



InterGenomics – HOL

Preliminary report of the research run

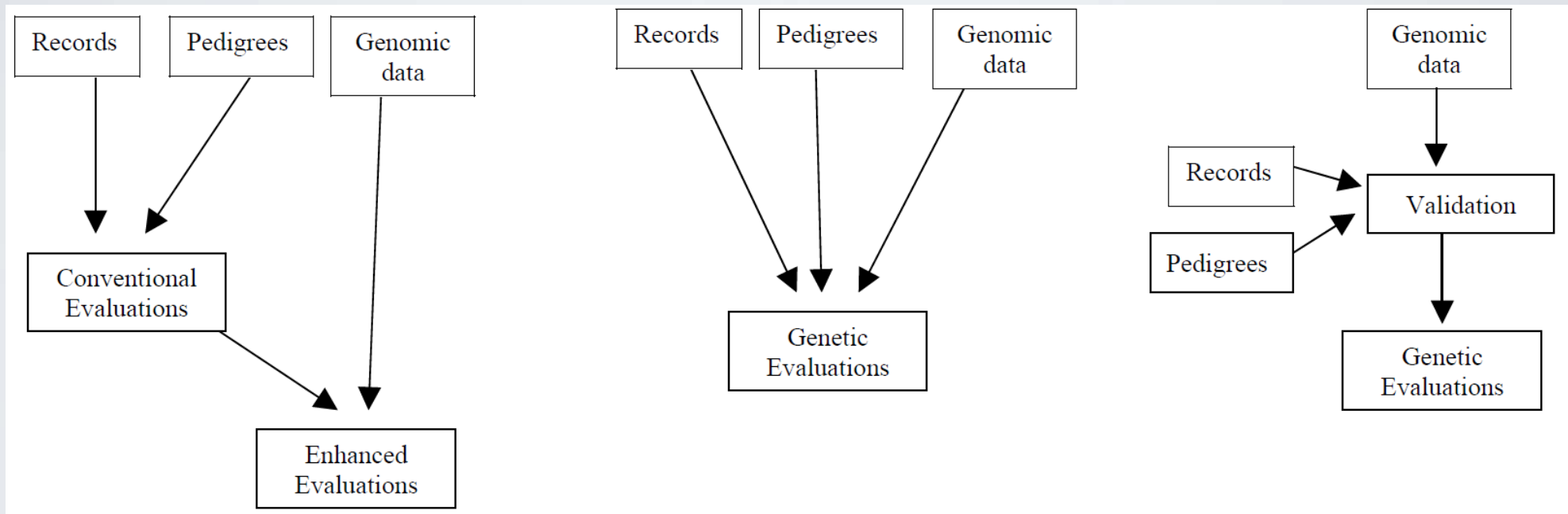
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ITBC Team



Introduction (1)

SAC report 2007 – National genomic models



2-Step method

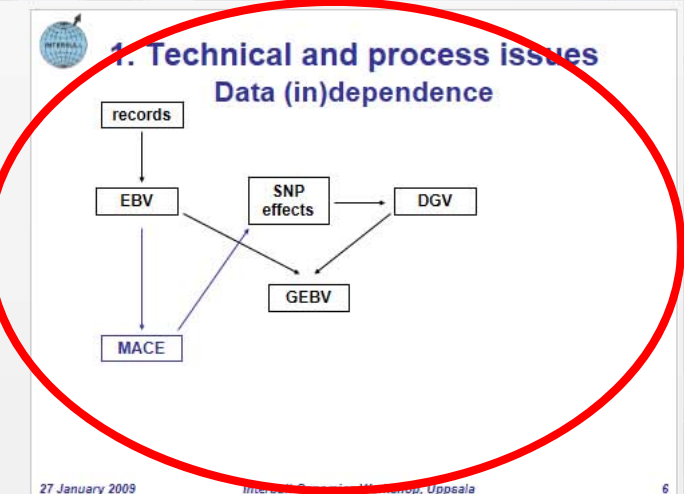
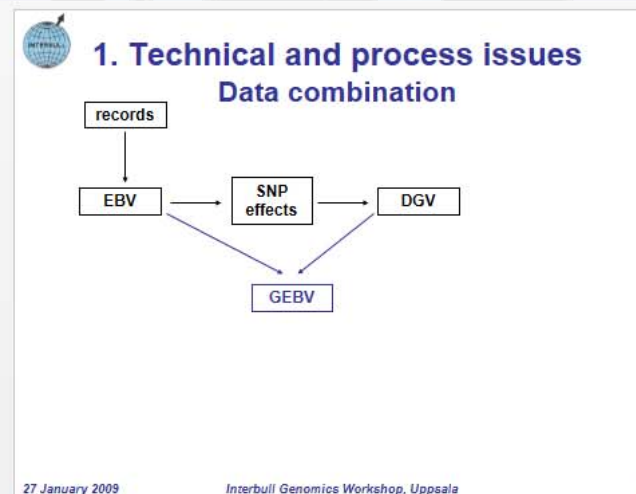
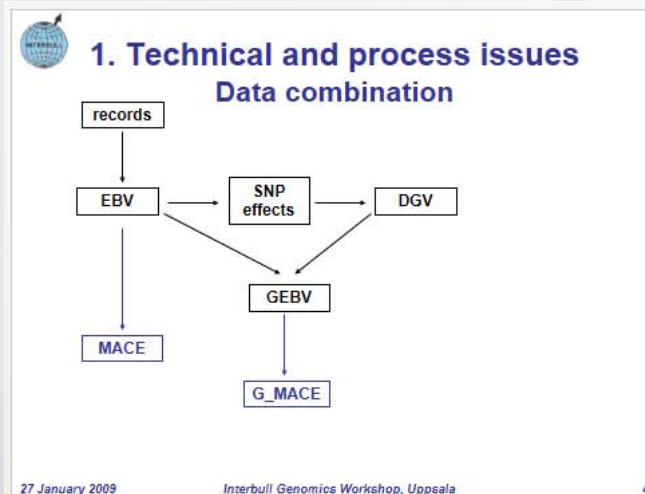
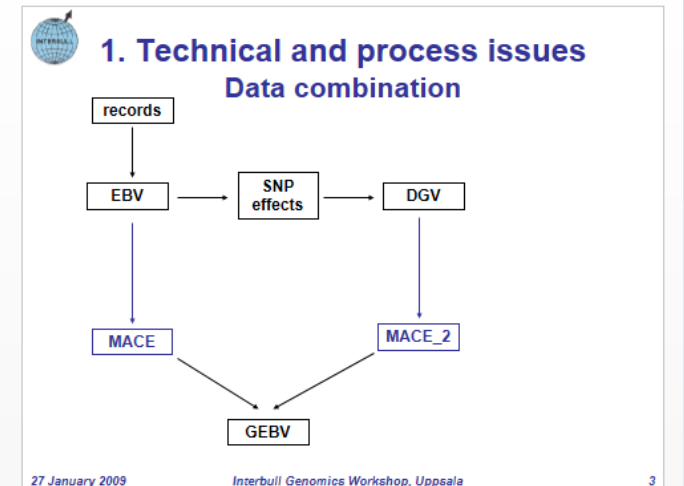
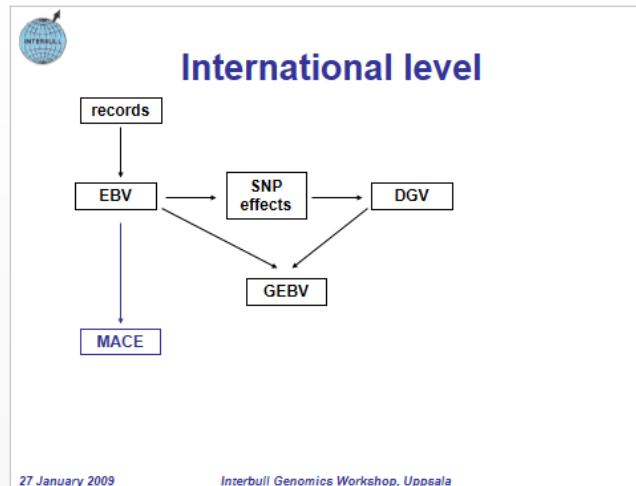
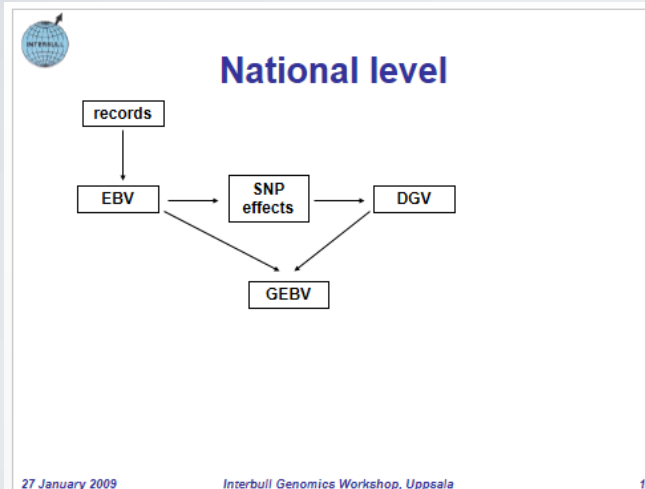
1-Step method

0-Step method



Introduction (2)

Interbull Task Force 2009 – International genomic models





A little bit of IG-BSW history

JAN 2009 – Interbull Technical **Workshop** on Genomics (Uppsala)

FEB 2009 – MAR 2009: Letter of intent

MAY 2009 – Project presentation (Innsbruck)

SEP 2009 – OCT 2009: InterGenomics BSW agreement

OCT 2009 – **IG-BSW TC**: Methods (Zug)

DEC 2009 – **APR 2010**: Data (genotype) submission

JUL 2010 – NOV 2010: **IG-BSW TC**: Preliminary results (Uppsala)

MAR 2011 – Interbull Technical **Workshop** on Genomics (Guelph)

MAR 2011 – **IG-BSW** approved as a new future service

DEC 2010 – **AUG 2011**: Validation

AUG 2011 – Green light from SC, IG-BSW MC (Stavanger)



A little bit of IG-HOL history

- Large international consortia exist for exchange of genotypes in order to perform genomic selection
- Small/other Holstein populations have been searching for ways of ensuring cost efficient solutions for genomic selection
- In small HOL populations are limited chances for commercial-driven implementation of genomic selection
- After the successful implementation of InterGenomics for BSW the idea of implementing this methodology for small/other HOL populations has arisen
- With some additional input would be possible to amend one additional and relevant project for these small/other HOL populations

Marija Klopčič, Toine Roozen, Brian Van Doormaal



Main steps of the project IgHol

- Interbull SC decision for supporting idea
- Interbull Centre find the possibilities to support idea/initiative
- Ask potential countries (HOL population) about interest for cooperation in the project
- Prepare data according Interbull file formats for InterGenomics
- Use of InterGenomics methodology for HOL interested populations (**feasibility / pilot run**)
- Test run
- Discussion of costs and interest of routine run
- Routine run

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Survey

Country	No progeny bulls	No young bulls	Each year
Belgium	21	233	50
Croatia	0	13	5 to 6
Czech Republic	1500	500	100 - 150
Estonia			
Hungary	550	1000	
Ireland	5.5	30	7
Latvia			
Portugal	1.896	28	120/200
Slovakia			
Slovenia	200		50 - 100
Macedonia			
Brazil	230		
Israel	1.427	545	400
South Africa	89	65	300
South Korea	300		50
Uruguay	200	65	n.a

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Number of Submitted HOL genotypes

Chip	HRV		IRL		PRT		SVN		URY		ZAF		SUM
	F	M	F	M	F	M	F	M	F	M	F	M	
2900			174	266									440
6909			2894	431									3325
18819			3940	1898									5838
26151												45	45
30105												34	34
53218			2965	144									3109
54001			99	249		263							611
54609	72		5	295		555	88		581	251			1847
76999						13	179	343				7	542
139480												2	2
777962			25	2									27
SUM M		0		3285		831		343		251		88	4798
SUM F	72		10102				267		581				11022
SUM F + M	72		10102	3285		831	267	343	581	251		88	15820



Pulling of genotypes

- All genotypes are converted to a "common map";
- "Common map" contains 55172 SNPs;
 - 50 K V1 + 50 K V2 – SNPS with unknown position;
 - Needs to be re-evaluated to accommodate new chips;
- Merge genotypes within and across countries;
 - Remove animals with no pedigree information;
 - Select one copy if there are any duplicate genotypes;
- Missing SNPs set to unknown;



Further handling of genotypes

- First parentage check (Mendelian conflicts);
- Identify and remove problematic SNPs (sire-son conflicts);
 - Sever pedigree link if necessary;
- Impute all genotypes to the level of "common map";
 - > 15000 genotypes imputed to higher densities;
 - HapMap (PVR, USDA);
 - Remove poorly imputed genotypes;
 - Needs to be fine-tuned for HOL;
- Remove uninformative SNPs;
 - (Call rate for animal and SNP, MAF >
- **What is left?**
 - **4656 bull genotypes with 45473 SNPs**



Prepare "phenotype"

- Bulls with MACE EBV → old bulls → Reference population
- Bulls without MACE EBV → young bulls
 - Parent average needed;
 - Country / sex / year average
 - Missing country / sex / year averages are predicted through regression



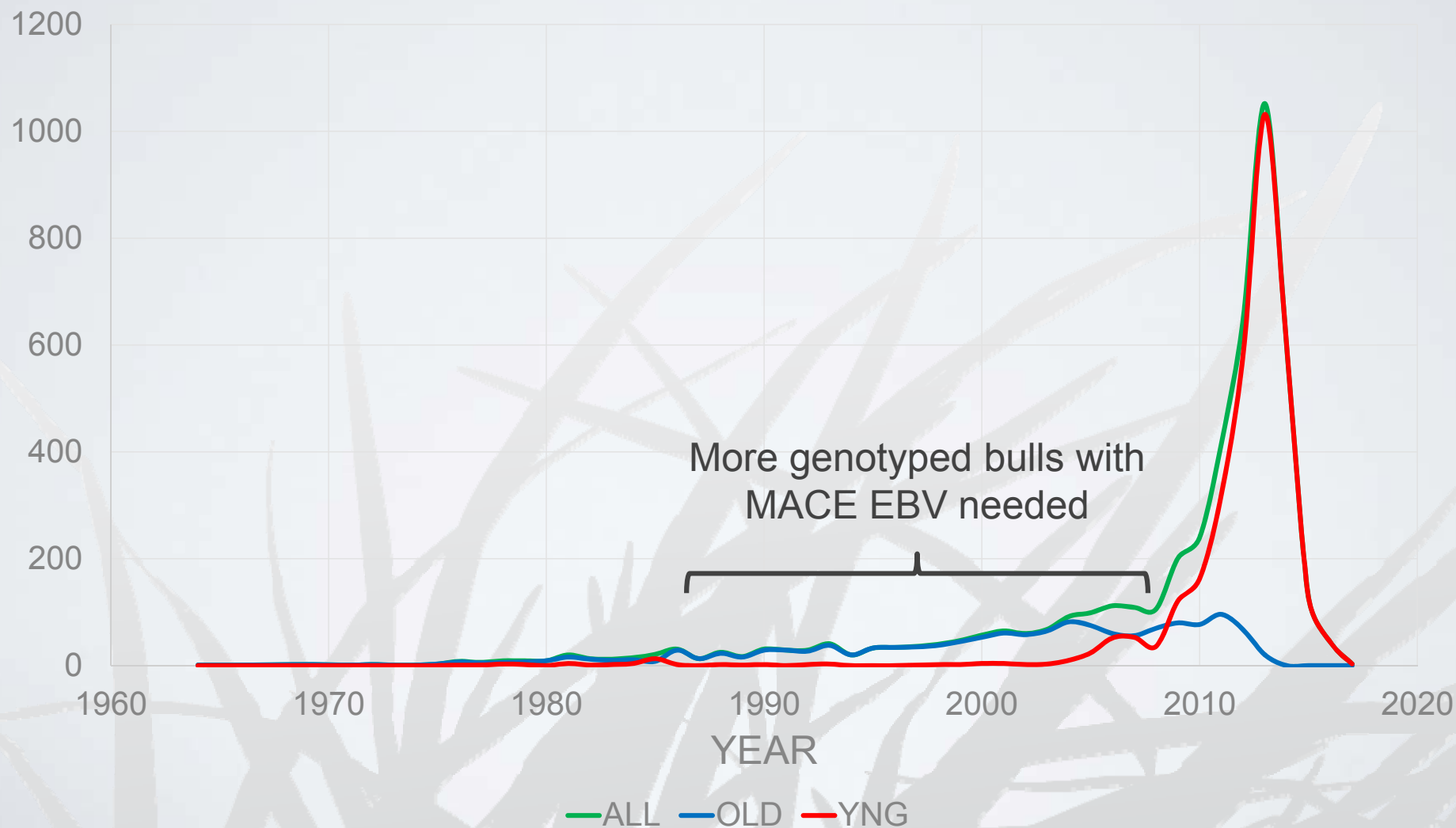
Size of the reference population

TRAIT	MACE EBV	NO MACE EBV	S + D	S	D	NO MACE EBV/PA
pro	1432	3224	125	2889	2	208
scs	1409	3247	128	2894	2	223
mas	1394	3262	135	2901	1	225
cwi	1328	3328	117	2923	2	286
rtp	1283	3373	132	2945	1	295
dlo	1259	3397	141	2958	6	292
int	1076	3580	151	3130	8	291



Age of bulls

Age Distribution PRO





Traits

- 26 traits;
- 6 country scales
 - HRV – 5 traits
 - IRL – 26 traits
- Total 105 country-trait combinations (GBLUP runs)



GBLUP

- VanRaden (2008)
- $DPGM = \text{mean} + \Sigma \text{genotypes}^* \text{effects} + \text{poly} + \text{error}$
 - $DPGM = PA + (PGM - PA) / REL_{\text{dau}}$
 - SNP variance 90%



Correlation (EBV, DGV, GEBV)

CORRELATIONS BETWEEN

				EBV DGV	EBV GEBV	DGV GEBV
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HOL	int	IRL	old	0.9731	0.9818	0.9981
			yng	0.7023	0.8117	0.9213
HOL	pro	IRL	old	0.9401	0.9482	0.9988
			yng	0.5907	0.8068	0.8876



r (REL, (Diff(EBV, GEBV))

BRD	TRT	COU	GRP	STAT
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HOL	int	IRL	old	-0.4081
			yng	-0.1740
HOL	pro	IRL	old	-0.7250
			yng	-0.1168



Reliability gain

				CALCULATED				
				EBV RELIABILITY		GEBV RELIABILITY		GAIN
				MEAN	STD	MEAN	STD	MEAN
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HOL	int	IRL	old	76.39	13.69	79.93	10.09	3.54
			yng	33.85	3.76	48.02	2.26	14.17
HOL	pro	IRL	old	70.58	17.38	76.56	12.56	5.98
			yng	34.93	3.79	51.06	2.07	16.13



Summary

- It was easy to adapt the IG-BSW machinery to the use for IG-HOL (and any other breed in the future);
- The number of available genotyped bulls with MACE EBV was low; \therefore More genotypes are needed;
- Despite the small size of the reference population, the prospects of achieving higher reliability values are good.



Thank you.

Any questions or comments?



CORRELATIONS BETWEEN

				EBV DGV	EBV GEBV	DGV GEBV
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BSW	int	DEA	old	0.8770	0.9047	0.9956
			yng	0.3273	0.4048	0.9907
BSW	pro	DEA	old	0.9345	0.9495	0.9937
			yng	0.6083	0.6794	0.9904

