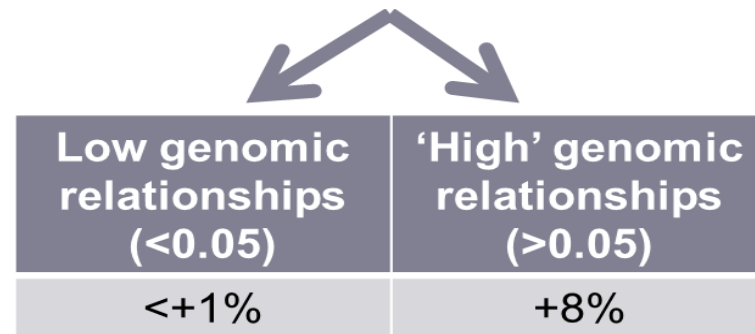
SNP-chip vs. WGS

- SNP chip
  - Sample of SNP (higher minor allele frequency)
  - Limited linkage disequilibrium depending on number of SNP
  - High informativity for imputation
  - Opportunity for custum made chip

- Sequence
  - Contains most variants (>20 mio SNP, indels, CNVs, etc)
  - Causative variants included (no bias in selection of SNP)
  - High linkage disequilibrium between markers and causative variants
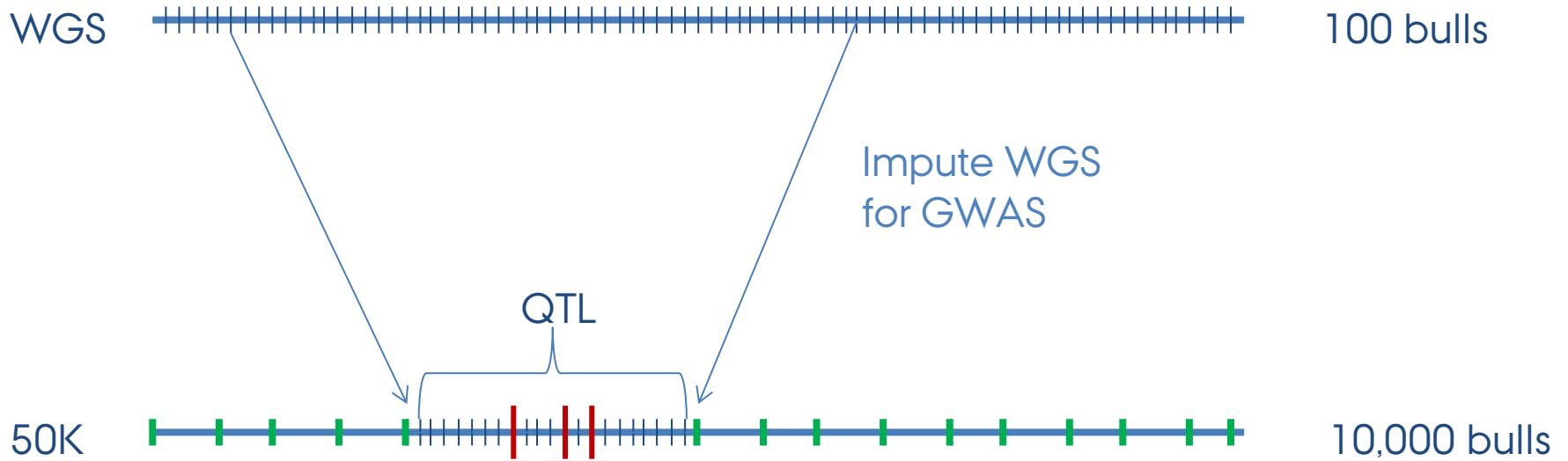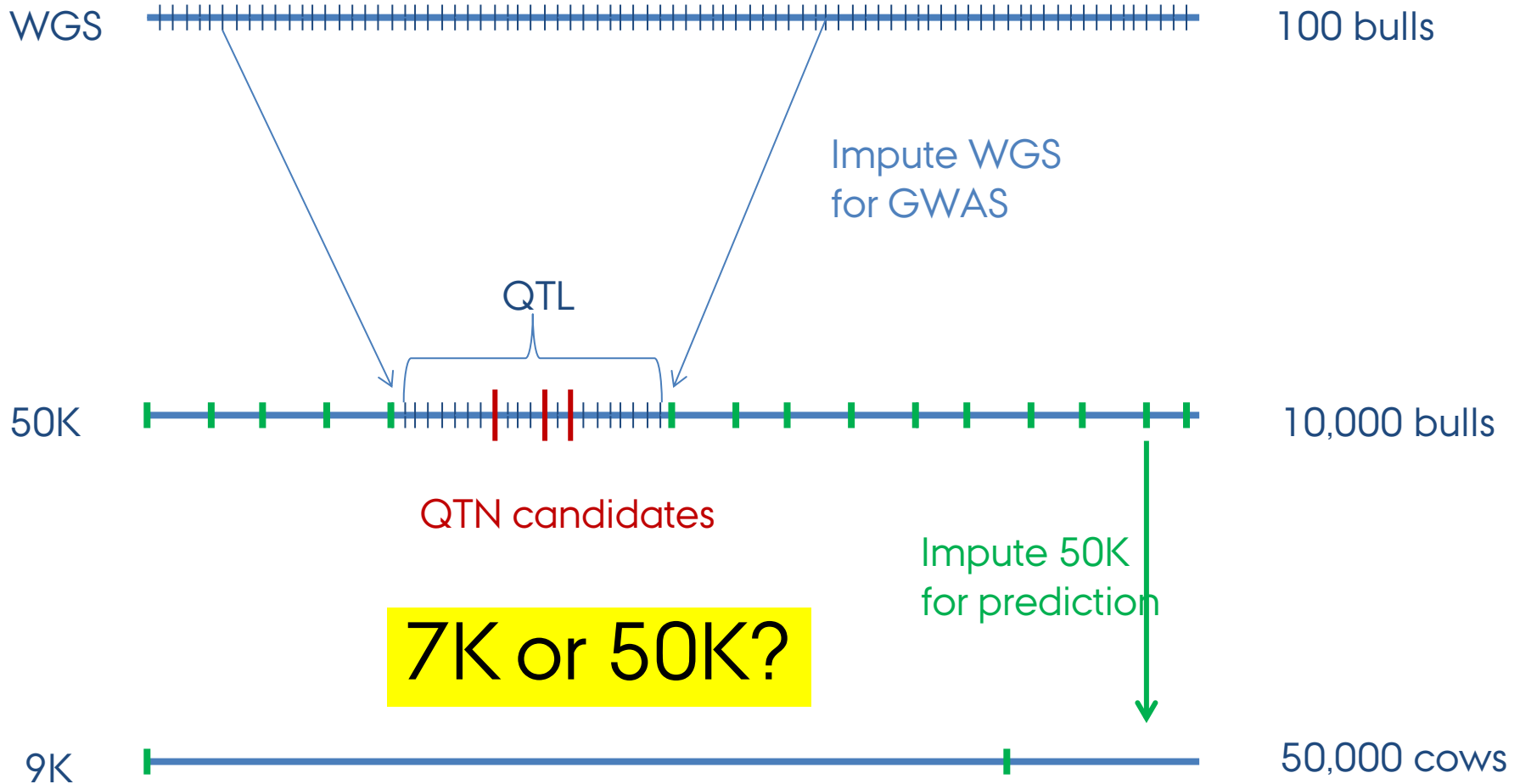 - Sequence GWAS improve associations substantially (Goutam)
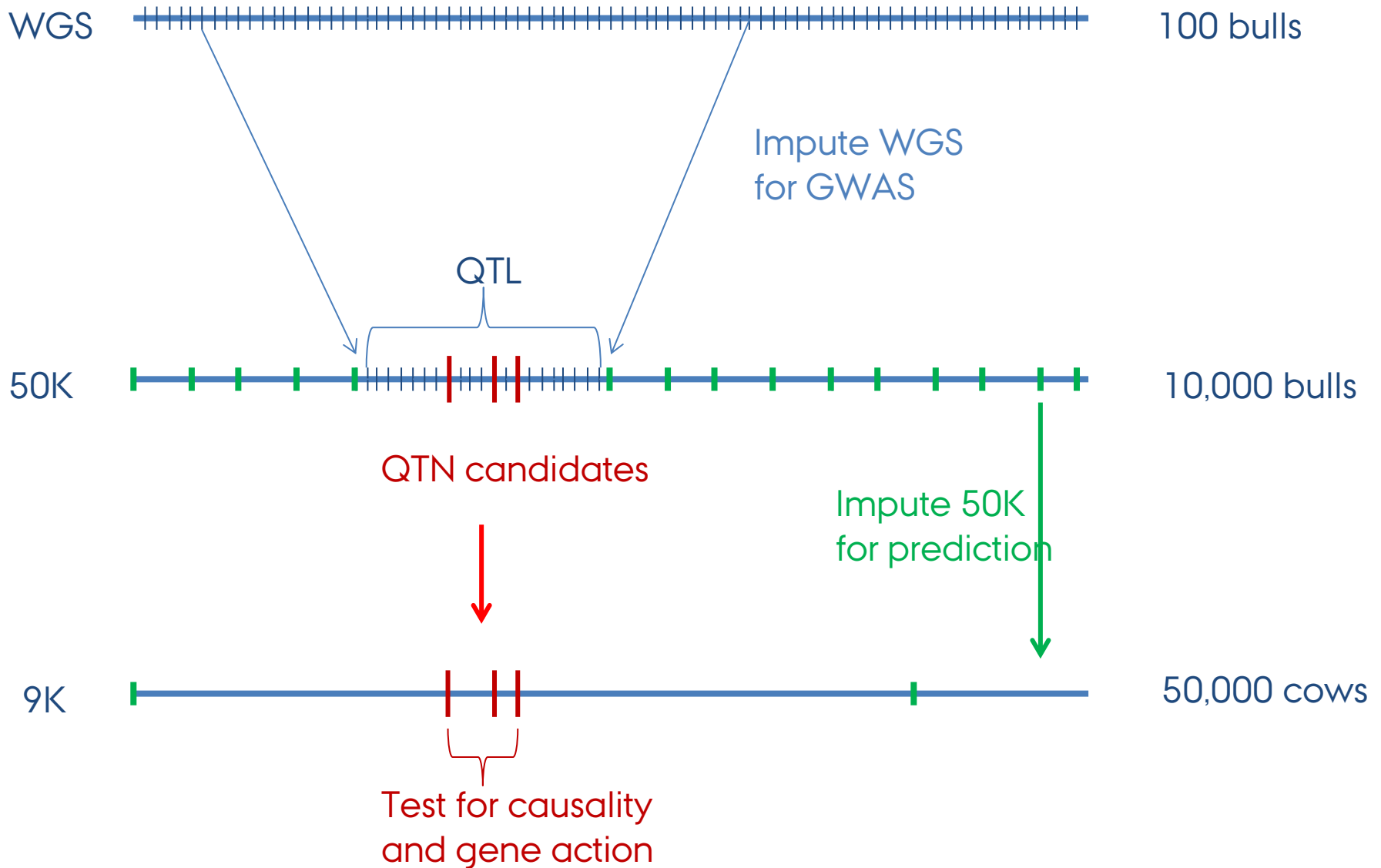
LD-chip

- **Imputation of all genotyped bulls to WGS level**

- **GWAS with 10 mill SNP with R^2>0.9**

- **Selection of 5-15 QTL for each index**

- **Selection 3-5 SNP**
  - P-values
  - Functional annotations

Number of QTL in the LD-chip

Chr	Trait	HF	RDC	JER
1	Birth	10	15	10
2	Body-confirmation	6	8	5
3	Calving	13	12	15
4	Fat	15	14	14
5	Fertility	19	15	15
6	Growth	8	9	5
7	Leg	17	18	10
8	Longevity	8	11	14
9	Mastitis	16	17	25
10	Milk	13	18	16
11	Milking-speed	5	7	5
12	NTM	6	8	9
13	Other-diseases	23	21	13
14	Protein	22	10	14
15	Temperament	6	7	0
16	Udder	8	8	8
17	Yield	16	8	13
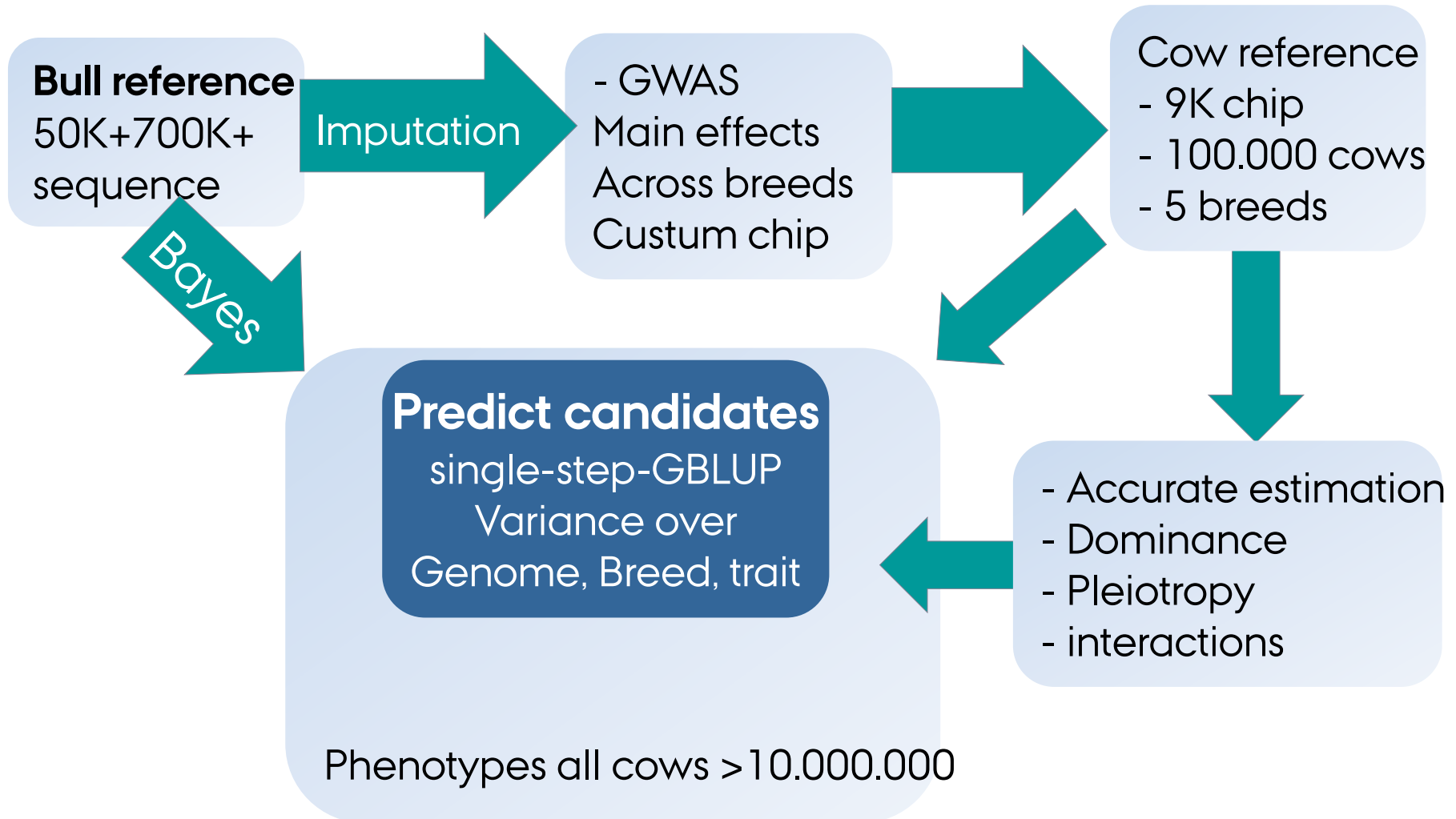
Where are we?

- **Strong strategy to integrate WGS and prediction in practice**

- **New traits on research farm level**

- **Bring to large scale is needed**
  - FE, metabolic diseases, Reproduction, milk spectra
  - Registration herds
  - Focus in new initiative

- **Breeding plans**

Bull reference

- **50K**
  - Capture most genetic variance within breed

- **700K**
  - Haplotype models
  - Prediction over generations (and breeds)

- **Sequence data**
  - Causative variants
  - Prediction over generations and breeds

9K for reference cows

- **More cows in reference (cheaper)**

- **High imputation accuracy**

- **Add many potential causative variants**
  - Non-additive effects
  - Testing for causative variants

- **Better predictions across breeds**

Models

- **GBLUP → infinitesimal model**
  - No improvement from sequence data
  - Needed for large scale predictions
  - Can be modified to prioritise specific SNPs

- **BayesianVS models → causality model**
  - Select causal SNP or few SNP in high LD
  - Needed to extract prior knowledge for GBLUP/SNP-BLUP

Examples

Product quality

J. Dairy Sci. 94:5683–5690
doi:10.3168/jds.2011-4520
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Predicting bovine milk protein composition based on Fourier transform infrared spectra

M. J. M. Rutten,[*1] H. Bovenhuis,[*] J. M. L. Heck,[†] and J. A. M. van Arendonk[*]
[*]Animal Breeding and Genomics Centre, Wageningen University, PO Box 338, 6700 AH, Wageningen, the Netherlands
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Fertility/ Energy balance

Acta Agriculturae Scand Section A, 2010; 60: 79–87

Taylor & Francis
Taylor & Francis Group

ORIGINAL ARTICLE

Predicting early lactation energy balance in primiparous Red Dairy Cattle using milk and body traits

P. MÄNTYSAARI[1] & E. A. MÄNTYSAARI[2]

[1]Animal Production Research, MTT Agrifood Research Finland, Jokioinen, Finland, and [2]Biotechnology and Food Research, MTT Agrifood Research Finland, Jokioinen, Finland

Health

J. Dairy Sci. 93:3065–3069
doi:10.3168/jds.2009-2847
© American Dairy Science Association®, 2010.

Short communication: Ketone body concentration in milk determined by Fourier transform infrared spectroscopy: Value for the detection of hyperketonemia in dairy cows

A. T. M. van Knegsel,[*1] S. G. A. van der Drift,[†2] M. Horneman,[‡] A. P. W. de Roos,[‡] B. Kemp,[*] and E. A. M. Graat[#]
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Emission

Animal (2012), 6:10, pp 1694–1701 © The Animal Consortium 2012
doi:10.1017/S1751731112000456

animal

Potential use of milk mid-infrared spectra to predict individual methane emission of dairy cows

F. Dehareng[1*†], C. Delfosse[1*], E. Froidmont[2], H. Soyeurt[3,4], C. Martin[5], N. Gengler[3,4], A. Vanlierde[1] and P. Dardenne[1]

Increased LD