Comparison of national genomic predictions of EuroGenomics exchanged young bulls

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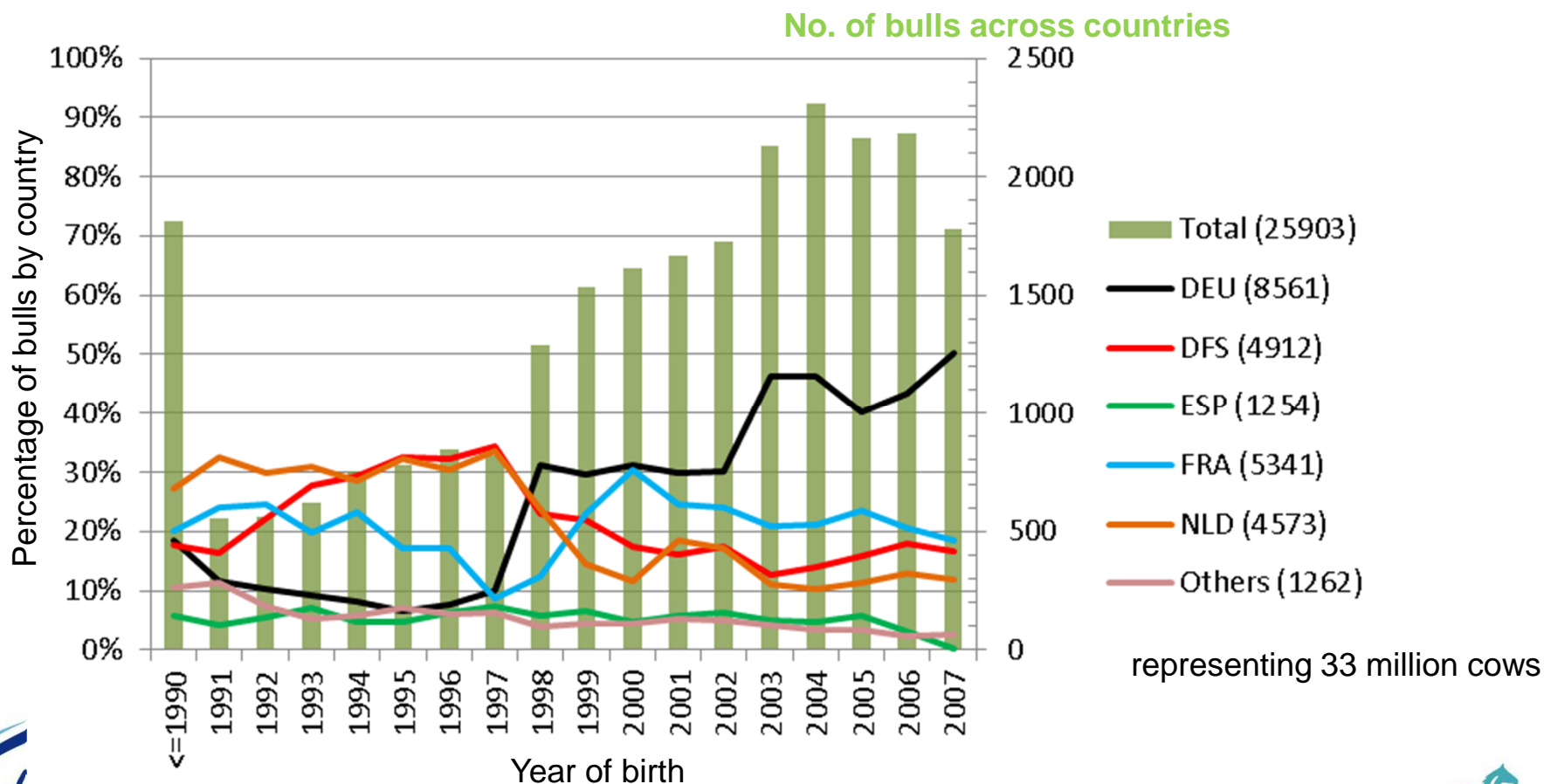# Introduction: EuroGenomics bull reference population

Six Holstein populations forming the largest bull reference population
(Germany, Nordic countries, Spain, France, The Netherlands/Flanders & Poland)

No. of bulls across countries

Legend:
- Total (25903)
- DEU (8561)
- DFS (4912)
- ESP (1254)
- FRA (5341)
- NLD (4573)
- Others (1262)

representing 33 million cows

Data from April 2013 genomic evaluation for milk yield

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Genomic evaluation models by EuroGenomics countries

- Lund et al. (2011) demonstrated a 11% increase in reliability of genomic prediction by upgrading national to EuroGenomics ref. pop.
- Genomic prediction models
  - DEU: BLUP SNP model (Liu et al. 2011) with a residual polygenic effect
  - DFS: GBLUP model (Lund et al. 2011)
  - NLD: Bayes stochastic search variable selection (Calus et al. 2008)
  - FRA: BLUP QTL model (Ducrocq et al. 2009) with a polygenic effect and ~ 400 QTLs/trait
- Combination of genomic with conventional information
  - DGV combined with male pedigree index in a posterior step
  - FRA: joint estimation of QTL and polygenic (with ~ 40% variance) effects
- Phenotypes for genomic prediction
  - Mixture of deregressed EBVs from MACE and national evaluations
  - FRA: DYD for bulls with sufficient number of daughters in France

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Data materials

- Goal of this study: comparing national genomic predictions using common young bulls
- Four countries exchanged genotypes and pedigree of young bulls born in 2010 (including culled candidates) in March 2013
    - DEU, DFS, FRA and NLD
- National GEBV and reliabilities provided for comparison
- Selected traits for joint analysis (December 2012 evaluation)
    - Milk production: protein yield (pro)
    - Conformation: udder depth (ude)
    - Udder health: somatic cell score (scs)
    - Female fertility: cow's ability to conceive (T4: cc2)
        - DEU, DFS and NLD: interval first to last insemination
        - FRA: cow conception rate
- Focus: correlations and regressions of national genomic predictions
    - also compared to conventional evaluations

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Data materials: exchanged genotypes and national GEBV

Country providing genotypes	DEU	DFS	FRA	NLD	Total
Genotypes (%)	5269 (43%)	1164 (9%)	4169 (34%)	1734 (14%)	12,336

Country providing national GEBV					Total
DEU	4888	1031	4102	1686	11,707
DFS	4809	988	4096	1661	11,554
FRA	4052	1048	4163	1344	10,607
NLD	4868	1159	4010	1747	11,784

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Results: country correlations for protein

- Conventional MACE country correlations above and h^2 on diagonal
- GEBV correlations below diagonal (ignoring reliability)

	DEU	DFS	FRA	NLD	average
DEU	0.48	.90	.85	.89	.88
DFS	**0.90**	0.42	.90	.89	.90
FRA	**0.79**	**0.79**	0.30	.87	.88
NLD	**0.90**	**0.91**	**0.85**	0.50	.89
average	**0.87**	**0.87**	**0.81**	**0.89**	

Results: country correlations for udder depth

- Conventional MACE country correlations above and h^2 on diagonal
- GEBV correlations below diagonal (ignoring reliability)

	DEU	DFS	FRA	NLD	average
DEU	0.27	.98	.97	.98	.98
DFS	**0.93**	0.37	.98	.98	.98
FRA	**0.78**	**0.78**	0.36	.98	.98
NLD	**0.91**	**0.92**	**0.82**	0.40	.98
average	**0.87**	**0.88**	**0.79**	**0.88**	

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Results: country correlations for somatic cell scores

- Conventional MACE country correlations above and h^2 on diagonal
- GEBV correlations below diagonal (ignoring reliability)

	DEU	DFS	FRA	NLD	average
DEU	0.23	.95	.94	.95	.95
DFS	**0.91**	0.23	.97	.95	.96
FRA	**0.79**	**0.79**	0.15	.94	.95
NLD	**0.89**	**0.90**	**0.84**	0.37	.95
average	**0.86**	**0.87**	**0.81**	**0.88**	

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Results: country correlations for fertility – cow's ability to conceive (T4: cc2)

- Conventional MACE country correlations above and h^2 on diagonal
- GEBV correlations below diagonal (ignoring reliability)

	DEU	DFS	FRA	NLD	average
DEU	0.01	.91	.84	.91	.89
DFS	0.85	0.02	.71	.91	.84
FRA	0.73	0.67	0.02	.79	.78
NLD	0.85	0.74	0.65	0.08	.87
average	0.81	0.75	0.68	0.75	

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Reliabilities by genotyping country (protein)

Country scale	DEU	DFS	FRA	NLD
DEU	73.1	72.4	72.7	72.9
DFS	56.3	57.4	56.1	56.0
FRA	68.0	66.6	68.9	67.8
NLD	65.5	65.2	65.3	66.0

All four countries had nearly equal R^2 in GEBV test.

Results: ratio of GEBV std dev of foreign to domestic bulls

Country scale: DEU

Country scale: DFS

SD(foreign)/SD(domestic) = 1
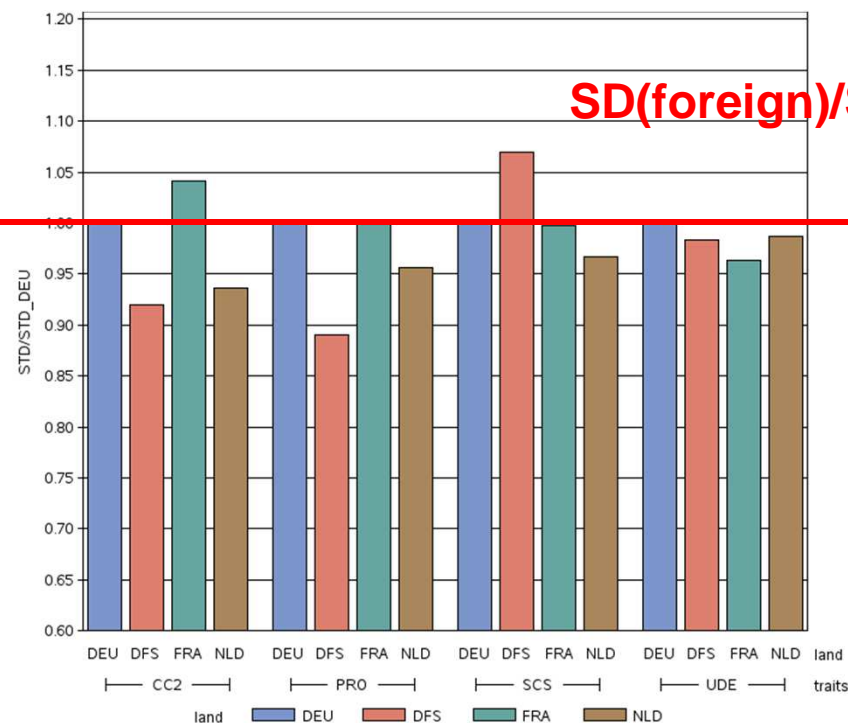
Country	μ_{STD}
DFS	0.966
FRA	1.001
NLD	0.962
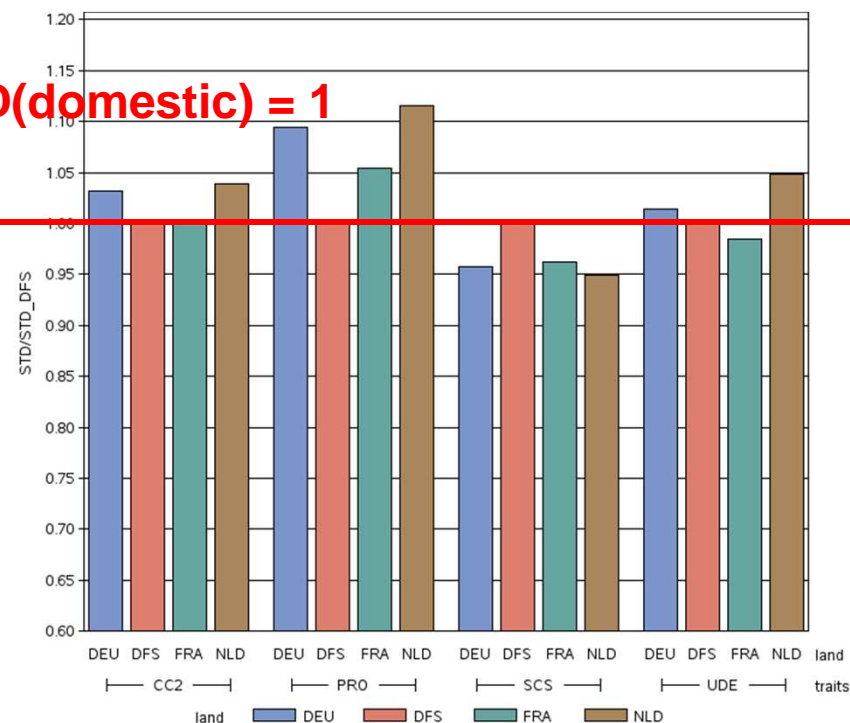
Country	μ_{STD}
DEU	1.024
FRA	1.002
NLD	1.038

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Results: ratio of GEBV std dev of foreign to domestic bulls

Country scale: FRA

Country scale: NLD

SD(foreign)/SD(domestic) = 1
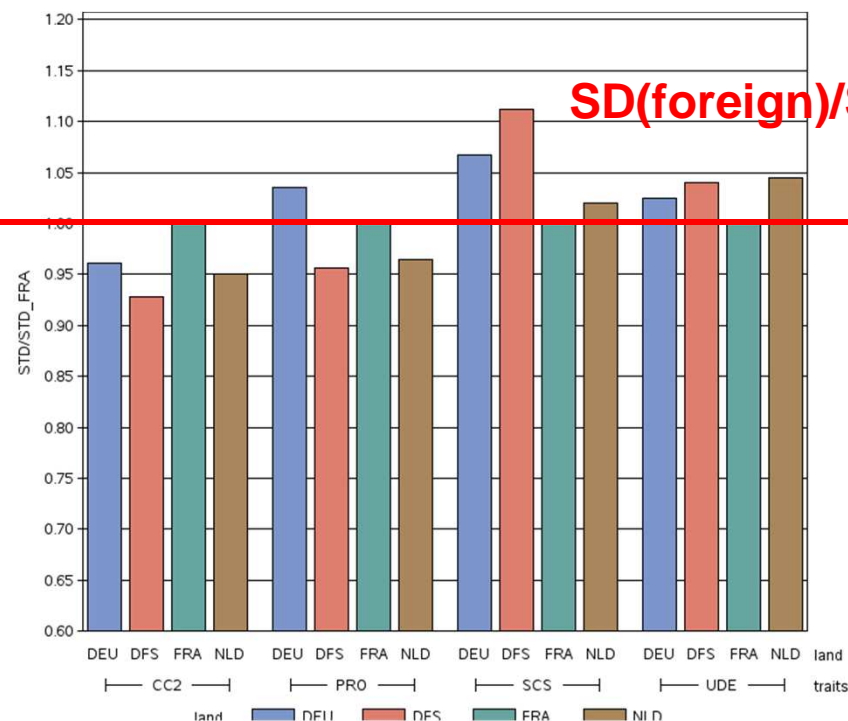
Country	μ_{STD}
DEU	1.022
DFS	1.001
NLD	0.995
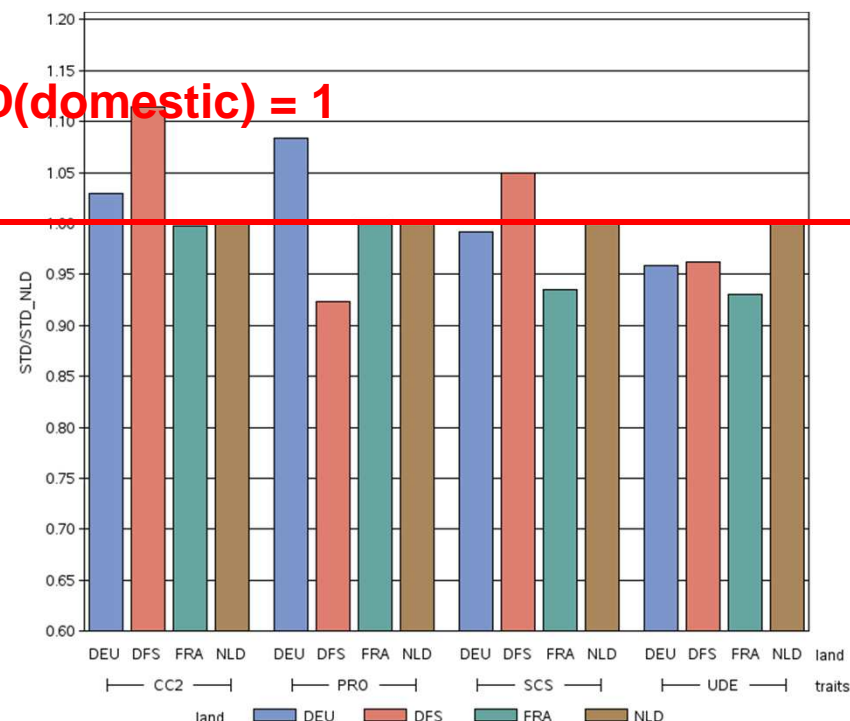
Country	μ_{STD}
DEU	1.016
DFS	1.013
FRA	0.967

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Results: no. of common bulls in top 1000/500 lists (protein)

Country scale	DEU	DFS	FRA	NLD
DEU		670	517	669
DFS	323		484	682
FRA	240	224		547
NLD	310	328	239	

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Summary and conclusions

- EuroGenomics national genomic predictions highly correlated
  - Using a common bull reference population & same pedigree
  - Using deregressed MACE / national proofs as phenotypes
  - Using MACE / national phenotypes for male pedigree index

- Two important procedures EG countries avoid bias in prediction
  - No cows are included in genomic reference population
  - Dam EBV are not used in pedigree index calculation

- Benefits of genotype exchanges
  - Foreign bulls have almost equal GEBV variance as domestic bulls
  - Avoid negative impacts of different trait definitions and low country correlations
  - Provide useful data for comparison to GMACE

- Calculation of GEBV reliability to be harmonised (Interbull WG)

- EuroGenomics national genomic predictions are highly consistent
  - High quality of EuroGenomics genomic models confirmed
  - Trust in EuroGenomics genomic predictions increased

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