



IT Solutions for
Animal Production

A Continuous Genomic Evaluation System for German Holsteins

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Introduction: frequency of genomic evaluation

- Genomic evaluation for German Holstein
 - 3 major evaluations following Interbull MACE
 - Deregressing national and MACE EBV of bulls
 - Estimating SNP effects for all traits
 - Monthly genomic evaluation
 - Official GEBV

- German industry demands on more frequent genomic evaluations
 - Reduce costs of keeping (culled) candidates on farm
 - Genomic selection of embryos on a weekly basis



A continuous genomic evaluation system for German Holsteins



- A genomic model with SNP effects for German Holsteins
 - SNP effects by traits and allele frequencies for DGV calculation
- Pedigree index automatically calculated in **vit** system for new (genotyped) animals

- Changes in genomic evaluation methods in the new system
 - Standard chip (50K) now with missing genotypes NOT filled via imputing
 - Selection index for TMI (RZG) replaced with a fixed formula (DGV)
 - No longer bottom-up wise for calculating TMI or sub-indices (GEBV)



Technical issues for implementation

- Source programs in Java/SQL instead of Fortran/SAS
- Parameter files obtained from official genomic evaluations
- Automatic notification of genotype providers about interim genomic evaluation results
- Animals in standard 50K chip get GEBV just-in-time (no imputation)
- Genotype imputing for non-standard chips
 - Most candidates genotyped with LD, EuroG10K, GGP, GHD, etc.
 - Imputing on a bi-weekly basis as currently requested
 - Embryos in 50K have lower call rates than real animals
 - Imputing on a weekly basis
 - Full imputation with findhap version 2
 - c.a. 2 hours on 40 CPUs and 100 Gb RAM for 113,910 genotyped animals
- The continuous system was introduced in March 2014





Ergebnisse Zuchtwertschätzung



HB-Nr.:
Orig.Name: Teddy
Besitzer:

Geschlecht: weiblich

Druckdatum: 07.03.2014
Schätzdatum:

Abstammung



Teil- und Gesamtindizes

	3-V-PI ¹	ZW (konv./VPI) ²	dGW ³	gZW ⁴
RZG	115	%	121 50%	123
RZM	101	%	116 49%	115
RZE	107	%	95 47%	97
RZS	116	%	113 74%	114
RZN	118	%	107 48%	109
RZR	113	%	116 29%	121
RZK m	111	%	112 50%	114

Milchmerkmale

	3-V-PI ¹	dGW ³	gZW ⁴	Funktionale Merkmale	3-V-PI ¹	dGW ³	gZW ⁴
Milchmenge		448	458	KON		116	118
Fettmenge		53	52	KV d		115	115
Eiweißmenge		29	29	TG d		114	114
Fettgehalt		0,36	0,36	RZK d		115	115
Eiweißgehalt		0,10	0,10	RZD		96	97
				MVH		89	91
				BCS		93	95

Exterieur

	dGW ³	gZW ⁴
Größe	94	94 groß
Milchcharakter	100	100 viel
Körperteile	95	95 viel
Stärke	95	95 stark
Beckenneigung	100	100 abfallend
Beckenbreite	100	100 breit
Hinterbeinwinkel	102	102 gewinkelt
Klauenwinkel	87	87 steil
Sprunggelenk	109	109 trocken
Hinterbein	95	95 parallel
Bewegung	98	98 gut
Hinterhöhe	101	101 hoch
Zentralbau	95	95 stark
Schulterhöhe	94	94 innen
Strichhöhe	97	97 innen
Vordereuteraufhängung	94	94 fest
Euterteile	96	96 hoch
Strichlänge	97	97 lang

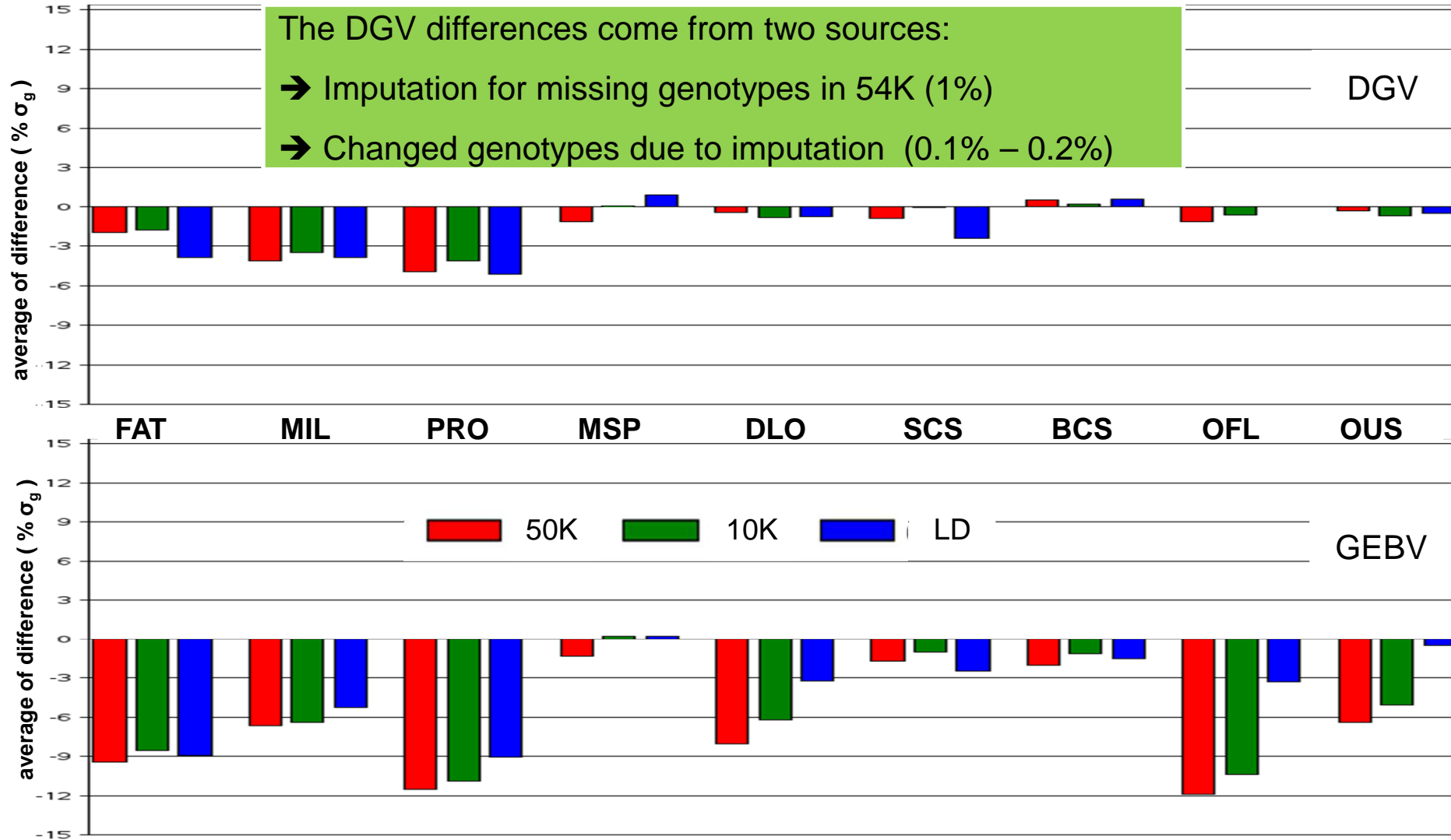


A validation study of the continuous system

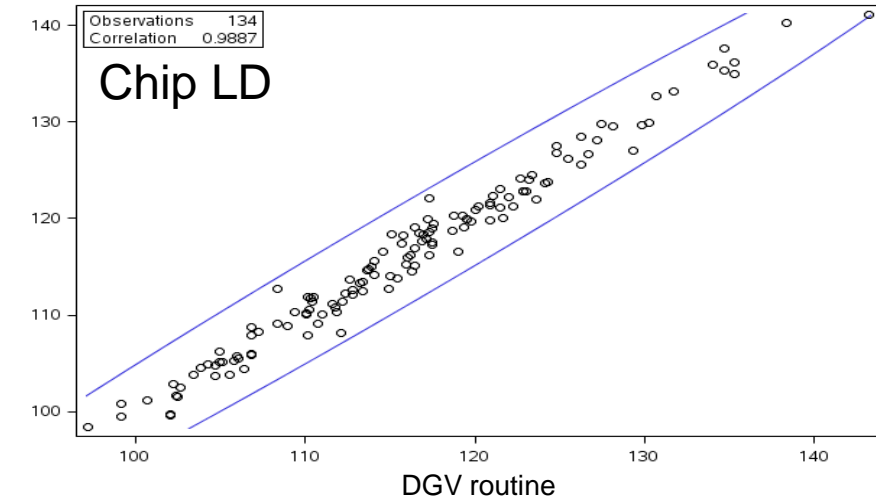
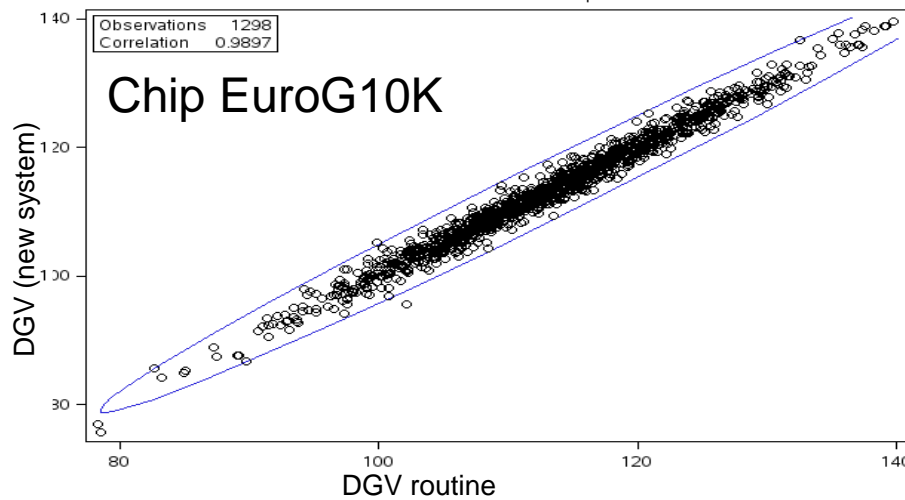
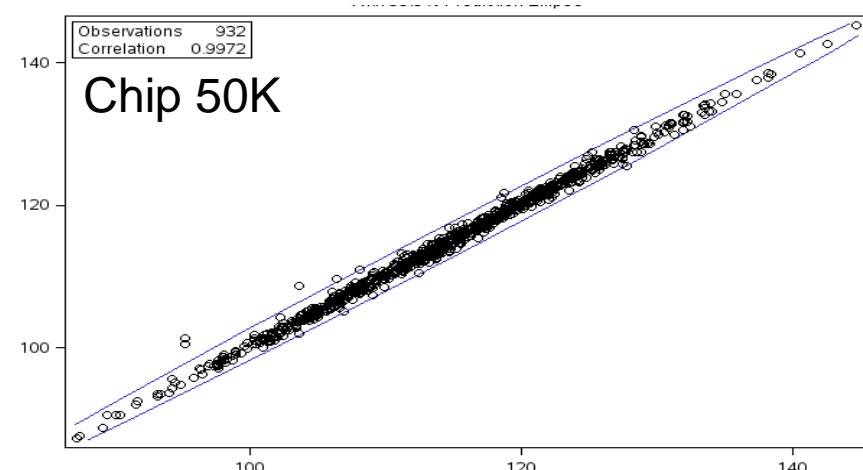
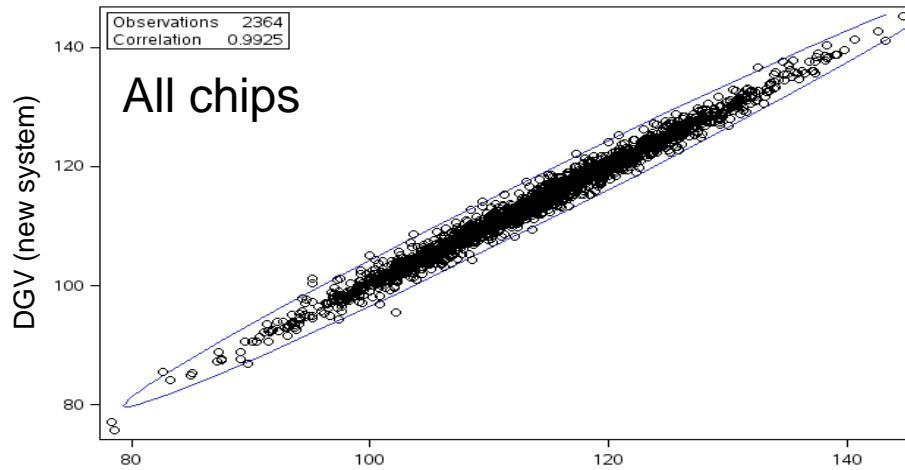
- Monthly genomic evaluation April 2014
 - 113,910 genotyped animals & 338,761 animals in pedigree
 - 45,613 SNPs for DGV calculation
 - 27,175 Holstein bulls in genomic reference population
- The continuous just-in-time genomic evaluation system
 - 921 animals and 60 embryos genotyped with 50K chip
 - 1340 animals genotyped with EuroG10K
 - 134 animals with Illumina LD chip
- Full genotype imputation with findhap v2
 - 34,115 animals with 50K v1 chip
 - 62,486 animals with 50K v2 chip (including embryos)
 - 14,221 animals with EuroG10K chip
 - 3,081 animals with LD chip



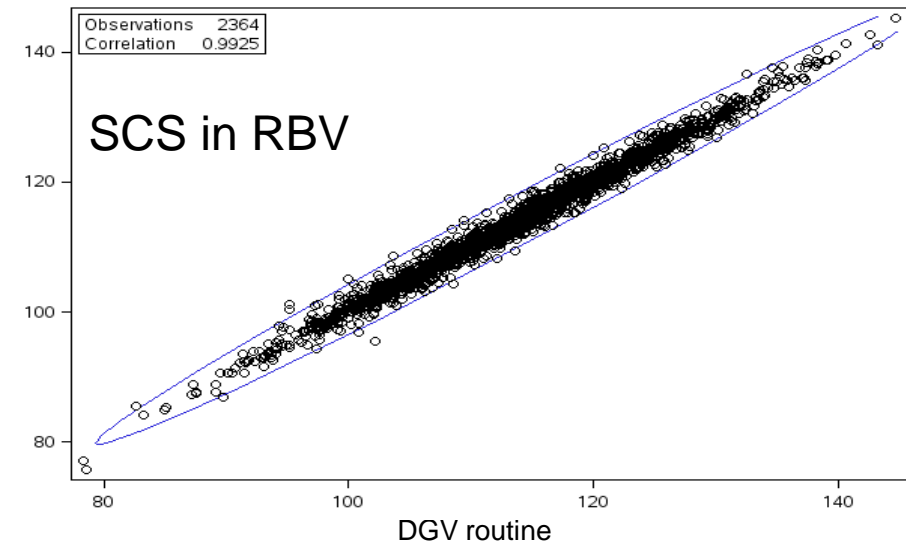
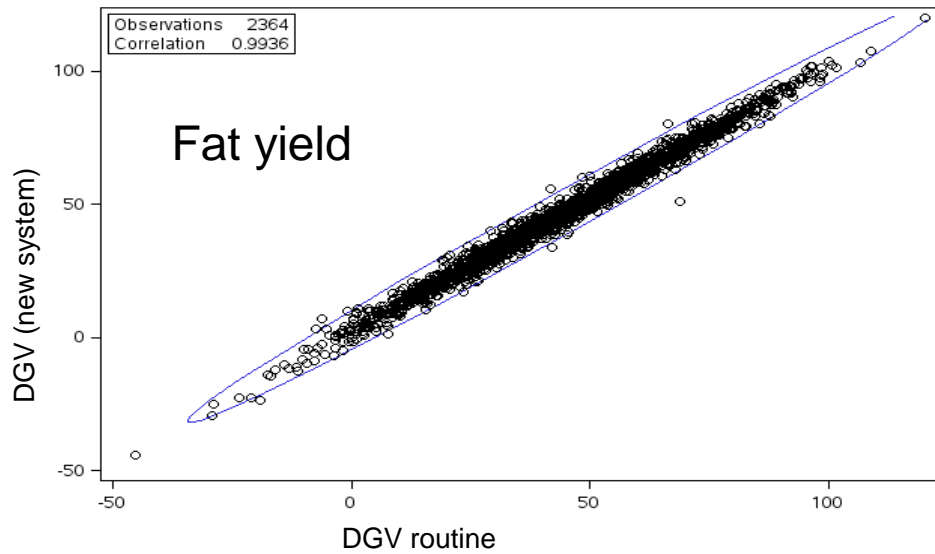
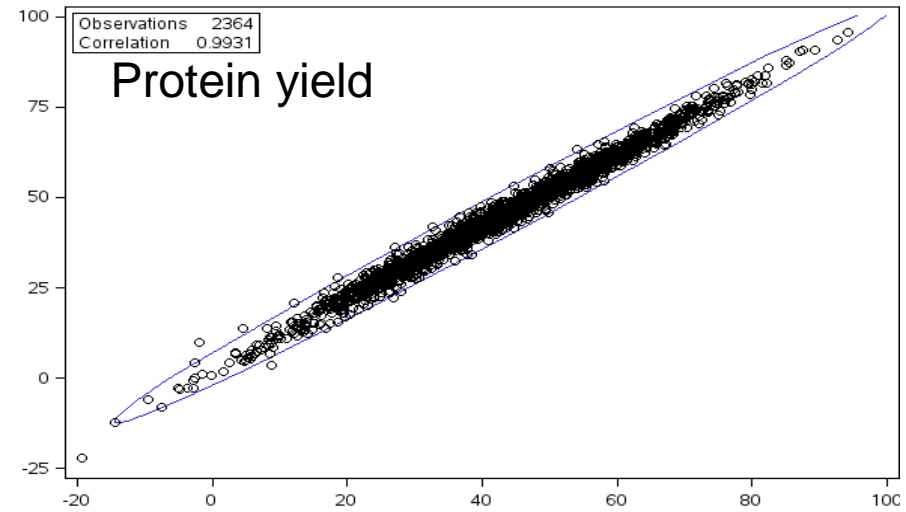
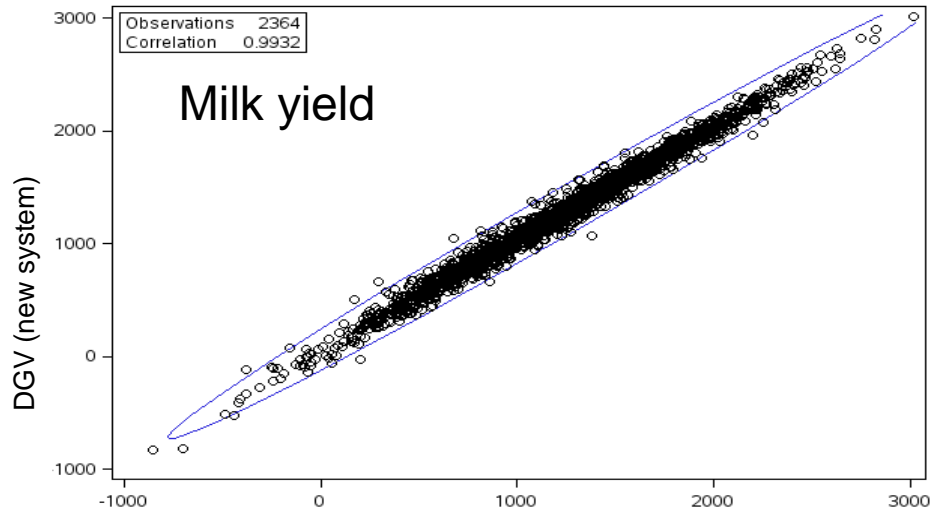
DGV and GEBV standardized differences between the continuous and routine genomic evaluations



GEV correlations between the continuous and routine evaluations for SCS in RBV by chips



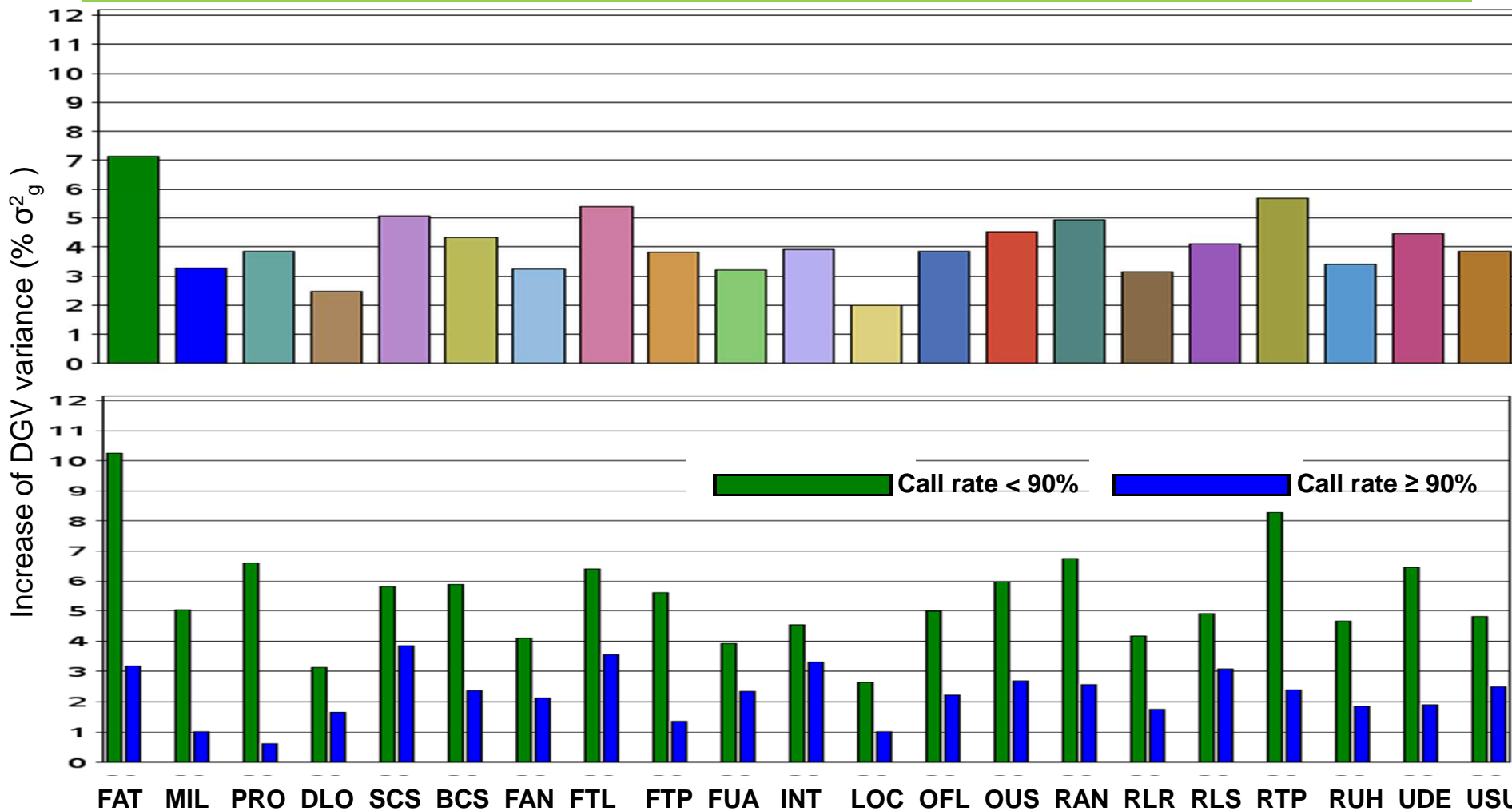
GEV correlations between the continuous and routine evaluations for traits



Increase of DGV variance due to imputing for embryos (N=372)



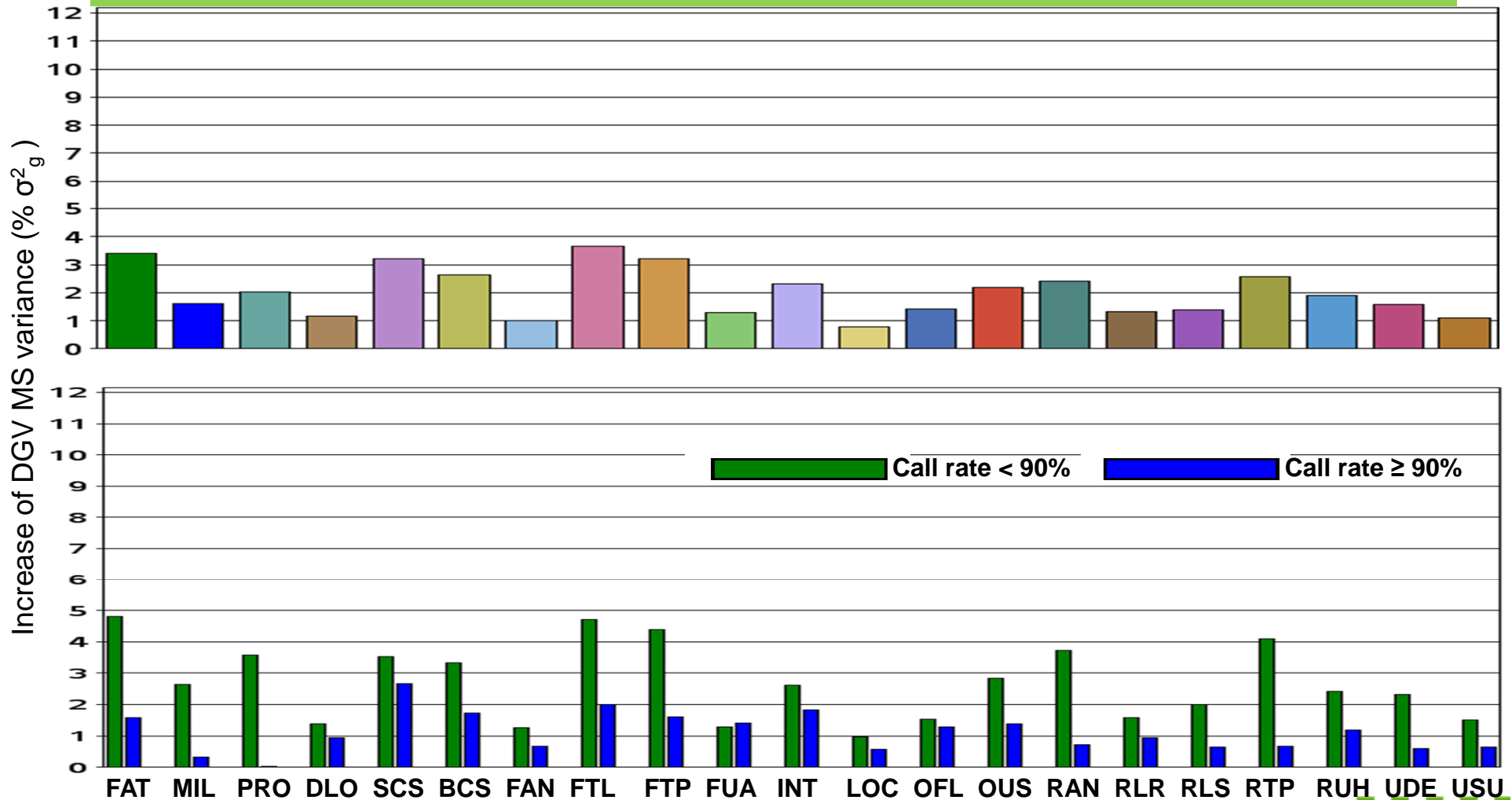
Included embryos → sire and dam genotyped → genotype inconsistency ≤ 5%



Increase of DGV Mendelian sampling variance due to imputing for embryos (N=372)



Included embryos → sire and dam genotyped → genotype inconsistency ≤ 5%

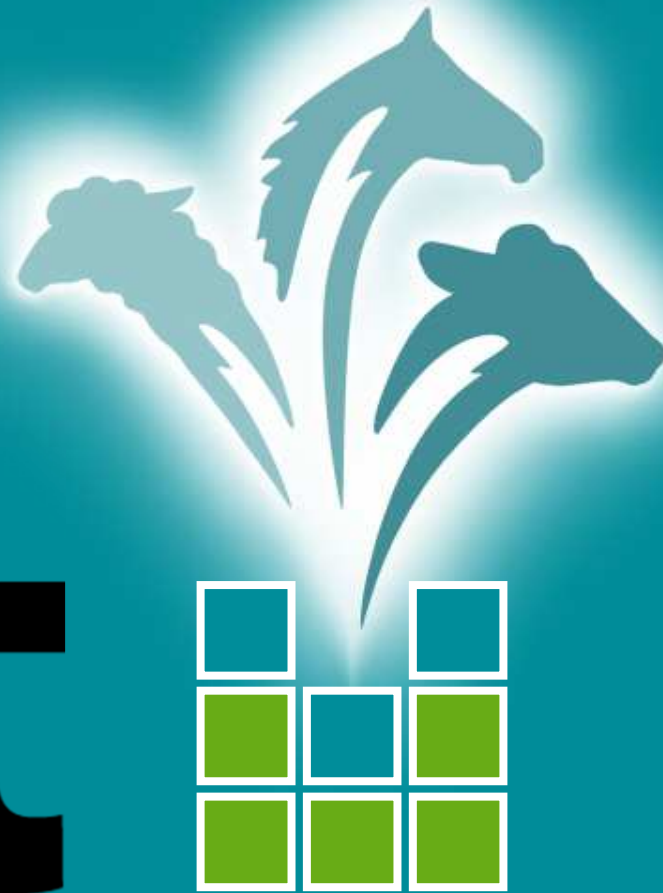


Conclusions and Summary

- The continuous genomic evaluation system implemented
 - As a supplement to official monthly genomic evaluations
 - With positive responses and support by the industry
- Results of the new system confirmed in a validation study
 - Correlations > 0.99 for all traits
 - Average of difference $-0.04 - 0.01 \sigma_g$
 - More changes in GEBV than DGV due to different PI calculations
- Genotype imputing important for embryos in 50K
 - Increase in DGV variance and Mendelian sampling variance
 - To improve genotypes using parents genotypes in future
 - To compare genotypes and DGV between embryos and calves in future
- Improve timely pedigree completeness of genotyped animals
- Routinely conduct validations for the new system
- Minimise differences in statistical methods with the official evaluation



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Thank you for your attention