

# IG-HOL

## Second Research run

Hossein Jorjani, Valentina Palucci

# Outline

- Background
- Data description
- Result description

# Background (1)

- Small/other Holstein populations have been searching for ways of ensuring cost efficient solutions for genomic selection
- In small HOL populations chances for commercial-driven implementation of genomic selection are limited.
- After the successful implementation of InterGenomics for BSW the idea of implementing this methodology for small/other HOL populations has arisen
- Marija Klopčič, Toine Roozen, Brian Van Doormaal

# Background (2)

- Interbull SC decision (supporting the idea)
- Ask potential countries (HOL population) about interest for cooperation in the project (survey)
- Use of InterGenomics workflow for HOL interested populations
- First feasibility/pilot run May-Aug 2017
- Second feasibility/pilot run May-July 2018

**DATA**

# Overall size of operations

	1705t	1805t
<b>Number of countries</b>	<b>6</b>	<b>8</b>
<b>Number of traits</b>	<b>27</b>	<b>31</b>
<b>Number of country-traits</b>	<b>105</b>	<b>148</b>
<b>Number of traits per country</b>		
– HRV	5	5
– IRL	26	30
– ISR	0	8
– KOR	0	24
– PRT	23	26
– SVN	24	27
– URY	5	5*
– ZAF	22	23

# Number of submitted genotypes

	1705t					1805t			
	FEMALE	MALE	ALL <sup>A</sup>	UNIQUE <sup>A</sup>		FEMALE	MALE	ALL <sup>A</sup>	UNIQUE
HRV	72	0	72	72		173	0	173	173
IRL <sup>B</sup>	10102	3285	13387	13387		9523	3166	12689	12689
ISR	0	0	0	0		3974	2194	6168	6168
KOR	0	0	0	0		1444	605	2049	2049
PRT	0	831	831	830		0	831	831	830
SVN	267	343	610	603		720	383	1103	1088
URY <sup>B</sup>	581	251	832	832		2790	363	3153	3153
ZAF	0	88	88	86		491	326	817	725
ALL	11022	4798	15820	15810 15778 <sup>C</sup>		19115	7868	26983	26875 26711 <sup>C</sup>
IMPUTED	11056	<b>4656<sup>D</sup></b>	15712 <sup>E</sup>	<b>15712<sup>E</sup></b>		17206 <sup>D,F</sup>	<b>7173</b>	24379 <sup>E</sup>	<b>24379<sup>E</sup></b>
IMPUTED Ancestors	<b>40</b>	<b>120</b>				<b>69</b>	<b>106</b>		

# New genotypes

- After the run was finished,  
we have received 1796 new genotypes from IRL.



# Duplicate genotypes

Number of bulls	Number of genotypes
4	4
16	3
120	2
7033	1

# Duplicate genotypes

	IRL	ISR	KOR	PRT	SVN	URY	ZAF
HRV							
IRL		34	50	35		43	4
ISR			36	31	2	36	5
KOR				53		41	6
PRT						25	1
SVN						1	
URY							5

# Bulls w/o National and MACE EBV

	GENOTYPED				PHENOTYPED	
COUNTRY	ANIMAL	MALE	BULL WITH OWN EBV		NAT EBV	GENOTYPED
HRV	173	0	0		721	119
IRL	12689	3166	270		2604	420
ISR	6168	2194	1229		1367	1238
KOR	2049	605	312		1284	454
PRT	830	830	444		2331	633
SVN	1088	370	202		501	289
URY	3153	363	75		998	222
ZAF	725	234	45		1272	221

# Bulls w/o National and MACE EBV

	GENOTYPED				PHENOTYPED	
COUNTRY	ANIMAL	MALE	BULL WITH OWN EBV		NAT EBV	GENOTYPED
HRV	173	0	0		721	119
IRL	<del>12689</del> <b>14485</b>	<del>3166</del> <b>4962</b>	<del>270</del> <b>1400*</b>		<b>2604</b>	<b>420 1546*</b>
ISR	6168	2194	1229		1367	1238
KOR	2049	605	312		1284	454
PRT	830	830	444		2331	633
SVN	1088	370	202		501	289
URY	3153	363	75		998	222
ZAF	725	234	45		1272	221

\* Not checked against cross reference file

# Size of the reference population

					PA BASED ON			
BREED	TRAIT	RUN	WITH OWN MACE EBV	WITHOUT OWN MACE EBV	S+D	S	D	NO EBV/PA
HOL	ofl	1705t	1296	3360	121	2929	2	308
		1805t	1705	5468	261	3952	16	1239
HOL	pro	1705t	1432	3224	125	2889	2	208
		1805t	3142	4031	271	3396	19	345

# RESULTS

# Expected (theoretical) reliability gain

				MACE EBV RELIABILITY		GEBV RELIABILITY		GAIN
				MEAN	STD	MEAN	STD	MEAN
HOL	ofl	IRL	all	37.43	16.72	53.97	11.22	16.55
HOL	ofl	IRL	old	61.22	18.38	70.58	11.91	9.36
HOL	ofl	IRL	yng	30.01	5.46	48.79	2.85	18.79
HOL	ofl	SVN	all	36.64	18.91	54.52	12.21	17.88
HOL	ofl	SVN	old	65.73	17.51	73.72	11.04	7.99
HOL	ofl	SVN	yng	27.57	5.24	48.54	2.6	20.97
HOL	pro	HRV	all	47.69	21.42	68.76	10.02	21.06
HOL	pro	HRV	old	70.25	10.99	79.24	5.59	9.00
HOL	pro	HRV	yng	30.11	4.08	60.58	1.26	30.47
HOL	pro	IRL	all	45.1	19.09	65.94	10.42	20.84
HOL	pro	IRL	old	60.89	18.68	74.63	10.43	13.73
HOL	pro	IRL	yng	32.78	5.53	59.16	1.92	26.38

# Comparison of the Expected (theoretical) REL gain

TRAIT	COUNTRY	BULLS	1705t	1805t
int	IRL	OLD	3.54	4.54
int	IRL	YNG	14.17	18.98
pro	IRL	OLD	5.98	13.73
pro	IRL	YNG	16.13	26.38



# Realized reliability gain

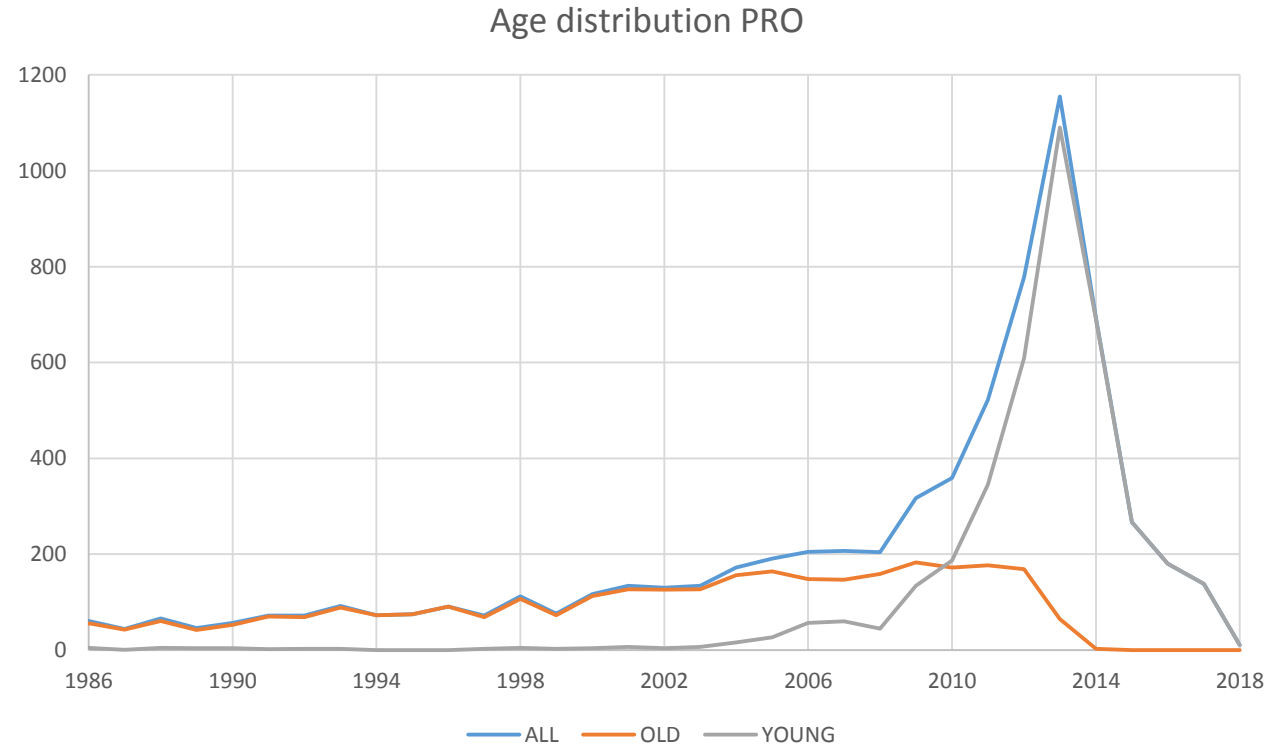
			Discount factor			
			100%	86%	70%	50%
<b>ALL</b>	<b>OLD</b>	<b>MEAN</b>	<b>7.6</b>	<b>6.5</b>	<b>5.3</b>	<b>3.8</b>
	<b>OLD</b>	<b>STD</b>	<b>2.9</b>	<b>2.5</b>	<b>2.0</b>	<b>1.4</b>
	<b>YNG</b>	<b>MEAN</b>	<b>23.8</b>	<b>20.5</b>	<b>16.7</b>	<b>11.9</b>
<b>ALL</b>	<b>YNG</b>	<b>STD</b>	<b>4.0</b>	<b>3.4</b>	<b>2.8</b>	<b>2.0</b>

# Validation

- Aim of validation
  - To determine the optimum level of polygenic effect
  - To determine the appropriate level of discounting
- Means of validation
  - GEBV-test
- Past experience
  - Two sets of runs: Full data and reduced data
  - In each set: polygenic effects = 0.0, 1.0, 0.1 (11 runs in each set)

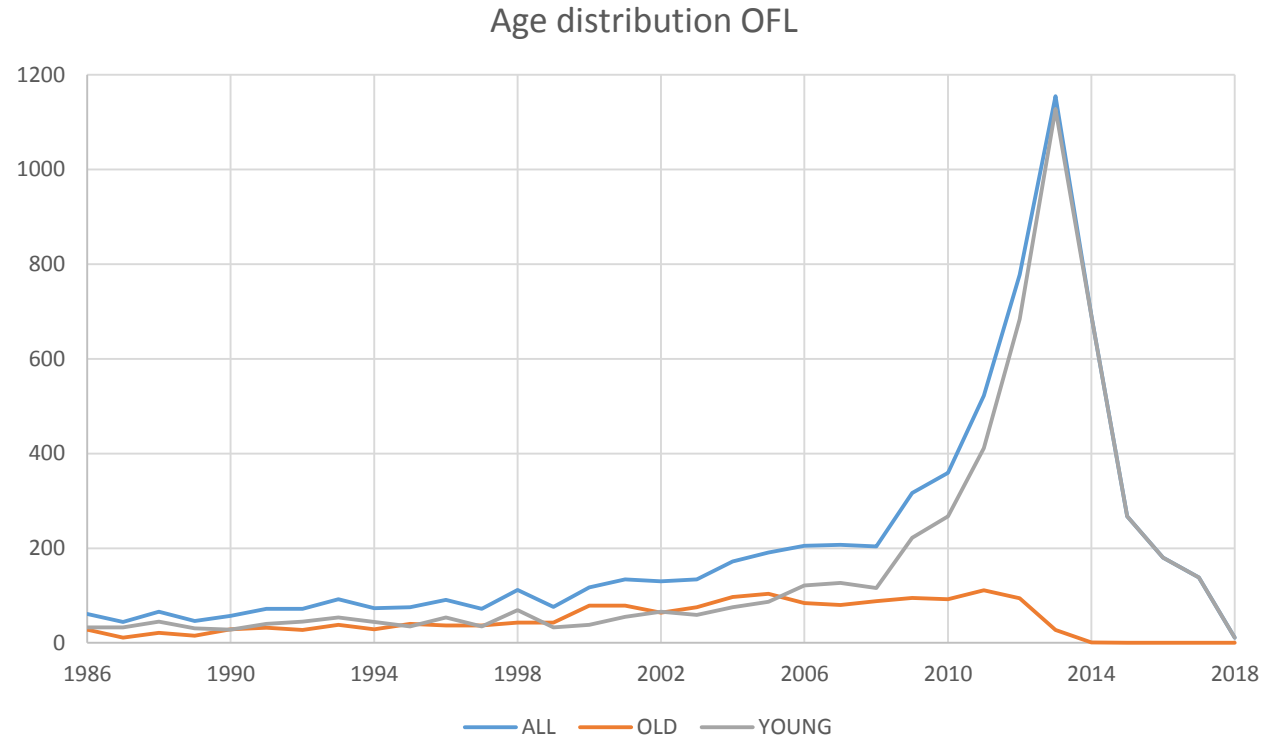
# Age distribution - PRO

- Bulls born 1986-2009: 2421
- Bulls born 2010-2013: 586
- There seems to be enough old bulls to perform GEBV-test



# Age distribution - OFL

- Bulls born 1986-2009: 1275
- Bulls born 2010-2013: 325
- There are still not enough old bulls to perform GEBV-test



# Consistency of the GEBV values

			CORRELATIONS BETWEEN	REGRESSION OF	
BREED	TRAIT	COUNTRY	CUR-PRV	CUR_ON_PRV	PRV_ON_CUR
HOL	ofl	IRL	0.979	0.959	0.999
HOL	ofl	SVN	0.973	0.979	0.967
HOL	pro	HRV	0.957	0.981	0.933
HOL	pro	IRL	0.958	1.314	0.698

# Consistency of SNP effects (incl. intercept)

COUNTRY		Previous SNP effect		Current SNP effect		Correlation
		MEAN	STD	MEAN	STD	
HRV	PRO	1.20E-05	8.58E-03	1.29E-05	1.07E-02	<b>0.9943</b>
IRL	PRO	1.87E-05	7.19E-03	1.22E-05	1.08E-02	<b>0.9941</b>
PRT	PRO	1.82E-05	3.84E-03	9.63E-06	1.01E-02	<b>0.9701</b>
SVN	PRO	2.17E-05	5.42E-03	1.69E-05	7.97E-03	<b>0.9865</b>
URY	PRO	1.37E-05	7.37E-03	5.59E-06	9.31E-03	<b>0.9921</b>
ZAF	PRO	5.59E-06	7.53E-03	5.32E-06	9.91E-03	<b>0.9931</b>
IRL	OFL	2.91E-07	9.33E-03	-4.70E-06	1.20E-02	<b>0.9988</b>
PRT	OFL	1.50E-05	8.03E-03	1.35E-05	1.15E-02	<b>0.9979</b>
SVN	OFL	5.29E-06	8.57E-03	2.17E-06	1.14E-02	<b>0.9982</b>

# Consistency of SNP effects (excl. intercept)

COUNTRY		Previous SNP effect		Current SNP effect		Correlation
		MEAN	STD	MEAN	STD	
HRV	PRO	5.19E-05	1.15E-03	6.25E-05	1.62E-03	<b>0.7259</b>
IRL	PRO	5.19E-05	1.18E-03	6.22E-05	1.64E-03	<b>0.7673</b>
PRT	PRO	3.53E-05	1.21E-03	5.62E-05	1.77E-03	<b>0.6422</b>
SVN	PRO	4.65E-05	1.20E-03	5.35E-05	1.63E-03	<b>0.7062</b>
URY	PRO	4.78E-05	1.15E-03	4.86E-05	1.61E-03	<b>0.7115</b>
ZAF	PRO	4.05E-05	1.15E-03	5.12E-05	1.61E-03	<b>0.7232</b>
IRL	OFL	4.38E-05	1.04E-03	5.15E-05	1.17E-03	<b>0.8977</b>
PRT	OFL	5.23E-05	1.07E-03	6.69E-05	1.21E-03	<b>0.8818</b>
SVN	OFL	4.51E-05	1.13E-03	5.52E-05	1.28E-03	<b>0.8909</b>

# Comparison of GMACE and IG-HOL

- PRO IRL

		<b>GMACE</b>	<b>IG-HOL</b>
Observations		11548	7173
In common		<b>36</b>	
GEBV (Mean)		16.40	18.38
GEBV (STD)		4.52	5.33
r (GMACE, IG-HOL)		<b>0.88</b>	
REL (Mean)		58.69	54.14
REL (STD)		3.58	1.27
r (GMACE, IG-HOL)		<b>0.59</b>	



# **CONCLUSIONS**

# Conclusions

- Large enough reference population for many traits
- Reasonable reliability gain
- Enough bulls with own EBV to make validation possible
- Consistent results between 1705t and 1805t
- Good agreement between IG-HOL and GMACE

?

# Origin of IG-HOL & GMACE common bulls

<b>HOLDEU</b>	<b>4</b>	<b>bulls</b>
<b>HOLDNK</b>	<b>1</b>	<b>bulls</b>
<b>HOLGBR</b>	<b>1</b>	<b>bull</b>
<b>HOLIRL</b>	<b>3</b>	<b>bulls</b>
<b>HOLNLD</b>	<b>5</b>	<b>bulls</b>
<b>HOLUSA/HOL840</b>	<b>22</b>	<b>bulls</b>