



IRISH CATTLE BREEDING FEDERATION

Estimation of across-country genetic parameters for Charolais



Research summary prepared by ICBF genetic team
for InterBeef Meeting 21/11/2013



Background

- CHA data
 - Received from IDEA June 2013
 - 6 countries : CHA, IRL, DNK, SWE, FIN, CZE
- Analysis
 - Sept. 2013
 - DMU

Table 1. Data received			
Type	Country of origin	N	
Pedigree	All countries	4,368,716	
Performance	FRA	3,472,920	95%
	SWE	99,691	3%
	CZE	24,371	1%
	IRL	22,031	0%
	FIN	17,185	0%
	DNK	15,556	0%

Data edits

- 4 major steps

Table 2. Animals successively edited				
Countries	1. ET	2. No sire or/and MGS	3. CG (min CG size)	4. Remaining animals
FRA	0	567,456	111,325 (5)	2,794,139
SWE	0	3,631	6,074 (5)	89,986
CZE	1,374	2,551	1,756 (5)	18,690
IRL	783	3,623	3,008 (5)	14,617
FIN	142	2,586	709 (5)	13,748
DNK	517	852	2,301 (5)	11,886

Pedigree pruning

- Using *Secateur* (Meyer, 2003)

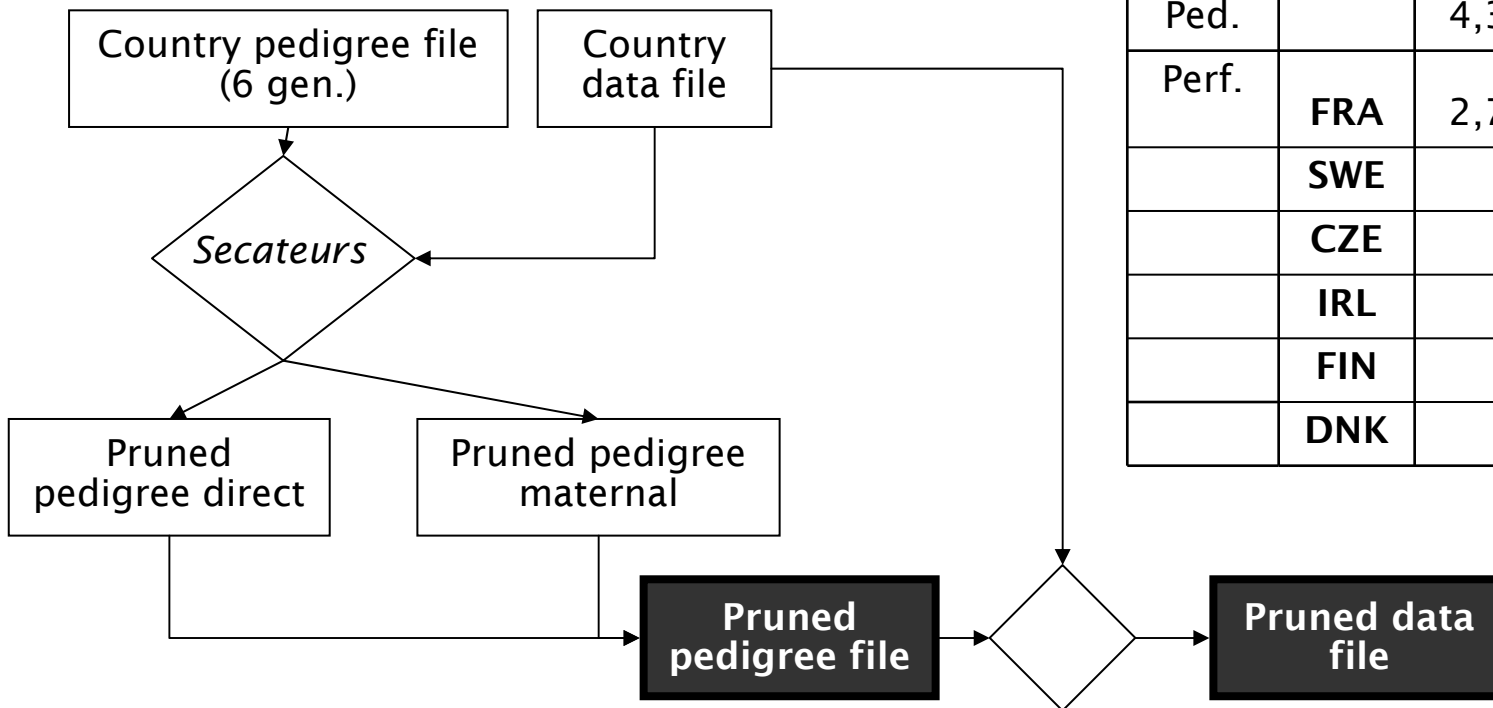


Table 3. Pedigree and data files before and after pruning

Type		N before	N after
Ped.		4,368,716	3,521,169
Perf.	FRA	2,794,139	2,784,099
	SWE	89,986	89,967
	CZE	18,690	18,679
	IRL	14,617	14,607
	FIN	13,748	13,735
	DNK	11,886	11,870

Connection (1/2)

- Sires

Table 4b.: Origin of sires across InterBeef countries - Detailed connection

		Sire country of 1 st registration					
		CZE	DNK	FIN	FRA	IRL	SWE
Animal country of 1 st registration	CZE		1CZE		272CZE 40DNK 33FIN 175FRA 25IRL 34SWE		2CZE 1DNK 1FIN 1SWE
	DNK				144DNK 40CZE 22FIN 87FRA 47IRL 30SWE		27DNK 1CZE 4SWE
	FIN		9FIN 3DNK 1SWE		54FIN 33CZE 22DNK 44FRA 13IRL 21SWE		132FIN 1CZE 57SWE
	FRA		3FRA 2DNK				1FRA 1SWE
	IRL				677IRL 25CZE 47DNK 13FIN 141FRA 24SWE		
	SWE		30SWE 8DNK 1FIN	5SWE	54SWE 34CZE 30DNK 21FIN 46FRA 24IRL		

Connection (2/2)

- Maternal-grand sires

Table 5b.: Origin of MGS across InterBeef countries - Detailed connection

		MGS country of 1 st registration					
		CZE	DNK	FIN	FRA	IRL	SWE
Animal country of 1 st registration	CZE		12CZE 10DNK		925CZE 44DNK 28FIN 830FRA 80IRL 28SWE		1CZE 1FIN 1SWE
	DNK				169DNK 44CZE 16FIN 112FRA 63IRL 29SWE		60DNK 6FIN 10SWE
	FIN		13FIN 6DNK 2SWE		42FIN 28CZE 16DNK 32FRA 10IRL 15SWE		221FIN 1CZE 6DNK 116SWE
	FRA		3FRA 1DNK				
	IRL				1336IRL 80CZE 63DNK 10FIN 515FRA 19SWE		
	SWE		41SWE 9DNK 2FIN	5SWE	52SWE 28CZE 29DNK 15FIN 35FRA 19IRL		

Models

- 2 x 2 analysis
- 3 models dep. on random terms
 - i) sire, ii) sire + dam-p.e., iii) sire, MGS, dam-p.e.
- Optimised connection

Table 6. Effects (except genetic effect) accounted for in the models**

FRA	IRL	DNK	SWE	FIN	CZE
	Sex	Sex	Sex	Sex	Sex Twin
Twin	Twin	Twin	Twin	Twin	
Parity x Age	Parity				
Season		Season	Season	Season	
Ind. situation					
CG	CG	CG	CG	CG	CG*
	Age #	Age	Age	Age	Age
					B. year

Results : raw r_g model iii)

Table 10a. Across-country genetic correlation* (standard error) for direct weaning weight (below diagonal) and maternal weaning weight (above diagonal)

r_{gm} r_{gd}	FRA	SWE	IRL	DNK	FIN	CZE
FRA		0.67 (0.229)	0.27 (0.370) ¹	<i>nc</i>	<i>nc</i>	<i>nc</i>
SWE	0.90 (0.102)		<i>nc</i>	0.99 (0.230)	0.90 (0.190)	0.82 (0.338)
IRL	0.77 (0.155)	<i>nc</i>		<i>nc</i>	<i>nc</i>	<i>nc</i>
DNK	<i>nc</i>	0.59 (0.226)	<i>nc</i>		<i>nc</i>	<i>nc</i>
FIN	<i>nc</i>	0.68 (0.213)	<i>nc</i>	<i>nc</i>		0.96 (0.375)
CZE	<i>nc</i>	0.79 (0.202)	<i>nc</i>	<i>nc</i>	0.83 (0.170)	

nc : non- converged

¹ : considered non-converged

Results : bended r_g model iii)

Table 10b. Bended across-country genetic correlation* (standard error) for direct weaning weight (below diagonal) and maternal weaning weight (above diagonal)						
r_{gm} r_{gd}	FRA	SWE	IRL	DNK	FIN	CZE
FRA		0.659	0.603	0.604	0.603	0.603
SWE	0.887		0.612	0.934	0.866	0.805
IRL	0.744	0.678		0.597	0.598	0.604
DNK	0.868	0.592	0.694		0.637	0.600
FIN	0.820	0.658	0.883	0.890		0.928
CZE	0.912	0.778	0.719	0.762	0.811	

non- converged $rg_{(dir)}$ defaulted to 0.90 (0.661)

non- converged $rg_{(mat)}$ defaulted to 0.62 (0.400)

Conclusion

- Experience from LIM analysis : speed-up process
- Across-country connection not as 'easy' as in LIM
 - FRA (and SWE) : main connecting countries
- Overall 'lower' rg's in CHA compare to LIM