Opportunities and challenges for small populations of dairy cattle

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To talk about my experiences in working with two groups of "small populations" in two projects:

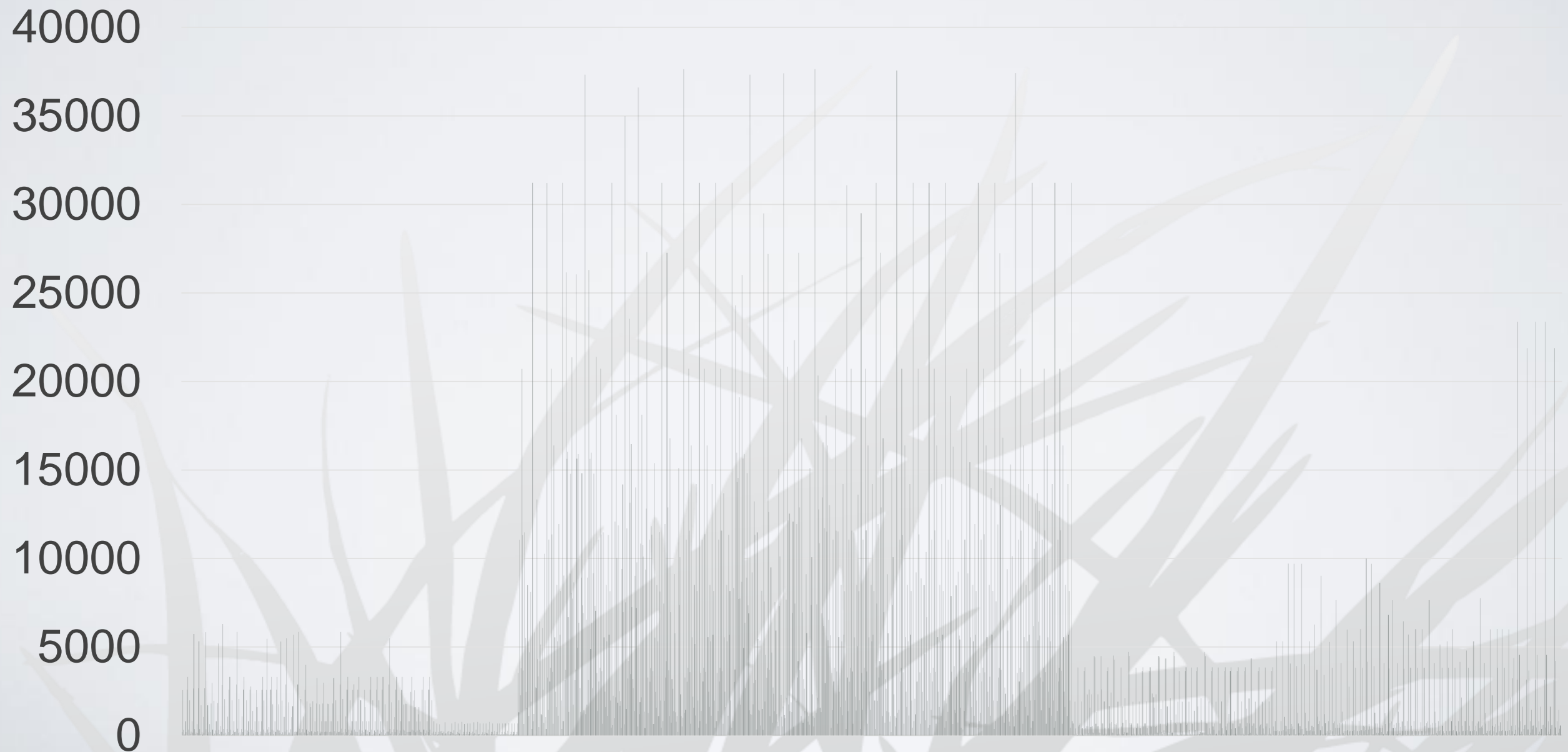InterGenomics – BSW

InterGenomics – HOL

Outline

- Some clarifications about "small population"

- Two examples of "small population"

- Thinking aloud

Small population?

Number of bulls / Trait / Breed / Country

Country-breed-trait combination

	Size (number of bulls)	Number of populations
All	**3657**	**1929**
10th Percentile	**< 93**	**190**
25th Percentile	**< 285**	**482**
10 bulls / birth year	**280 (HOL) / 330 (OTH)**	**523**
Arbitrary	**< 500**	**649**

Consequences of "small population"

- Small population / Smaller farms / smaller industry

- Weaker economic resources? Weaker infra-structure? Lack of full-time (devoted) staff?

- Is there a correlation between the number of churches and pubs in towns?

- Smaller population ←

  - Smaller university departments / research institutes ←

  - Smaller government support

Smallest populations

TRAIT	BSW	GUE	HOL	JER	RDC	SIM
cc2	52	40	1213	MAX→ 133	60	
dlo	48	56	513	122	35	43
pro	51	60	197	86	38	45
scs	49	57	506	84	37	45
sta	MIN → 19	52	446	36	31	
TRAIT	BSW	GUE	HOL	JER	RDC	SIM
cc2	NZL	CAN	ZAF	NLD	IRL	
dlo	NZL	NLD	SVN	NLD	CAN (M)	USA
pro	NZL	NZL	MEX	CHE	CAN (M)	USA
scs	NZL	NZL	SVN	CHE	CAN (M)	USA
sta	GBR	AUS	SVN	NLD	CAN (M)	

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scs	NZL	NZL	SVN	CHE	CAN (M)	USA
sta	GBR	AUS	SVN	NLD	CAN (M)	

- You cannot maintain a Genetic Evaluation System (GES) for a really small breed, unless the marginal cost of maintaining such a GES is very small because it is part of a much larger GES.

- **Challenge**: Small population
- **Opportunity**: Attach it to a larger program

- This is by no means an unusual phenomena:

  - Smaller breeds in each country could be included in a larger breed → each of the six ITBC evaluation breeds contain many smaller breeds;

  - A small country's data, in its entirety, can be included in another country's GES;

  - Part or all of the GES of a country can be outsourced to a different country;

- Why do we keep these small populations?
- Why do they need an independent GES?
- Why not let the dairy cattle become like poultry/pig?

- Schaeffer (2006):

- A system of cooperator herds or a consortium of herds should be established by the AI organization with approximately 10 000 cows in total.

- **In essence, the dairy industry would become more like the poultry and swine industries.**

- There are many reasons that Dairy cattle INDUSTRY will not become like poultry and pig INDUSTRY:

- Long generation interval

- Low natural reproductive rate

- …

- Standardized housing, feeding, disease control, management,…, not possible as it is in poultry and pig

G x E (estimated Genetic correlations for PRO)

CB > 0	FREQ	MIN	MEAN	MEDIAN	MAX
BSW	45	**0.773**	0.849	0.859	0.916
GUE	15	**0.761**	0.833	0.825	0.933
HOL	465	**0.750**	0.836	0.852	0.929
JER	55	**0.752**	0.834	0.857	0.923
RDC	91	**0.755**	0.855	0.874	0.931
SIM	66	**0.757**	0.860	0.864	0.932
CB > 100	FREQ	MIN	MEAN	MEDIAN	MAX
BSW	14	**0.852**	0.864	0.856	0.916
GUE					
HOL	343	**0.750**	0.837	0.852	0.929
JER	19	**0.752**	0.820	0.852	0.920
RDC	9	**0.755**	0.819	0.790	0.920
SIM	14	**0.851**	0.870	0.856	0.932

- If for nothing else, there is a need for independent GES for the dairy cattle breeds that have adapted to the local environment, which is manifested in GxE, and re-ranking of animals.

- **Challenge**: There is no escape from GxE interaction
- **Opportunity**: The world's sum of dairy cattle genetic resources is at your disposal to select from.

Would genomics change anything?

- Can genomics change the population size?
- Can genomics change the GxE interaction?

- Can genomics resolve the shortage of (**financial**) resources for the small populations?

- **Challenge**: How should small populations deal with the new costs?
- **Opportunity**: Stronger cooperation

- InterGenomics
  - BSW: 2009 - …
  - HOL: 2017 - …

Number of bull genotypes

- InterGenomics – BSW ← 8 BSW populations
- May 2010:   3392 Bull genotypes
- October 2010:   3775 Bull genotypes
- November 2011:   6202 Bull genotypes

Size of the reference population at first general successful validation test (November 2011)

Trait	Countries	Old bulls	Reference	Validation
ANG	3	**1844**	1394	450
INT	2	2242	1637	605
FTP	4	3215	2288	927
CC2	3	3305	2383	922
MSP	3	4038	2980	1058
FAN, RUH	5	4232	3125	1107
FTL	5	4235	3128	1107
RAN, RLS, STA	5	4236	3129	1107
SCS	5	4537	3319	1218
FAT, MIL, PRO	6	4775	3505	1270
DLO	5	4412	3756	656

IG – BSW

Number of:	Dec 2014	Dec 2015	Dec 2016	Dec 2017
Countries	8	8	8	8
Country-trait combinations	212	219	277	280
Unique submitted genotypes	16,599	20,561	26,794	32,344
Genotypes entering imputation & genomic evaluation	15,808	19,500	24,352	28,329
Distributed international GEBVs	N.A.	4,202,064	6,770,134	7,932,400

Palucci, Jorjani, Benhajali, Hjerpe, Sendecka, Pedersén, Wasserman, Roozen (2018) Interbull Centre. Interbull Bulletin 52, pp 46

IG-HOL genotypes

- IG-HOL: 1705 and 1805

	1805t		
	FEMALE	MALE	ALL
HRV	173	0	173
IRL	9523	3166	12689
ISR	3974	2194	6168
KOR	1444	605	2049
PRT	0	831	831
SVN	720	383	1103
URY	2790	363	3153
ZAF	491	326	817
IMPUTED	17206	**7173**	24379
IMPUTED Ancestors	**69**	**106**	

Expected (theoretical) reliability gain

				MACE EBV RELIABILITY			GEBV RELIABILITY		GAIN
				MEAN	STD		MEAN	STD	MEAN
HOL	ofI	IRL	old	61.22	18.38		70.58	11.91	9.36
HOL	ofI	IRL	yng	30.01	5.46		48.79	2.85	18.79
HOL	ofI	SVN	old	65.73	17.51		73.72	11.04	7.99
HOL	ofI	SVN	yng	27.57	5.24		48.54	2.6	20.97
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	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

Consistency of SNP effects

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

Comparison of GMACE and IG-HOL

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

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

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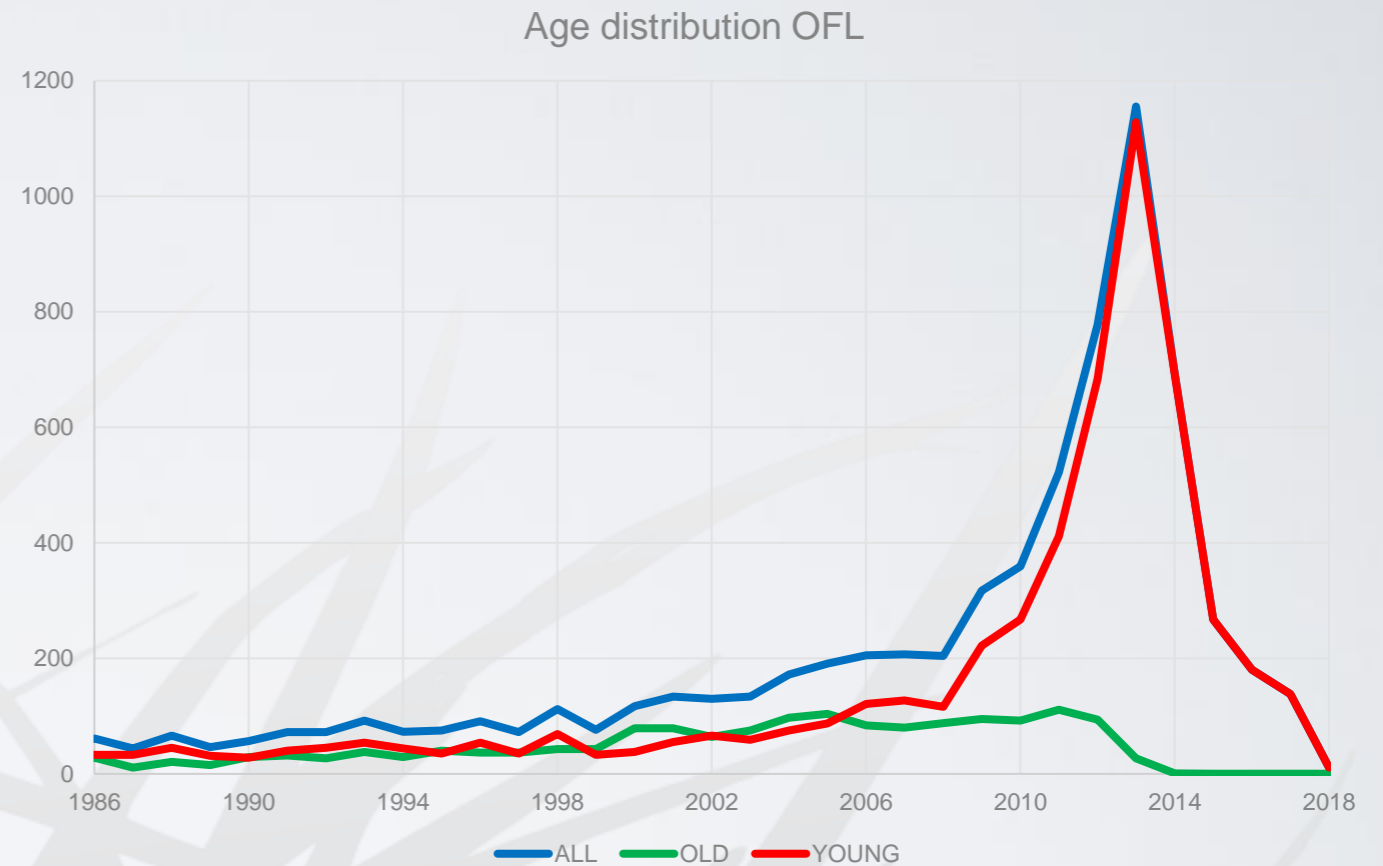
- Bulls born 1986-2009: 2421
- Bulls born 2010-2013: 586
- There seems to be enough old bulls to perform GEBV-test

- Schaeffer (2006)
- Nicholas & Smith (1983)

$$R = \frac{i \; \rho \; \sigma_a}{L}$$

$$MM, MF, FM, FF$$

Thinking aloud

- Schaeffer (2006)

	Selection %	Accuracy		Generation	
		i	r_{TI}	Interval, L	l x r_{TI}
Sire of bulls	5	2.06	0.99	6.50	**2.04**
	5	2.06	0.75	1.75	1.54
Sire of cow	20	1.40	0.75	6.00	1.05
	20	1.40	0.75	1.75	1.05
Dams of bulls	2	2.42	0.60	5.00	1.45
	2	2.42	0.75	2.00	**1.82**
Dams of cows	85	0.27	0.50	4.25	0.14
	85	0.27	0.50	4.25	0.14
Total				21.75	4.68
				9.75	4.55

Thinking aloud

- Nicholas & Smith (1983)

- Generation interval
- Juvenile scheme: 22 months = 1.83 years
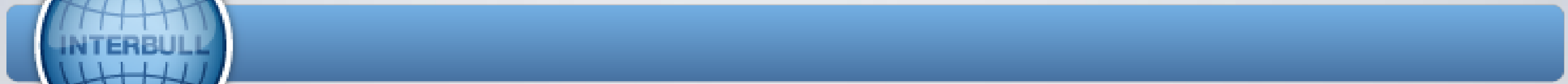- Adult scheme: 44 months = 3.67 years

?

Evaluation	Estimation	Genetics
	Prediction	Genetics
Selection		Macro-economics Micro-economics

Macro-economic decisions made by ?

Micro-economic decision made by ?