Addressing over-prediction in ICBF dairy genomic evaluations
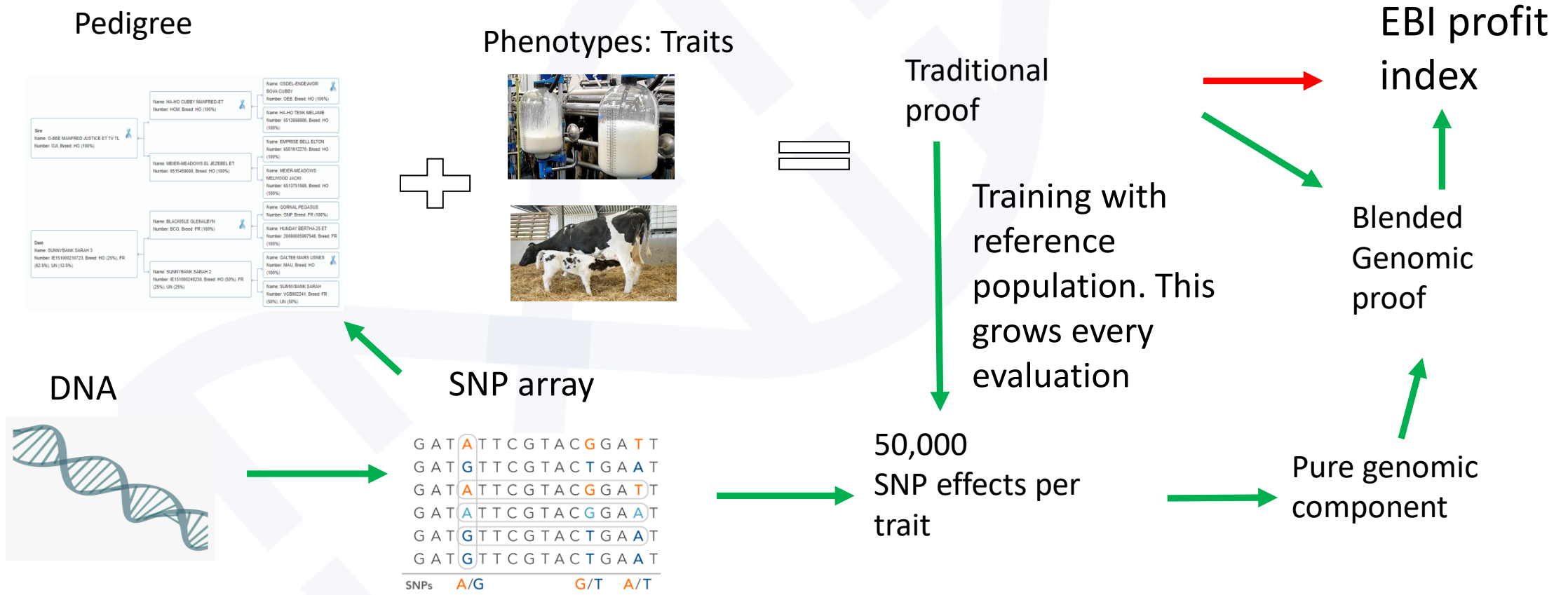
Date: 6th August 2020

AgTech - it's in our DNA

Overview

1. Outline of ICBF genomic evaluation process
2. Benefit of genomics
3. Impact of genomics on usage of young sires
4. Impact of genomics on generation interval
5. Challenges with large scale usage of genomic sires
6. Solution being implemented to address over-prediction
7. Impact on AI sires and genotyped animals

AgTech – it's in our DNA

1: Genomic Evaluations: The process

- Genomics combines pedigree based evaluations with genotypes => genomic proof

Pedigree

Phenotypes: Traits

Traditional proof

EBI profit index

DNA

SNP array

50,000 SNP effects per trait

Training with reference population. This grows every evaluation

Blended Genomic proof

Pure genomic component

AgTech – it's in our DNA

2: Benefit of genomics

- How is the benefit measured? Using well recognised validation techniques
  - ❖ Daughter data is censored for a group of sires and their prediction with no data is compared with their subsequent daughter proven proof (262 AI sires born since 2010 with a min of 50 daughters in milk)
- A correlation describes the strength of an association between 2 variables
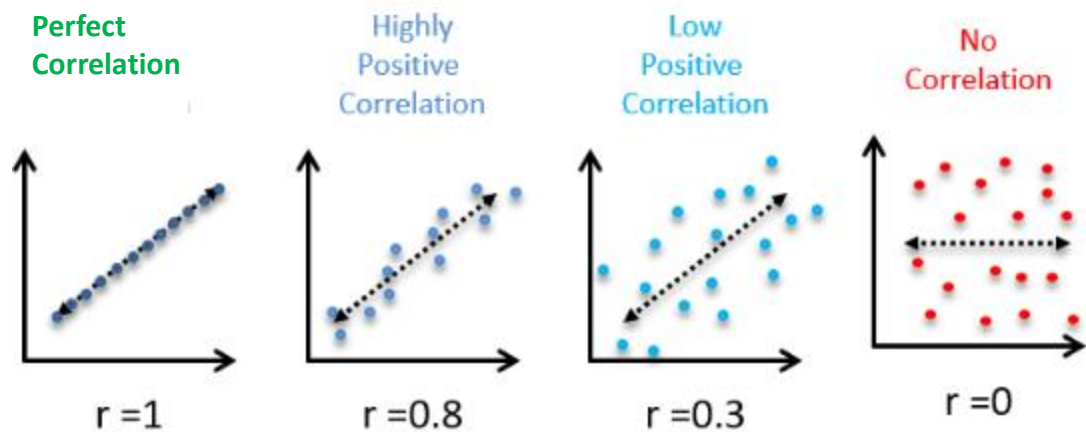
Traits	Parent average no genomics	Genomics with males only reference	Genomics with males & females reference
Milk	0.61	0.68	0.73
Fat	0.43	0.56	0.62
Protein	0.51	0.64	0.68
SCC	0.58	0.62	0.68
Calving interval	0.37	0.40	0.43

- Genomic rankings are a better predictor of the subsequent daughter proven rankings
- Highly heritable traits (Milk, fat, protein) predict better than lower heritable traits (fertility)
- Male and female trained genomics are better than male only. Females added to training in Jan 2020

3: Impact: Young Sire usage

Calving year	Average number of calves			Max number of calves		
	Sires = 263 2000_2008	Sires = 401 2009_2014	Sires = 363 2015_2020	2000_2008	2009_2014	2015_2020
1	135	191	282	925	1,743	1,924
2	135	605	1,046	3,275	13,937	20,754
3	121	546	671	9,396	27,323	27,323

- 2000- 2008: pre-genomics
- 2009 – 2014: early genomics era
- 2015-2020: later genomics era

- Genomic era has resulted in much heavier use of young sires

AgTech – it's in our DNA

4: Impact of genomics: generation interval

Generation Inteval change in AI sired HF calves
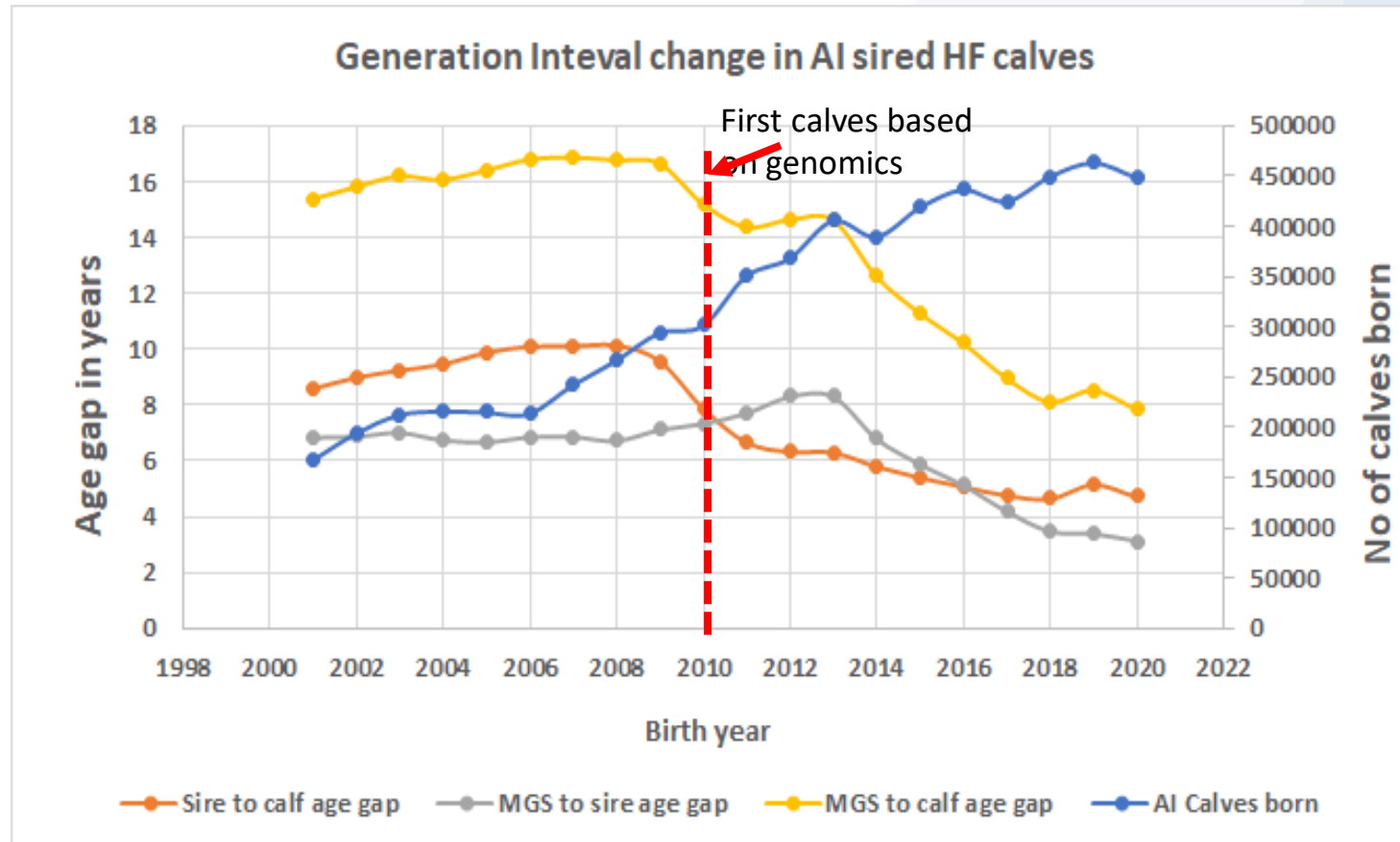
- Increase in level of AI sired calves

- Significant reduction in generation interval at both Maternal grand sire to AI sire level and at AI sire to calf level

# 5. Challenges with large scale adoption of genomics

	2016	2017	2018	2019	2020
Genotyped calves born	8,677	8,726	9,201	8,993	11,256
Sire to calf age gap	4.0	3.5	3.7	4.0	3.2
MGS to sire age gap	4.4	3.6	2.9	2.8	2.9
MGS to calf age gap	8.4	7.2	6.6	6.8	6.1
% of sires in Milk reference	98%	98%	96%	73%	19%
Sire Milk reliability excluding genomics	98%	97%	95%	81%	53%
% of sires in Fertility reference	98%	95%	84%	63%	17%
Sire Fertility reliability excluding genomics	90%	82%	76%	64%	39%

- Reduced generation interval is good for genetic gain:
  - ❖ = Younger sires and sires of sons
  - ❖ = But a wider relationship gap is emerging between young sires and the proven animals in reference. One of the known reasons for overprediction. Called "second generation" genomic selection.

ICBF.com

6. Solution being implemented

- Applied in US genomic evaluations
- Involves identifying the optimum weighting between genomic component and the parental average in order to
  - ❖ Maximise the prediction accuracy (correlation described earlier)
  - ❖ Minimise the over-prediction.
  - ❖ Each trait potentially has a different optimum
    - ❖ Milk traits: max weighting is 70% on pure genomic component
    - ❖ Fertility traits: max weighting is 50% on pure genomic component
    - ❖ Health (SCC): max weighting is 90% on pure genomic component
    - ❖ Calving already implemented since Spring 2020
- Weightings will be reviewed annually.

AgTech – it's in our DNA

7. Impact: AI sire and genotyped calves

Mean EBI by Year of birth
All AI sires
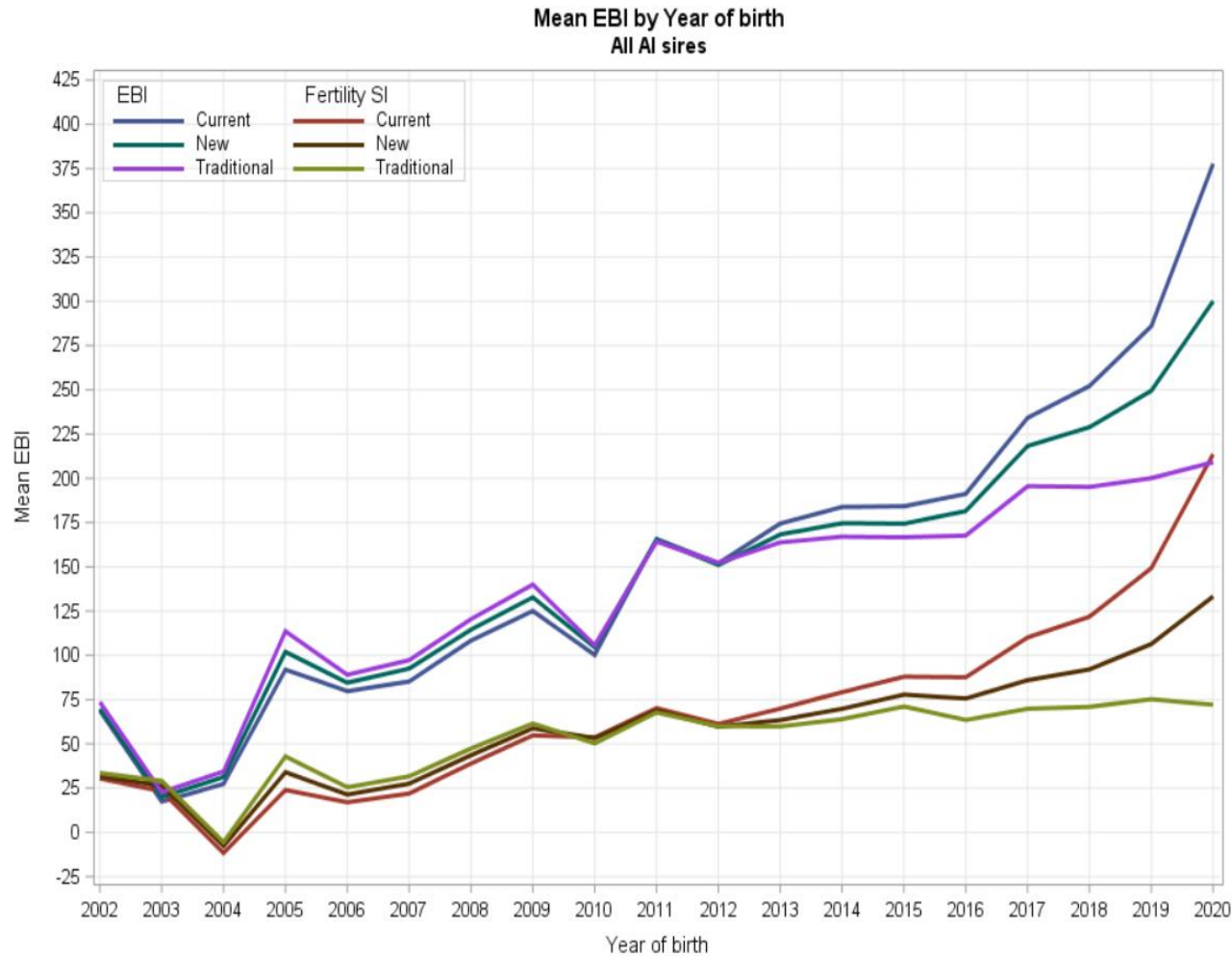
Year of birth	count	Average drop	Max change	New EBI	Correlation old v new
2010	138	€3	-€45 to €58	€100	0.97
2011	183	€1	-€46 to €45	€139	0.98
2012	171	€2	-€35 to €45	€132	0.97
2013	187	-€2	-€48 to €40	€143	0.97
2014	184	-€4	-€53 to €78	€147	0.95
2015	228	-€2	-€78 to €67	€139	0.96
2016	178	-€5	-€107 to €68	€144	0.96
2017	177	-€8	-€74 to €54	€167	0.97
2018	115	-€22	-€74 to €50	€209	0.94
2019	78	-€37	-€108 to €35	€249	0.9
2020a	136	-€78	-€125 to €-33	€300	0.85
2020b	21,274	-€31	-€136 to €77	€216	0.93

- 2020a = AI procured calves
- 2020b = All genotyped calves

Summary

- Internationally recognized validation tests applied to Irish data show that genomics outperforms conventional parental average predictions

- As the adoption of the technology has grown over years the overprediction has become a bigger issue

- Solution being applied is published and implemented in the largest genomic evaluation in the world (US)

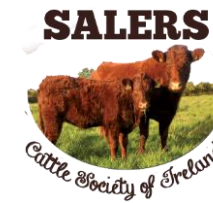- Changes will be implemented in the October evaluation run (6th Oct publication date)

AgTech – it's in our DNA

Our Farmer & Government Representation

Our AI & Milk Recording Organisations

Our Herdbooks

Acknowledging Our Members