## Genetic parameter estimation survey for weaning weight

## List of participants in survey

No.	First name	Last name	Email address	Country	Main activity?	Involved with National weaning weight evaluation?
1	Japie	Van der Westhuizen	japie@studbook.co.za	South Africa	Genetic evaluations	Yes
2	Gerben	de Jong	Gerben.de.jong@crv4all.com	The Netherlands	Genetic evaluations	NO
3	Kaisa	Sirkko	kaisa.sirkko@faba.fi	Finland	Genetic evaluations	Yes
4	Zdena	Vesela	vesela.zdena@vuzv.cz	Czech Republic	Academics	Yes
5	Mohammad	Nilforoosham	Mohammad.Nilforooshan@slu.se	INTERBULL	Academics	NO
6	Eric	Venot	eric.venot@jouy.inra.fr	France	Genetic evaluations	Yes
7	Ross	Evans	revans@icbf.com	Ireland	Genetic evaluations	Yes
8	Friedrich	Reinhardt	friedrich.reinhardt@vit.de	Germany	Genetic evaluations	Yes
9	Thomas	Schmidt	dr.schmidt@rind-bw.de	Germany		NO
10	Anders	Fogh	ADF@vfl.dk	Denmark	Genetic evaluations	Yes
11	Kirsty	Moore	Kirsty.moore@sac.ac.uk	UK	Genetic evaluations	Yes
12	Jan-ake	Eriksson	jan-ake.eriksson@svenskmjolk.se	Sweden	Genetic evaluations	Yes
13	Clara	Diaz	cdiaz@inia.es	Spain	Other	Yes

Q1	Age limits for weaning weight				
	Minim	Minimum age		um age	
Country	VCE	BVE	VCE	BVE	
South Africa	150	150	270	270	
Finland	150	150	250	250	
Czech Rep.	171	171	290	290	
France					
Ireland	150	150	250	250	
Germany	90	90	280	280	
Denmark					
UK	365	3645	4380	5475	
Sweden	125	125	250	250	
Spain	300	300	60	<mark>6</mark> 0	

Q2	Do you exclude phenotypic outliers based on weight?				
Country	Different for Yes/No males and Minin females		Minimum	Maximum	
South Africa	Yes	No	100	333	
Finland	No	No	70	495	
Czech Rep.	Yes	No	150	450	
France	No	Yes	<4 sds	>4 sds	
Ireland	Yes	No	105	600	
Germany	Yes	No	<3.5 sds	>3.5 sds	
Denmark	Yes	Yes			
UK	Yes	No	<3sd	>3sd	
Sweden	Yes	No	<4sds (50kg)	>5sds (600kg)	
			5 sd (31 to 485) to 200 days (CH)	5 sd (31 to 451) to 200 days (LM)	
Spain	Yes	No	1 percentile (146.4)	99 percentile (375.9)	

Q3	Do you exclude phenotypic outliers based ADG?					
Country	ry Yes/No males and Minimum females		Minimum	Maximum		
South Africa	No	No				
Finland	No	No				
Czech Rep.	No	No				
France	No	No				
Ireland	Yes	No	0.4	2		
Germany	Yes	No	<0.300 kg/day	>2.000 kg/day		
Denmark	Yes	Yes				
UK	No	No				
Sweden	No	No				
Spain	Yes	No	0	2.5		

Q7, Q8, Q9	Do you exclude animals:				
Country	With an unknown sire?	With an unknown dam?	With an unknown maternal grandsire?		
South Africa	Yes	Yes	No		
Finland	Yes	Yes	Yes		
Czech Rep.	Yes	No	Yes		
France	No	Yes	No		
Ireland	Yes	Yes	Yes		
Germany	Yes	Yes	No		
Denmark	N/A	Yes	Yes		
UK	Yes	Yes	No		
Sweden	Yes	Yes	Yes		
Spain	No	Yes	No		

	Q10	Q11	Q12	Q12a	Q13	Q13a
Country	CGs same for VCE and BVE?	Exclude CGs with no phenotypic variation?	Min no. anims per CG?	Q12a.Specify minimum no.	Minimum no. of sires per CG?	specify minimum number
South Africa	No	Yes	Yes	10	Yes	2
Finland	Yes	No	Yes	20	No	
Czech Rep.	Yes	Yes	Yes	5	Yes	2
France	Yes	No	Yes	2 for BVE	Yes	Yes for VCE. No for BVE. Depends (CHA v AUB)
Ireland	No	Yes	Yes	5	Yes	2
Germany	Yes	No	Yes	5	Yes	2
Denmark	Yes	Yes	Yes		Yes	
UK	Yes	Yes	Yes	5	Yes	2
Sweden	Yes	No	No		No	
Spain	Yes	Yes	Yes	5	No	

	Q16	Q16a	Q17	Q17a	Q17b
Country	Apply Connected- ness between herd and population?	Specify how	pedigree file confined to number of generations?	specify the number of generations	pedigree birth date restriction
South Africa	No		Yes	5	
Finland	No		No		
Czech Rep.	No		Yes	3	1970
France	Yes	"CACO" software	Yes	8	
Ireland	No		Yes	5	
Germany	No		No		
Denmark	Yes		Yes		
UK	No		Yes	5, (3 for large datasets/ complex models)	
Sweden	No		Yes	4	
Spain	No		No		

	Q18	Q18a	Q18b	Q18c
Country	VCE separately each breed?	What breeds combined?	Crossbreds included?	How do you adjust for breed?
South Africa	Yes		N/A	
Finland	Yes		N/A	
Czech Rep.	No	All beef breeds	Yes	pedigree groups in the pedigree file
France	Yes		No	Salers and Aubrac: sire breed effect in the animal model.
Ireland	No	All beef breeds	Yes	pedigree groups in the pedigree file
Germany	Yes		N/A	
Denmark	Yes		N/A	
UK	Yes		N/A	
Sweden	Yes		N/A	
Spain	Yes		N/A	

	Q19	Q20	Q20a
Country	Type of model for VCE	Univariate model?	Other traits involved?
South Africa	Animal model	No	Birth, Weaning, Yearling, 18 Months, Mature Weight
Finland	Animal-Dam model	No	birth, 1 year, and slaughter weight
Czech Rep.	Animal model	No	calving ease, birth wt, 120d wt, weaning wt, yearling wt
France	Animal model	No	Univariate for Charolais and Partenaise only
Ireland	Animal-Dam model	No	50-150 day, 250-350 day, 350-450 day, 450-500 day
Germany	Sire-MGS model	No	Birth, Yearling, muscle score 200d, muscle score 365d
Denmark	Animal-Dam model	No	Yearling, slaughter, performance test, slaughter wt for crosses
UK	Animal-Dam model	Yes	
Sweden	Animal-Dam model	No	postweaning gain, carcass gain, grade and fat.
Spain	Animal-Dam model	Yes	

	Q21	Q22	Q23	Q24	Q25
Country	Include a dam pe effect	Non-genetic fixed effects similar for VCE and BVE	Treatment of CG	Adjust for birth year	Replicates
South Africa	Yes	Yes	Fixed	Yes	No
Finland	Yes	Yes	Fixed	Yes	No
Czech Rep.	Yes	Yes	Random	Yes	Yes
France	Yes	Yes	Fixed	Yes	No
Ireland	Yes	Yes	Random	Yes	Yes
Germany	No	Yes	Random	No	No
Denmark	Yes	Yes	Fixed	Yes	Yes
UK	Yes	Yes	Fixed	Yes	No
Sweden	No	Yes	Fixed	No	No
Spain	Yes	Yes	Fixed	No	No

Q27	
Country	Software used for VCE
South Africa	VCE
Finland	DMU
Czech Rep.	F90
France	ASREML
Ireland	Mix99
Germany	MTDFREML
Denmark	DMU
UK	ASREML
Sweden	DMU
Spain	TM and own

	Q28	Q28a	Q28b
	Does your database:		
Country	Store only pure bred animals?	Store multiple breeds?	Database specifics
South Africa	Yes	Yes	Breed and Breed fraction are indicated
Finland	No	N/A	Breed of sire and dam stored
Czech Rep.	No	N/A	Storing main beef breed proportion information
France	No	Yes	No breed proportion, genetic and evaluation breed
Ireland	No	N/A	Breed and breed fraction. Crossbred animals have multiple entries
Germany	No	Yes	Breed and breed composition is stored for each animal.
Denmark	No	N/A	Breed proportions are calculated on all animals
UK	No	N/A	breed 16th values of up to 4 different breeds
Sweden	No	N/A	we are storing breed proportion for each animal
Spain	Yes	N/A	

	Q29				
Country	Handling of founder ancestors with unknown breed?				
South Africa	Assume as purebred				
Finland	Assign unknown breed status				
Czech Rep.	Assume as purebred				
France	Older animals given unknown status				
Ireland	Other				
Germany	Assume as purebred				
Denmark	Assign unknown breed status				
UK	Assume as purebred				
Sweden	Assign unknown breed status				
Spain	Assign unknown breed status				

Country	Q31. How often are genetic parameters re-estimated (years)?				
South Africa	Every 5 years				
Finland	15				
Czech Rep.	5				
France	10 years				
Ireland	5				
Germany	5				
Denmark	Only done once				
UK	Not done for a long time and are just about to start parameter estimation				
Sweden	seldom				
Spain	aprox. 5 (1 generation)				

Country	Q32. Do you have any additional comments and/or recommendations?				
Czech Rep.	No estimation of direct genetic effect only. Animal model with direct and maternal genetic				
France	Some questions confusing. Maximising genetic links between countries in the data subset used. list of "connecting bulls", 2x2, maybe 3x3 with France. 3. Important to maintain CG structure for environmental effects				
UK	Reestimation of genetic parameters about to commence				
Sweden	Operate a multiple trait evaluation with birth, weaning and yearling weight. Important to include all traits in VCE and BVE. recorded birth weight an edit.				
Spain	Include crossbred data for carcass traits, Not in weaning due to potential bias. Bayesian approach for VCE				

## Variance components submitted

Country	Genetic	Maternal	Dam PE	Residual	Total	Difference
South Africa	113.002	62.63	60.907	284.545	545.8528	521
Finland	257	144	102	693	1196	1196
Czech Rep.	309.8	197.3	80.9	374.2	2677.7	962
France	240	96.1	105.6	586.4	960.32	1028
Ireland	450	194	45	647	1336	1336
Germany	383	326	0	719	1905	1428
Denmark						
UK	268	55	63	421	807	807
Sweden	170	120	80	500	870	870
Spain	136.3	67.73	43.39	294.1	690.4	542

France and Finland quoted Charolais parameters

Forgot to ask for genetic correlations between direct and maternal!!!

## **SUMMARY**

Useful exercise

Genetic parameters useful reference point for subsequent work