Calving ease
Estimation of cross-country genetic parameters for Limousin cattle

Research report prepared by the Czech Research Team

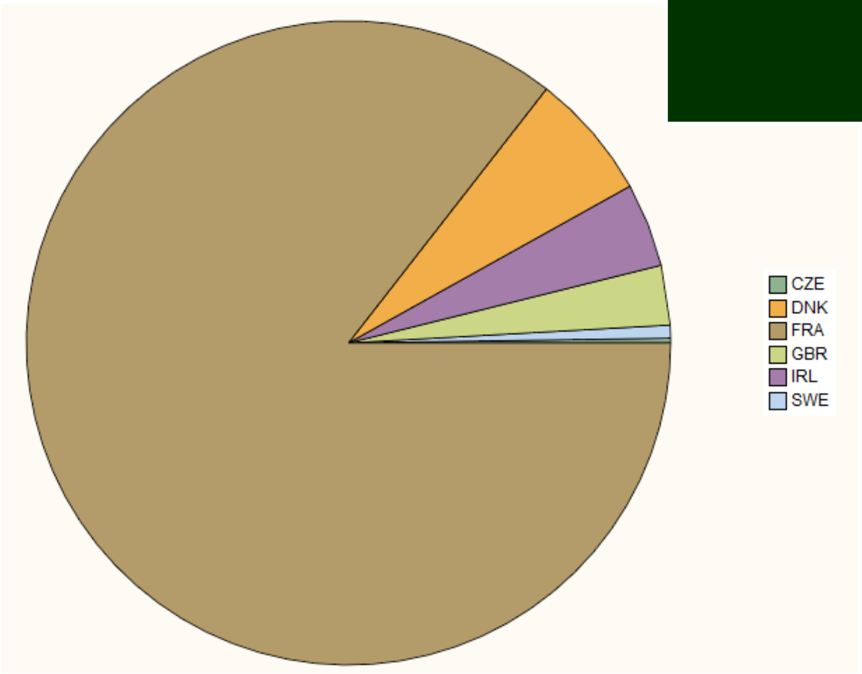
VÚŽV, v.v.i.
INSTITUTE OF ANIMAL SCIENCE
PRAHA UHŘÍNĚVES

Českomoravská společnost chovatelů, a.s.

Český svaz chovatelů masného skotu

Data

Type	Country of origin	N	
Pedigree	All countries	4,523,586	
Performance	FRA	3,468,854	85.5%
	DNK	258,448	6.4%
	IRL	170,856	4.2%
	GBR	121,407	3.0%
	SWE	26,369	0.6%
	CZE	9,554	0.2%
	All	4,055,485	



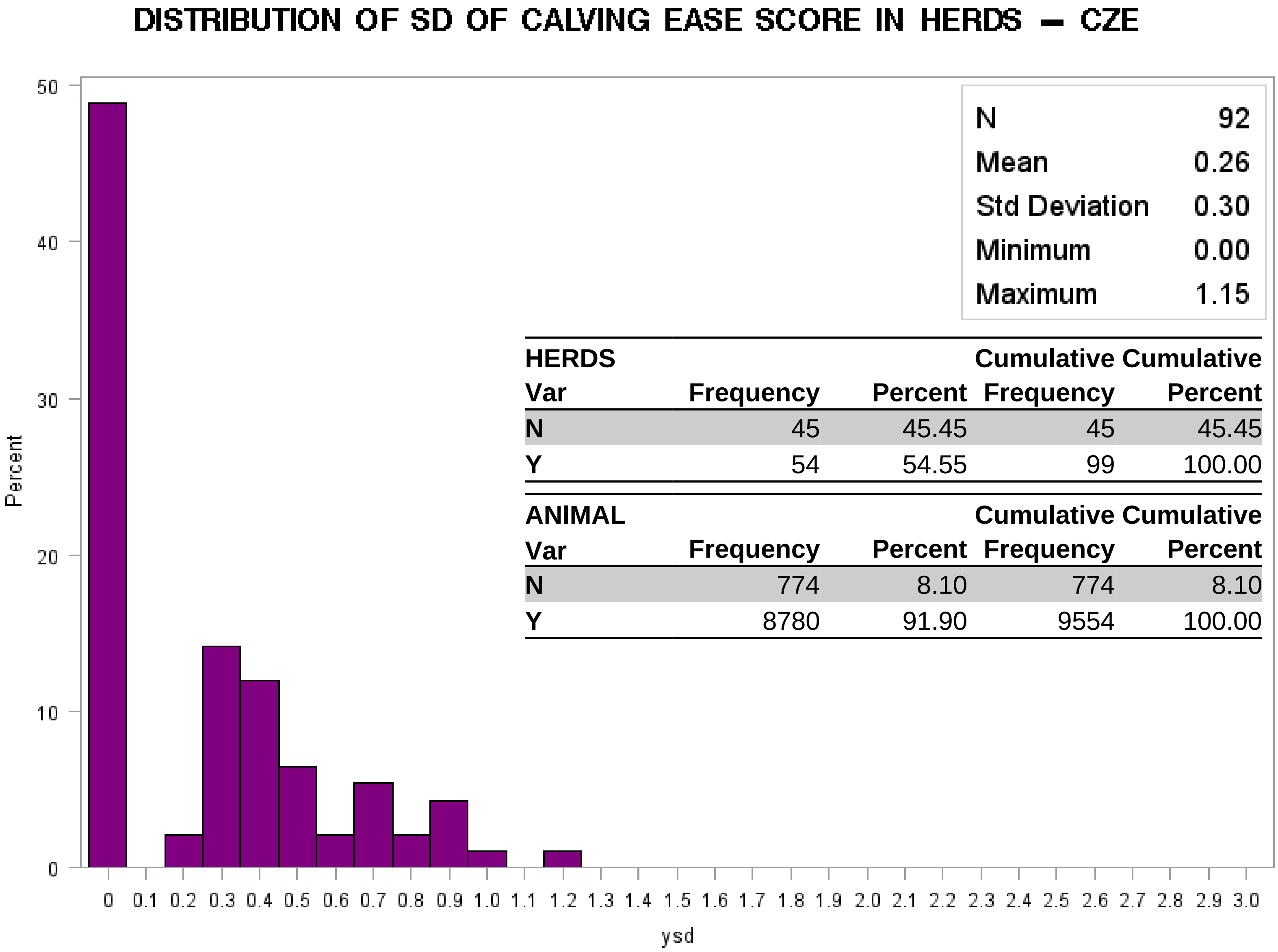
Data edits

- Pedigree of calves without official registration number (dead calves)
  - „UUUUUUUUUUUUUUUUUUUU“
    - CZE – 4.53%
    - DNK – 3.82%
    - FRA – 0%
    - GBR – 0%
    - IRL – 0%
    - SWE – 2.98%

Data edits

Countries	1. Herds without variation	2. ET	3. No sire or/and MGS	4. CG (min CG size 5)	Remaining animals
FRA	68,908	0	947,524	93,754	2,358,665
DNK	18,259	22	100,824	17,402	121,938
IRL	38,272	2,051	27,867	25,292	77,374
GBR	15	3,376	2,307	7,891	107,818
SWE	1230	0	3,467	1,161	20,511
CZE	774	552	387	622	7,219

Herds without variation



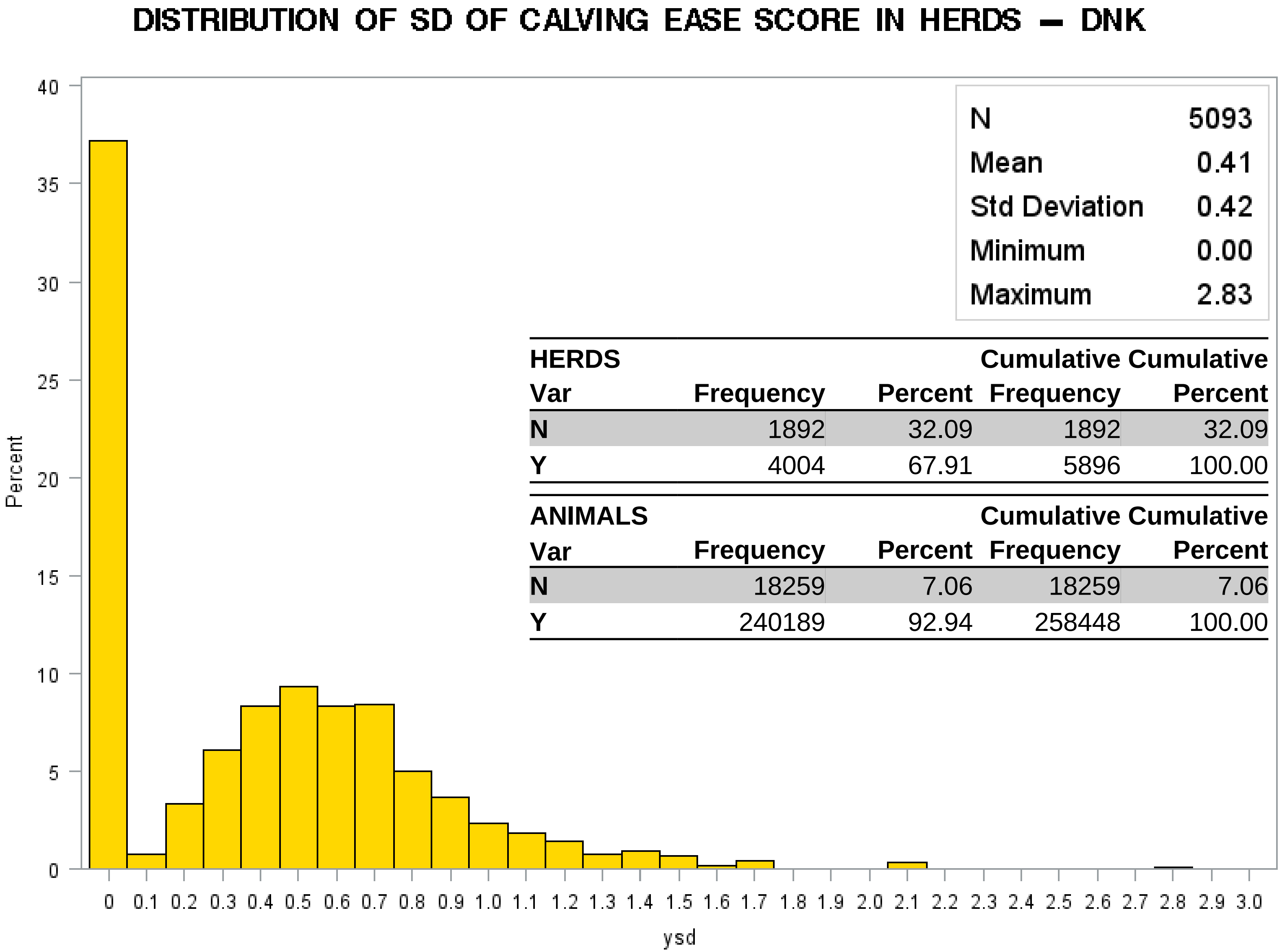
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS – CZE

N	92
Mean	0.26
Std Deviation	0.30
Minimum	0.00
Maximum	1.15

HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	45	45.45	45	45.45
Y	54	54.55	99	100.00

ANIMAL Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	774	8.10	774	8.10
Y	8780	91.90	9554	100.00

Herds without variation



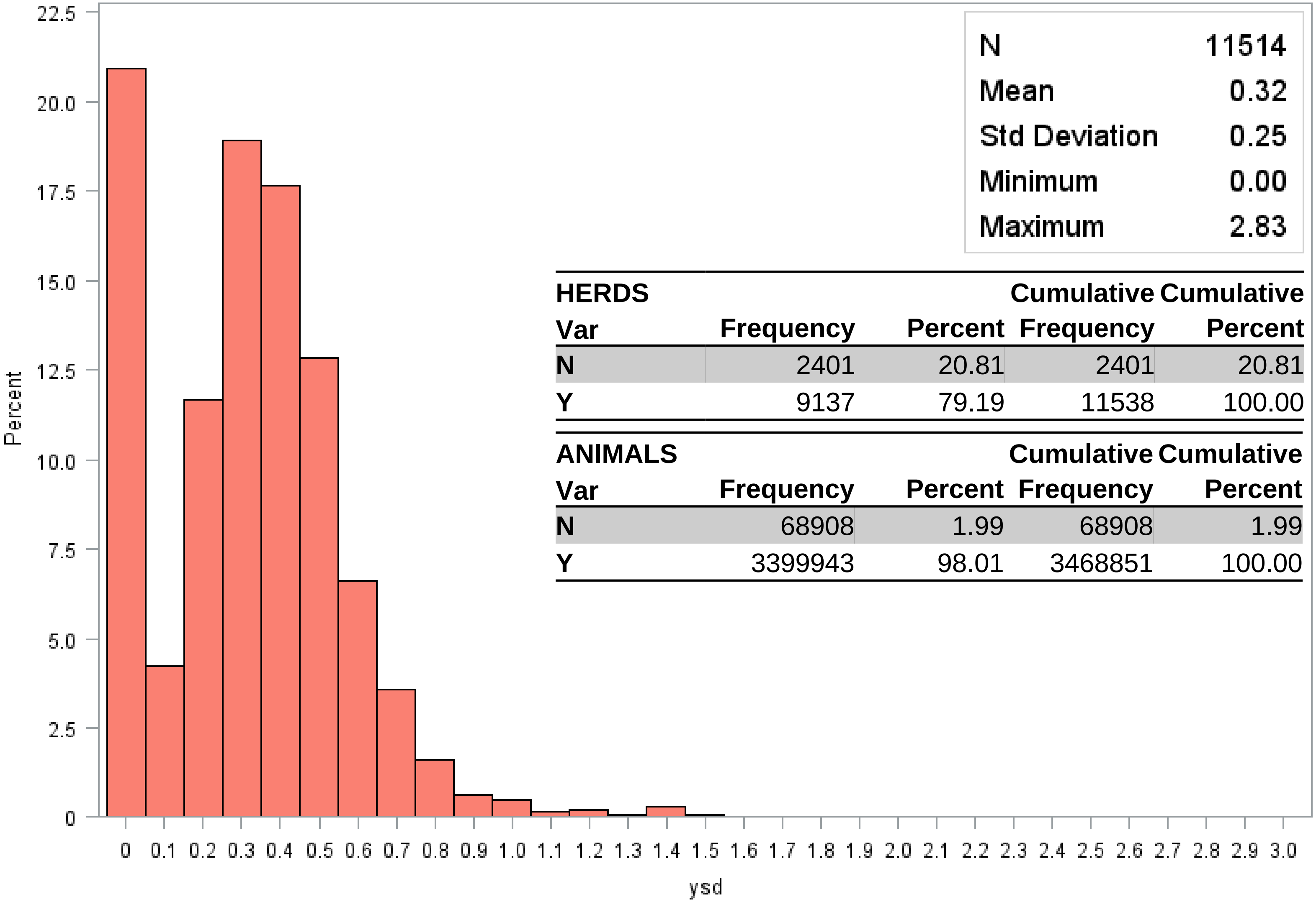
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS – DNK

N	5093
Mean	0.41
Std Deviation	0.42
Minimum	0.00
Maximum	2.83

HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	1892	32.09	1892	32.09
Y	4004	67.91	5896	100.00

ANIMALS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	18259	7.06	18259	7.06
Y	240189	92.94	258448	100.00

Herds without variation



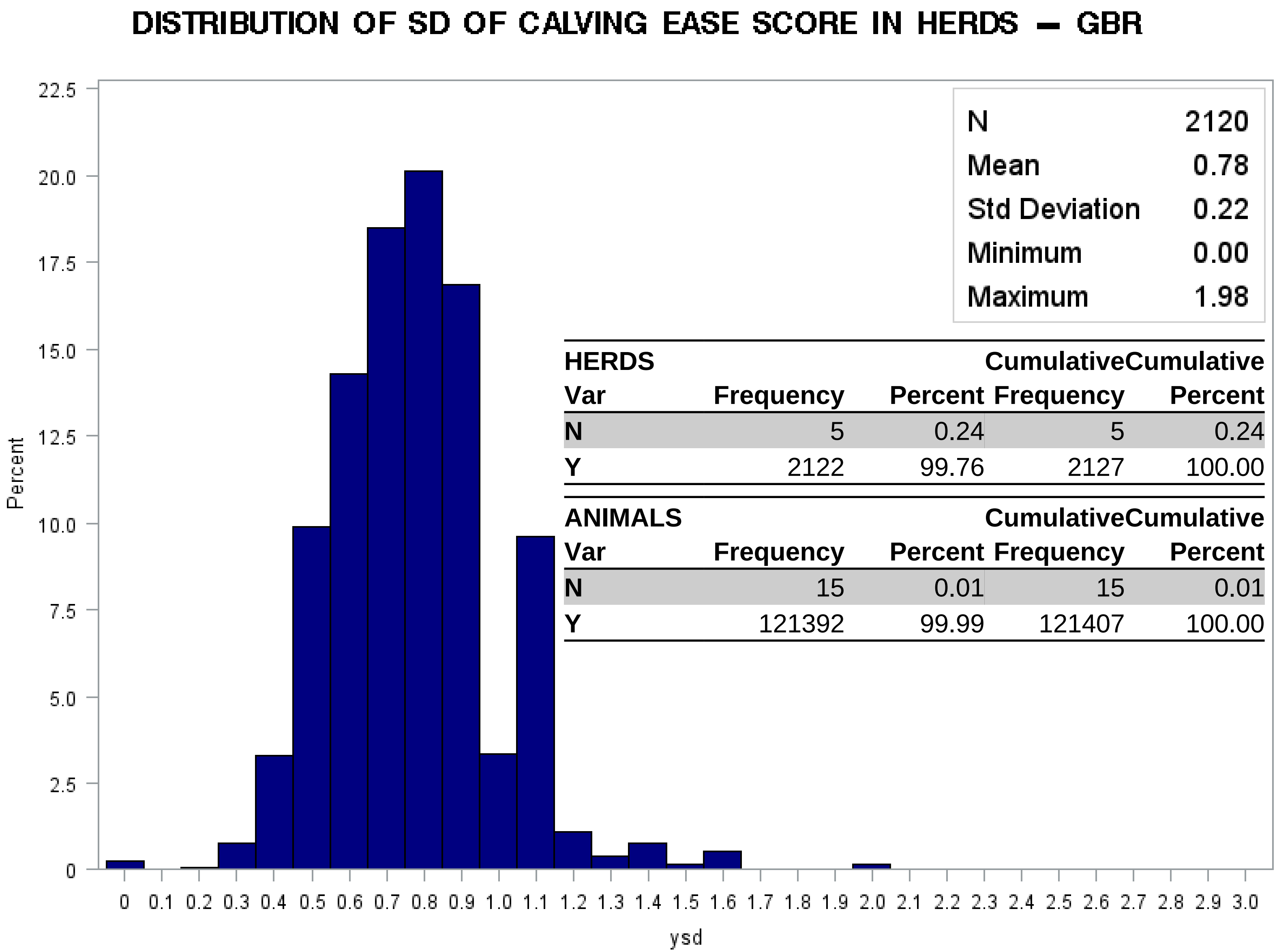
DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS – FRA

N	11514
Mean	0.32
Std Deviation	0.25
Minimum	0.00
Maximum	2.83

HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	2401	20.81	2401	20.81
Y	9137	79.19	11538	100.00

ANIMALS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	68908	1.99	68908	1.99
Y	3399943	98.01	3468851	100.00

Herds without variation



DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS – GBR

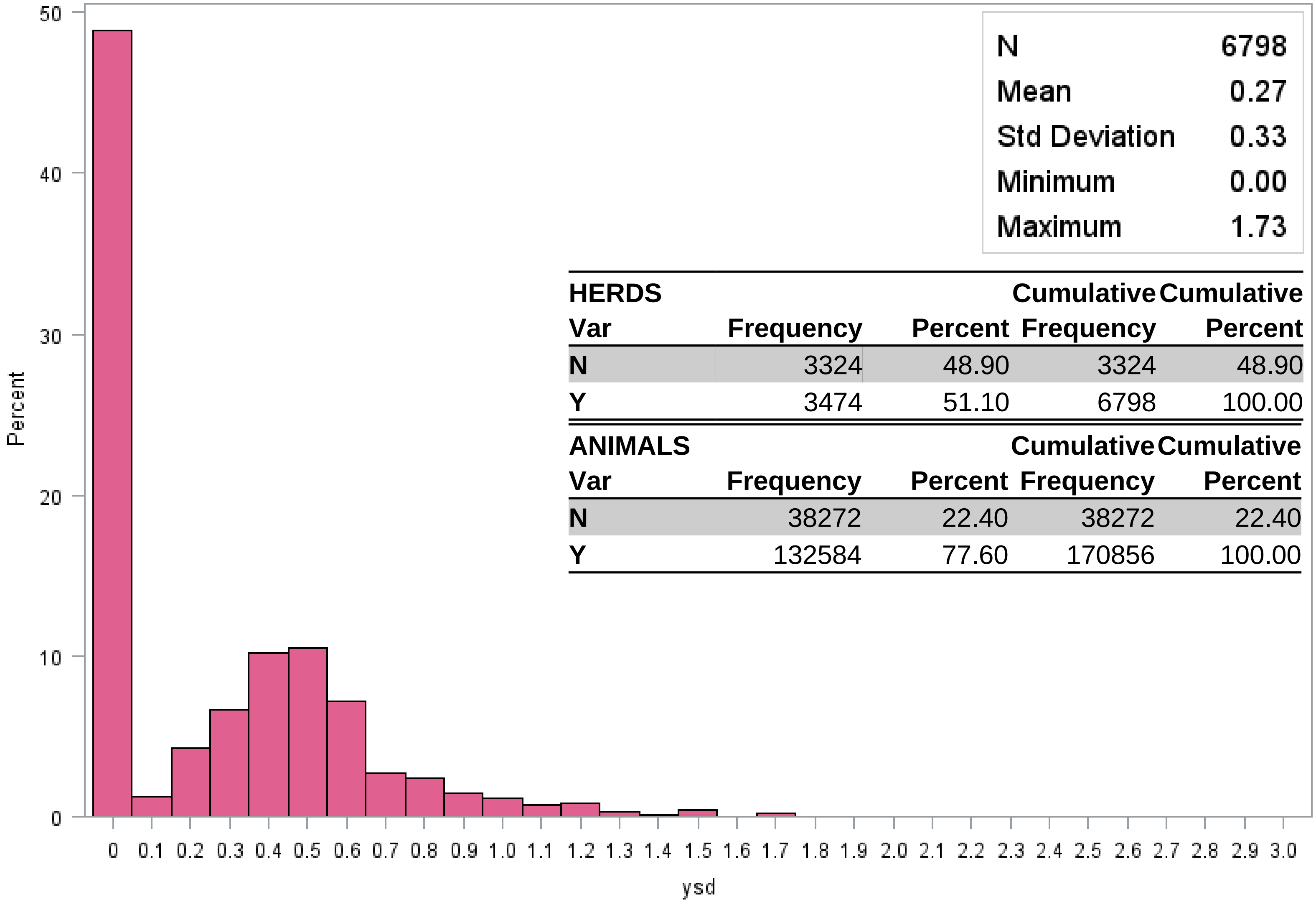
N	2120
Mean	0.78
Std Deviation	0.22
Minimum	0.00
Maximum	1.98

HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	5	0.24	5	0.24
Y	2122	99.76	2127	100.00

ANIMALS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	15	0.01	15	0.01
Y	121392	99.99	121407	100.00

Herds without variation

DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS – IRL

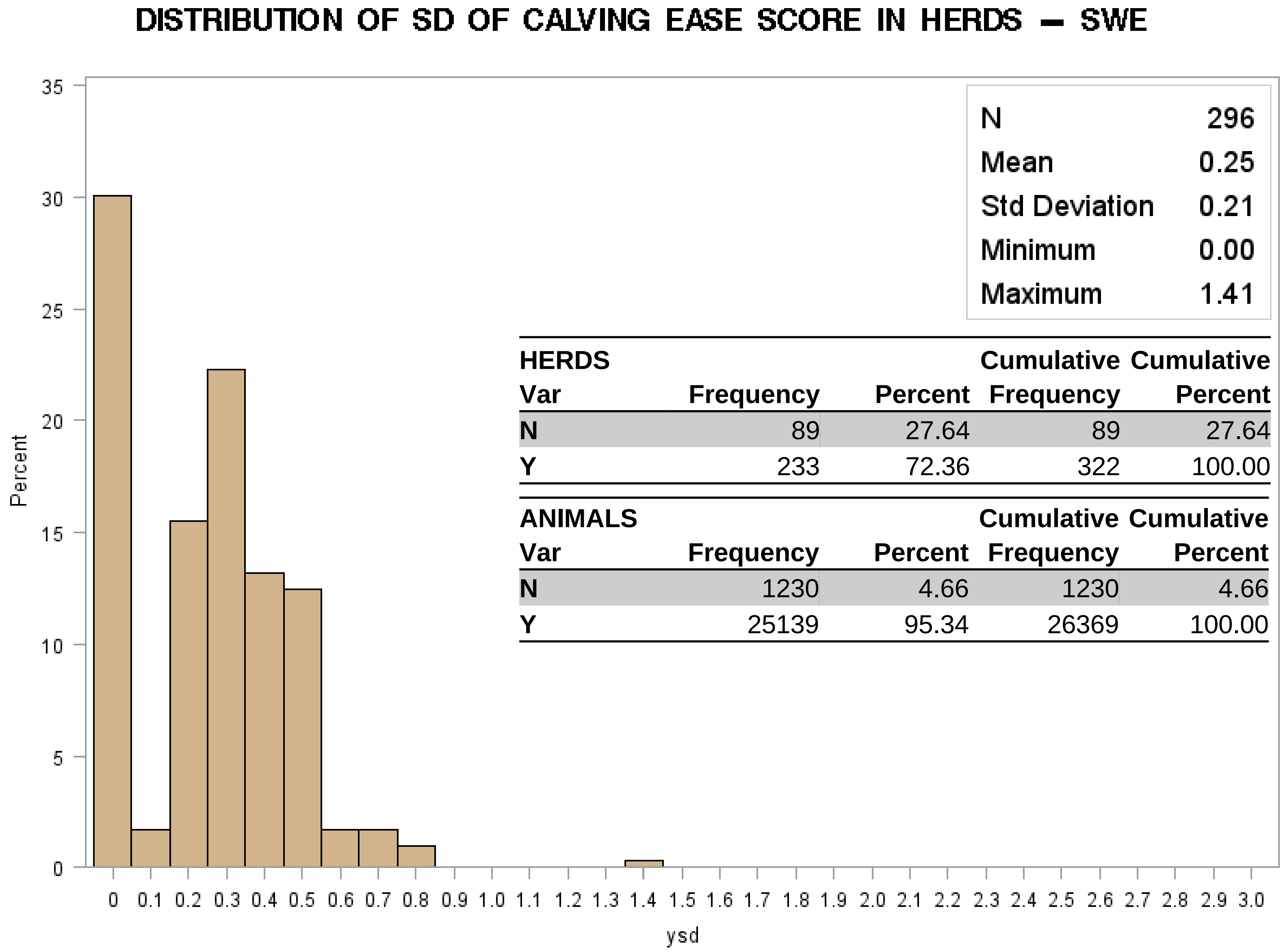


N	6798
Mean	0.27
Std Deviation	0.33
Minimum	0.00
Maximum	1.73

HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	3324	48.90	3324	48.90
Y	3474	51.10	6798	100.00

ANIMALS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	38272	22.40	38272	22.40
Y	132584	77.60	170856	100.00

Herds without variation



DISTRIBUTION OF SD OF CALVING EASE SCORE IN HERDS – SWE

N	296
Mean	0.25
Std Deviation	0.21
Minimum	0.00
Maximum	1.41

HERDS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	89	27.64	89	27.64
Y	233	72.36	322	100.00

ANIMALS Var	Frequency	Percent	Cumulative Frequency	Cumulative Percent
N	1230	4.66	1230	4.66
Y	25139	95.34	26369	100.00

Building files for REML

- Method and software from ICBF
  - Connection within 3 generations

- 7 subsets for FRA according to random selection of herds
  - Followed by the weighted mean
  - Weights – SE

$$\mu^* = \frac{1}{SW}\sum_{i=1}^{7}\frac{\mu_i}{SE_i^2} \qquad SW = \sum_{i=1}^{7}\frac{1}{SE_i^2}$$

Models

CZE	DNK	FRA	GBR	IRL	SWE
*CG**	CG	CG	CG	CG	CG
	season	season			
birth year					
			birth month		
sex × twi	sex			sex	sex
	twi				
		parity × age	parity × sex	parity	parity
age	age			age**	age
			birth type		
			purebred status		

* random effect

** fixed regression

Models

- 2 x 2 analysis
- Linear model

1. AM with direct genetic effect and MPE
    - residual correlation = 0
    - Software: airemlf90

2. AM with direct and maternal genetic effect and MPE
    - residual correlation = 0
    - direct – maternal correlation = 0
    - Software: gibbs1f90

Results – 1. AM-DE-MPE

	CZE	DNK	FRA	GBR	IRL	SWE
CZE						
DNK	0.95 (0.027)					
FRA	0.53 (0.129)	0.89 (0.019)				
GBR	0.95 (0.017)	0.68 (0.042)	0.59 (0.044)			
IRL	0.19 (0.250)	0.60 (0.089)	0.98 (0.004)	0.79 (0.032)		
SWE	nc	0.47 (0.102)	0.66 (0.080)	0.48 (0.007)	nc	

Average direct genetic correlation = 0.71

Results – 2. AM-DE-ME-MPE

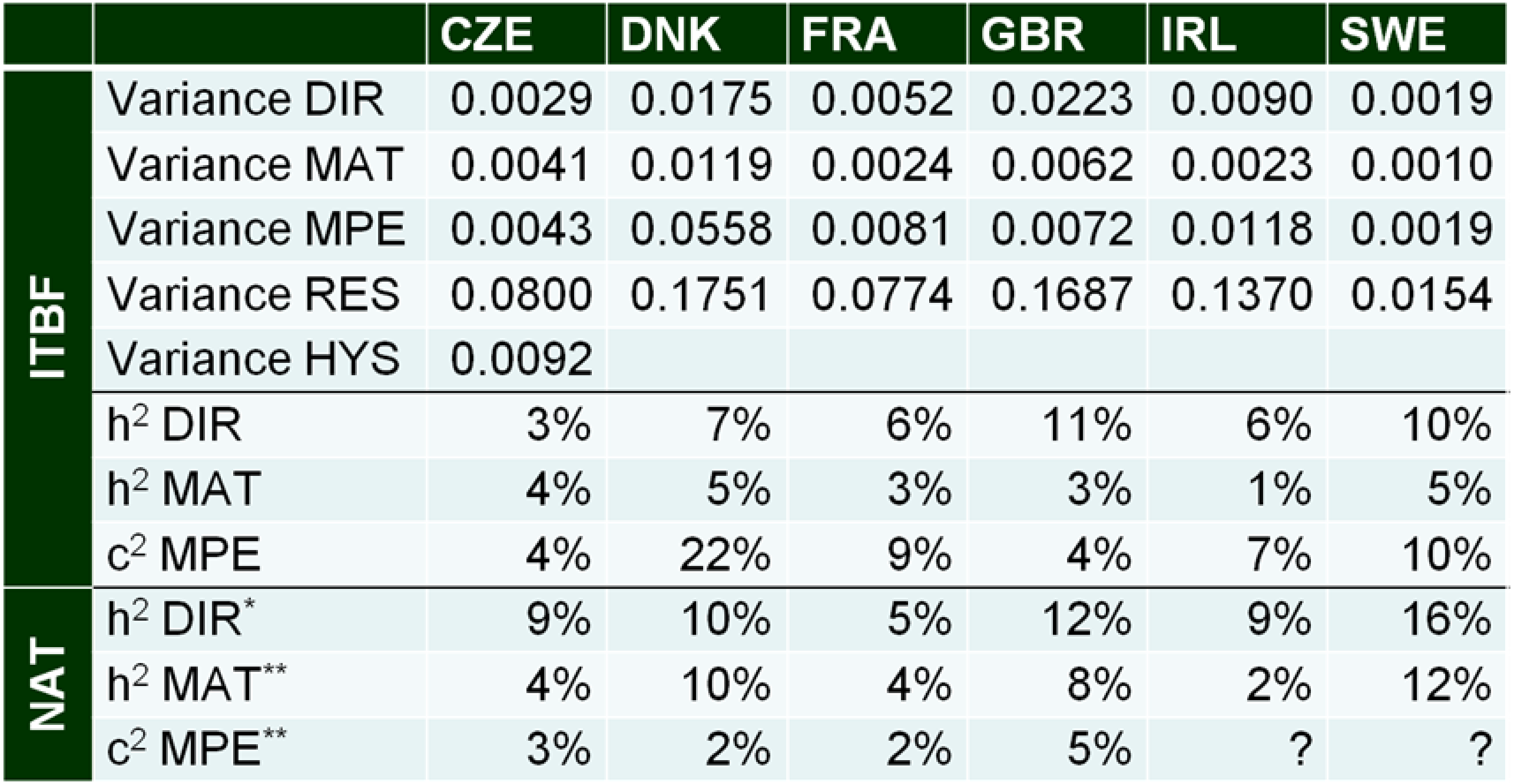
Direct (below diagonal) and maternal effect (above diagonal)

	CZE	**DNK**	**FRA**	**GBR**	**IRL**	**SWE**
CZE		nc	0.20 (0.13)	nc	nc	nc
DNK	nc		0.63 (0.073)	nc	nc	0.39 (0.107)
FRA	0.62 (0.079)	0.92 (0.015)		0.63 (0.081)	0.55 (0.093)	0.56 (0.104)
GBR	nc	nc	0.77 (0.031)		0.47 (0.106)	nc
IRL	nc	nc	0.88 (0.021)	0.68 (0.048)		nc
SWE	nc	0.42 (0.109)	0.64 (0.081)	nc	nc	

Average direct genetic correlation = 0.70; Average maternal genetic correlation = 0.53

Results – 2. AM-DE-ME-MPE

Weighted means from 2 x 2 analysis from AM-DE-ME-MPE



		CZE	DNK	FRA	GBR	IRL	SWE
ITBF	Variance DIR	0.0029	0.0175	0.0052	0.0223	0.0090	0.0019
	Variance MAT	0.0041	0.0119	0.0024	0.0062	0.0023	0.0010
	Variance MPE	0.0043	0.0558	0.0081	0.0072	0.0118	0.0019
	Variance RES	0.0800	0.1751	0.0774	0.1687	0.1370	0.0154
	Variance HYS	0.0092					
	h^2 DIR	3%	7%	6%	11%	6%	10%
	h^2 MAT	4%	5%	3%	3%	1%	5%
	c^2 MPE	4%	22%	9%	4%	7%	10%
NAT	h^2 DIR*	9%	10%	5%	12%	9%	16%
	h^2 MAT**	4%	10%	4%	8%	2%	12%
	c^2 MPE**	3%	2%	2%	5%	?	?

* From 603 files

** From “Description of National Genetic Evaluation Systems for beef cattle as applied in different Interbeef member countries“

Results – 3. Full matrix

1. CORRELATION MATRIX DIRECT EFFECT

- All correlations non-converged and correlations < 0.2 from 2. AM-DE-ME-MPE were set to their value from AM-DE-MPE.
- All correlations non-converged from both models and correlations < 0.2 were set to 0.71 with SD 0.25 (largest SD).
- Bending - SD of estimated correlations were used for weighting.

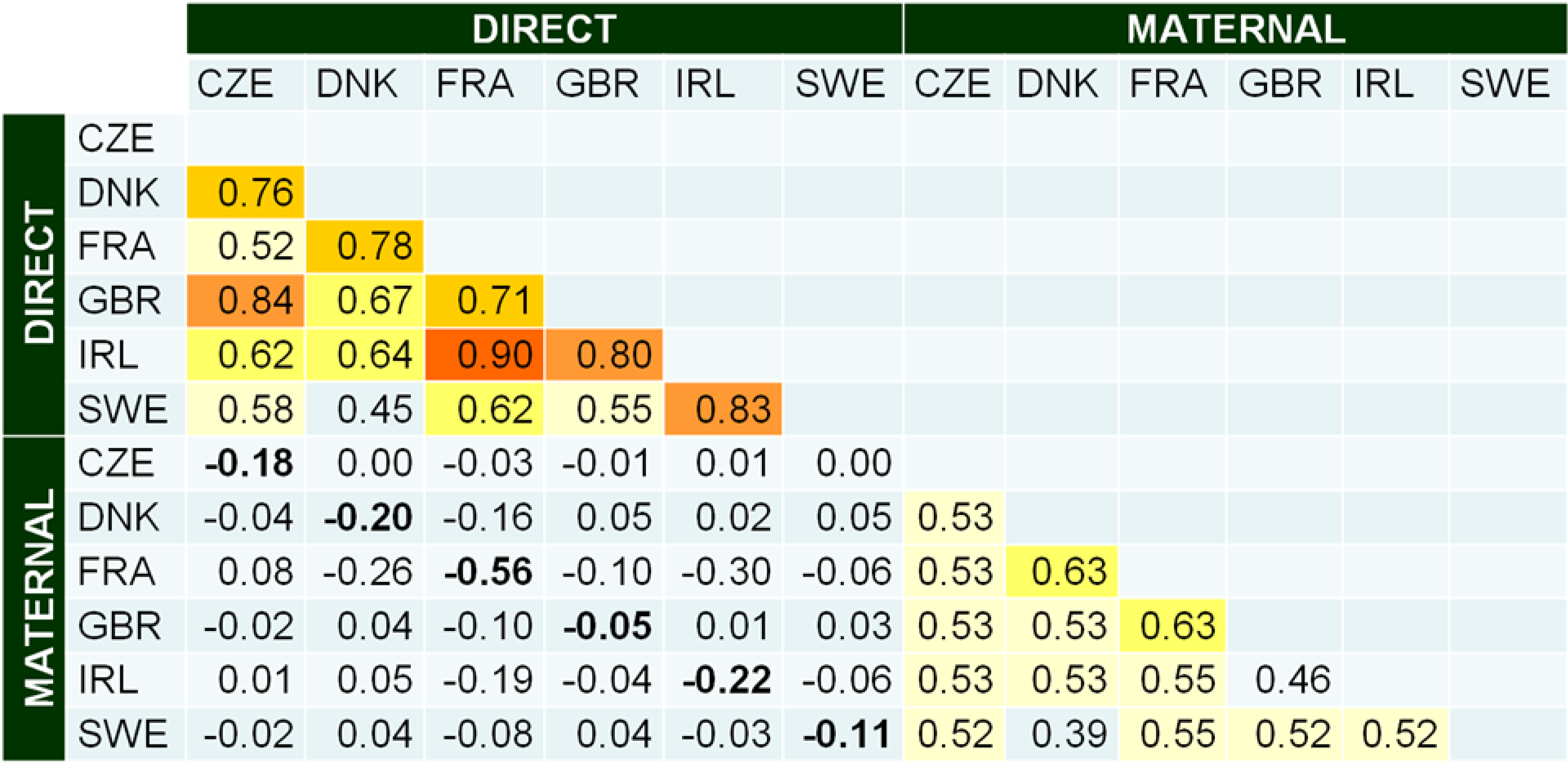
2. CORRELATION MATRIX FOR MATERNAL EFFECT

- All correlations non-converged and correlations < 0.25 were set to 0.53 with SD 0.13.
- Bending - SD of estimated correlations were used for weighting.

3. FULL CORRELATION MATRIX

- Correlations between direct and maternal genetic effect from national genetic evaluation in participant countries
- Banding - Numbers of bulls and common bulls used for weighting.

Results – 4. Full banded matrix



		DIRECT						MATERNAL					
		CZE	DNK	FRA	GBR	IRL	SWE	CZE	DNK	FRA	GBR	IRL	SWE
DIRECT	CZE												
	DNK	0.76											
	FRA	0.52	0.78										
	GBR	0.84	0.67	0.71									
	IRL	0.62	0.64	0.90	0.80								
	SWE	0.58	0.45	0.62	0.55	0.83							
MATERNAL	CZE	**-0.18**	0.00	-0.03	-0.01	0.01	0.00						
	DNK	-0.04	**-0.20**	-0.16	0.05	0.02	0.05	0.53					
	FRA	0.08	-0.26	**-0.56**	-0.10	-0.30	-0.06	0.53	0.63				
	GBR	-0.02	0.04	-0.10	**-0.05**	0.01	0.03	0.53	0.53	0.63			
	IRL	0.01	0.05	-0.19	-0.04	**-0.22**	-0.06	0.53	0.53	0.55	0.46		
	SWE	-0.02	0.04	-0.08	0.04	-0.03	**-0.11**	0.52	0.39	0.55	0.52	0.52	

Average direct genetic correlation = 0.68; Average maternal genetic correlation = 0.53