

# Genomic selection in the Icelandic dairy cattle population

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# Current breeding programme

- Established in 1974 – BLUP animal model in 1992
- Farmers Association runs AI station and is responsible for running the breeding scheme
- AI station buys 70-75 bull calves annually, acquired by screening based on BLUP merit
- 25-30 bulls go to progeny testing annually

# Current breeding programme

- 6-8 used as proven bulls, thereof 3-5 as sires of bulls
- Number of AI is ~50.000 annually
- 70% of animals are from AI and 30% from natural matings
- Annual genetic progress 10% of genetic SD ( $\sigma_G$ ), where 16% is theoretically possible
  - Output 65% of capacity....
- Generation interval (2000-2009)
  - Sire of bulls 7,9 yr.
  - Sire of cow 5,6 yr.
  - Dams of bulls 6,0 yr.
  - Dams of cows 4,3 yr.

# Project started 1. October 2016

1. Genomic relationships and genomic inbreeding in Icelandic cattle
2. Collecting DNA samples from cows and heifers
3. Implementing genomic selection in Icelandic dairy cattle population  
– Ph.D. study

# Genomic inbreeding in Icelandic cattle

- HD analysis of 47 AI bulls b. 1981-2015
  - Genetic contribution
  - Genetic merit (high, low, unproven)
  - Relationship with other animals in the study (no half-sibs or father-son)
- Other data from Center for Quantitative Genetics and Genomics, Aarhus University and „1000 Bulls Genomes Project Run 4 data“
- Study made by Dr. Bernt Guldbbrandtsen, CQGG, AU.

# Genomic inbreeding in Icelandic cattle

- Icelandic population is very uniform
  - 29 bulls have 100% "Icelandic", origin
  - 16 bulls have 95-99,9% "Icelandic" origin
  - 2 bulls have ~14% "imported" origin
- Loss of genetic diversity is much less of a concern than the history of the breed would suggest
  - Population size was ~9.800 animals in late 18. century after "Móðuharðindi" in 1783-5

# Genomic inbreeding in Icelandic cattle

Breed	Sub-breed	% Heterozygote	Number	Min % ROH	Mean % ROH	Max % ROH
Angler	Old-style	36.8	31	2.9	9.6	20.5
Brown Swiss	Czech	34.2	39	2.1	10.1	22.7
Brown Swiss	German	34.1	24	2.9	9.9	18.8
Brown Swiss	Italian	33.6	16	4.6	12.6	18.1
Brown Swiss	USA	33.0	41	7.0	13.8	24.8
Holstein Cattle	Danish	35.7	158	3.7	10.5	11.9
<b>Icelandic Cattle</b>		<b>31.8</b>	<b>47</b>	<b>4.6</b>	<b>11.1</b>	<b>18.2</b>
Jersey Cattle	Danish	32.1	420	7.8	16.7	28.3
Red Dairy Cattle	Modern Danish	37.9	245	0.0	4.4	16.7
Red Dairy Cattle	Finnish	35.6	243	2.7	9.8	17.6
Red Dairy Cattle	Norwegian	36.6	382	0.7	7.4	20.6
Red Dairy Cattle	Swedish	36.6	246	0.2	7.6	18.9
Jutland Cattle	Reconstructed	34.4	15	3.2	11.6	40.0
Black-and-White	Danish 1965	34.7	42	2.1	10.6	26.6
Shorthorn Cattle	Danish	28.1	60	0.3	28.8	46.9
Red Dairy Cattle	Old Danish	31.7	135	0.2	19.3	48.3

# Collection of DNA samples from cows and heifers














- 551 proven AI bulls with phenotypic data, b. 1990-2012
  - Semen available from 498
  - Proven bulls have 62.000 offspring
  - DNA samples from 183 bulls b. 2013-2018
- To compensate for low number of bulls, sampling DNA from 5.000 cows recommended by scientists at Aarhus University



# Collection of DNA samples from cows and heifers

- 124 farms in sampling with good data quality
- Regular reporting and regular collection of milk samples from individual cows
- Delivered milk 90-99,9% of produced milk in 2014-2016
- Minimum 75% of cows and heifers from AI bulls in 2014-2016
- 122 farms participated

**DNA sýnataka** 06.09.2017

Gröpunúmer	Nafn	Kyn	Einstaklingarnúmer	Sýni númer
0843	Doti	Kýr	201215283510843	 122628
0850	Þóll	Kýr	201215283510850	 122637
0859	Flík	Kýr	201215283510859	 122555
0861	Gylling	Kýr	201215283510861	 122594
0862	Mána	Kýr	201215283510862	 122641
0874	Malin	Kýr	201215283510874	 122563
0879	Íveta	Kýr	201315283510879	 122618
0890	Kemba	Kýr	201315283510890	 122583
0893	Geotrjúður	Kýr	201315283510893	 122629
0894	Móna	Kýr	201315283510894	 122647
0896	Hosa	Kýr	201315283510896	 122639
0899	Linda	Kýr	201315283510899	 122638
0900	Rauðhumla	Kýr	201315283510900	 122603

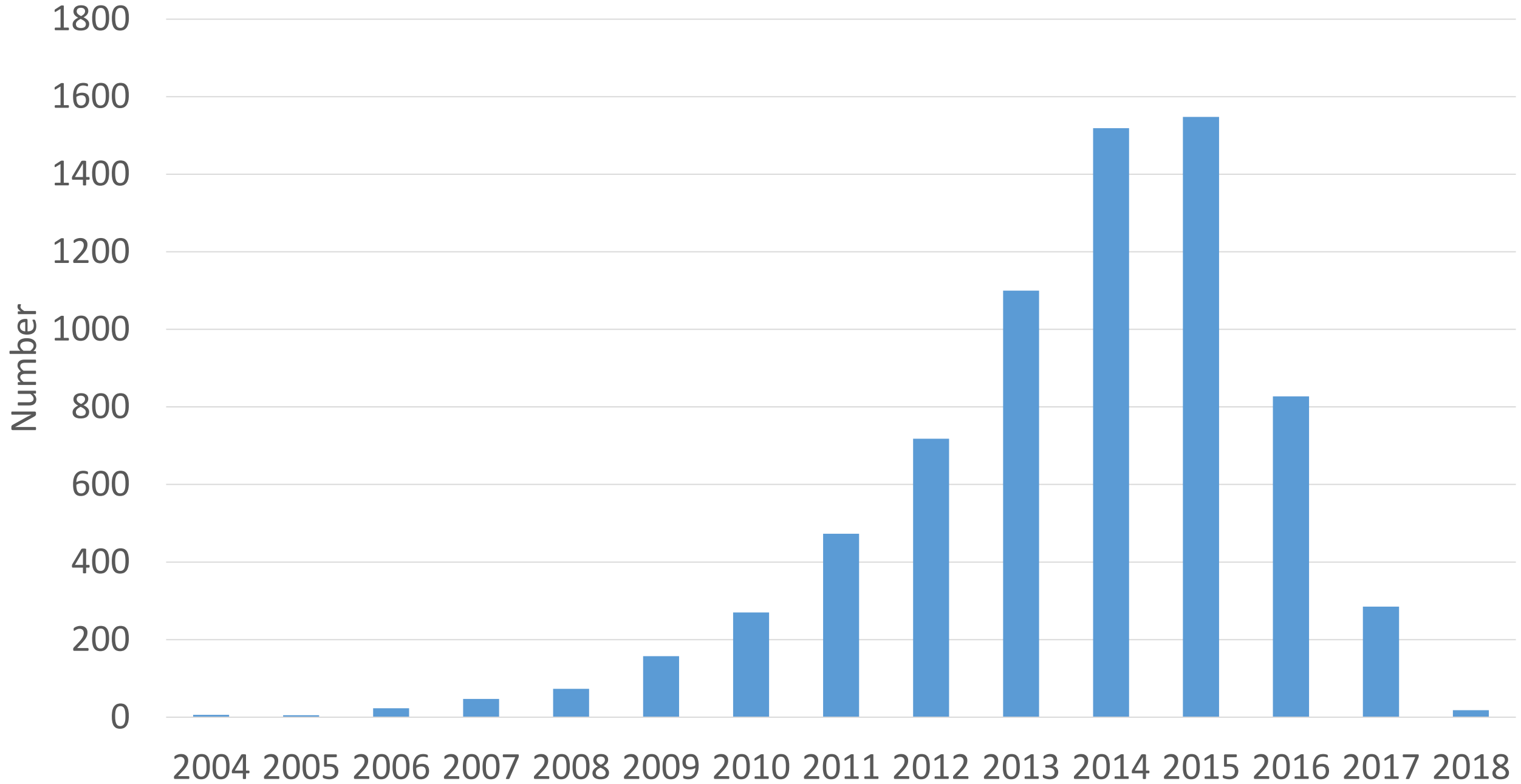
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# DNA collected from 7.521 cows and heifers

## Yfirlit sýnatöku

Svæði	Fjöldi sýna	Fjöldi bóa	Kýr	Kvígur	Naut
Kjalarnesþing	47	2	46	0	1
Borgarfjörður	1361	14	538	154	669
Snæfellsnes	225	4	205	20	0
Vestfirðir	36	2	36	0	0
Húnaþing og Strandir	600	14	558	42	0
Skagafjörður	508	8	478	30	0
Eyjafjörður	1412	16	1246	166	0
S-þing.	312	8	277	35	0
Austurland	381	6	345	36	0
A-Skaft.	97	1	79	18	0
V-Skaft.	21	1	19	2	0
Rangárvallasýsla	672	11	534	138	0
Árnessýsla	2530	39	2191	328	11
<b>Samtals</b>	<b>8202</b>	<b>126</b>	<b>6552</b>	<b>969</b>	<b>681</b>

# Birth year of animals with DNA samples



# Analysis of DNA

- All animals genotyped with 50k SNP chip
- Done by GenoScan – Eurofins in Aarhus, Denmark
- Data available by August 2018

# Ph.D. study on genomic selection

- Egill Gautason, Ph.D. student at Aarhus University will commence his project on genomic selection 1.9.2018
- Project consists of four papers
  1. Genomic relationships with other breeds, with three main questions in mind:
    - a) Genomic differentiation between breeds
    - b) Preservation of linkage phase
    - c) Identification of shared IBD segments
  2. Effect of incorporating GWAS data on prediction accuracies of Icelandic cattle
    - a) To what extent do the same genes explain variation in breeds that have been isolated for over 1.000 years?
    - b) To what extent do the same polymorphisms explain variation in breeds that have been isolated for over 1.000 years?
    - c) To what extent can imputation, or weights on chromosome regions, derived from other breeds improve the prediction accuracies of a distantly related population?

# Ph.D. study on genomic selection

- Ph.D. project, cont.

3. Impact of genomic selection on inbreeding in a small population

- a) The rate of inbreeding is directly related to loss of genetic variation, impact of inbreeding depression, probability of favorable mutations surviving, rate of spread of deleterious alleles in a population, and predictability of future genetic gain

4. Monitoring and managing inbreeding in a small population undergoing genomic selection

- a) Currently, the most efficient way of managing inbreeding is by using optimal contribution selection (OCS). Optimal contribution selection considers contributions of animals over the long term as measured by the expected increase in coancestry. OCS allows maximization of genetic gain at a fixed rate of inbreeding.

# Discussion

- Genomic selection is biggest revolution in cattle breeding for 75 yrs.
- Has conquered all over the world in less than a decade
- Successful implementation of genomic selection is of utmost importance for sustainable breeding of the Icelandic dairy cattle.
  - Do – or die.

# Hrepphólar – Icelandic Dairy herd of the year 2018



Thank you for your attention!