IRISH CATTLE BREEDING FEDERATION

Genomic selection for Irish beef cattle

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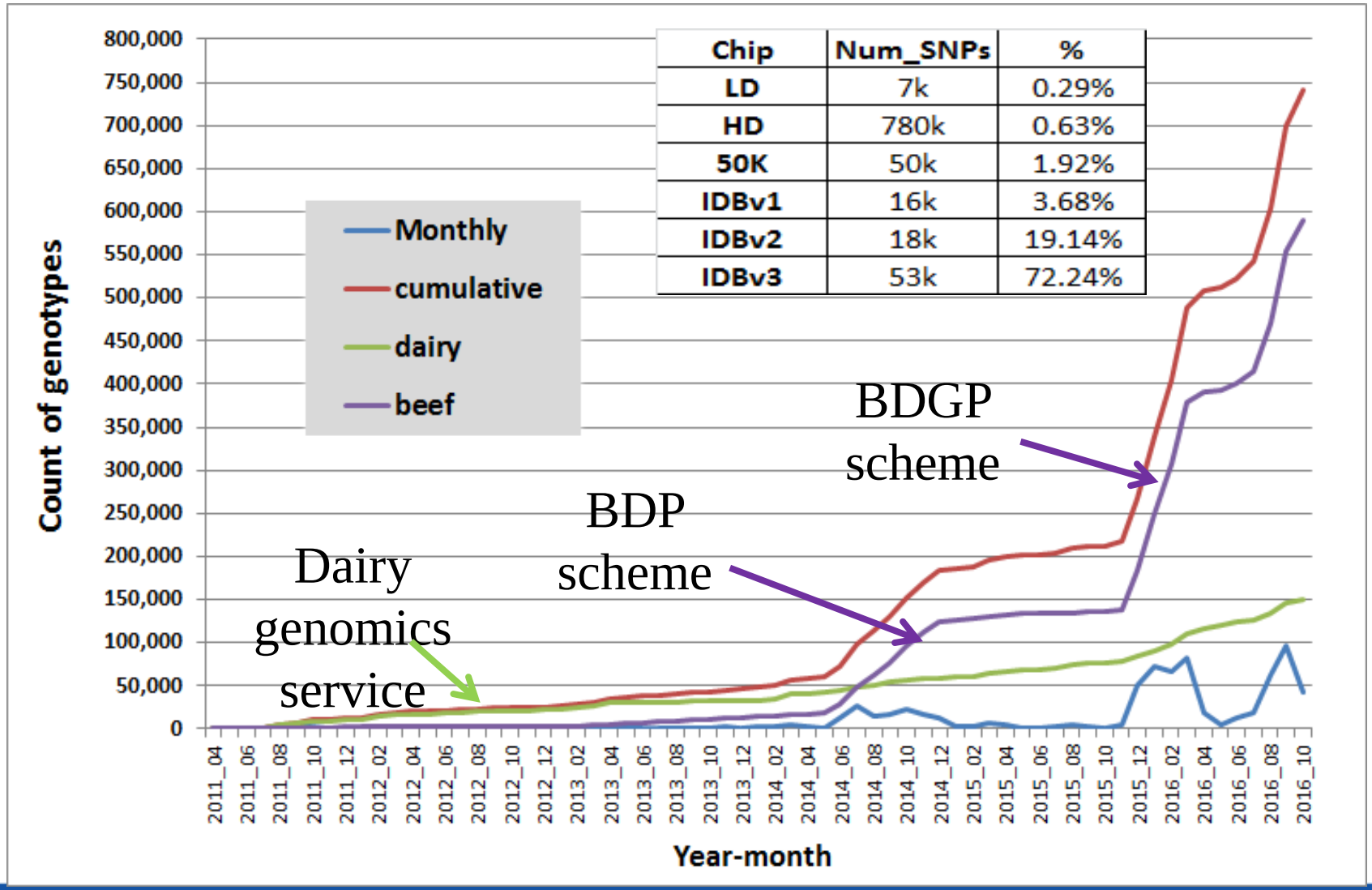
Genotyping history at ICBF



Evolving genotype quality control process

Parentage prediction based on 800 SNPs
200 ISAG (minus 5, clustering and low MAF)
605 additional based on high MAF >45% across 50 breeds in reference population

460,000 animals put through prediction process with either no sire or sire not genotyped
130,000 predicted
Last 6 months 76k predicted out of 172k (44%)

Sire error rate 9.5%
5% in pedigree animals

Characteristics of genotyped animals July'16 = 500,033)

breed/breed cross	Count
Holstein_Friesian	55,258
Limousin	28,943
Charolais	26,777
Limousin_Holstein	25,212
Limousin_Charolais	23,346
Charolais_Limousin	21,569
Limousin_Simmental	19,408
Angus_Holstein	14,619
Limousin_Angus	14,246
Limousin_Hereford	14,235
Angus	13,908
Limousin_unknown	13,642
Holstein	11,627
Charolais_Simmental	11,617
Hereford_Holstein	10,715
Limousin_Belgian Blue	10,385

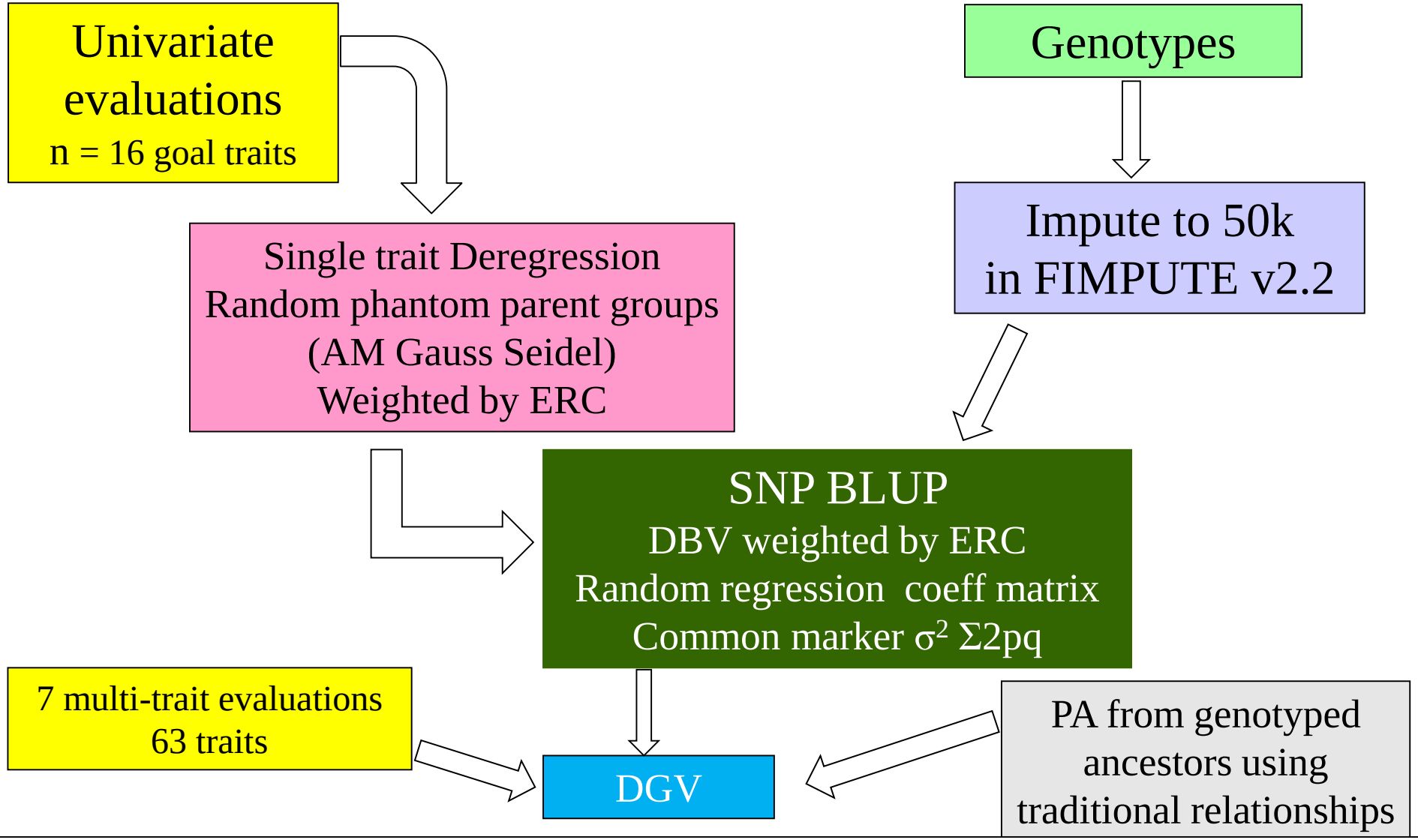
Category by genotyped pedigree	Count
Sire also genotyped	219,663
No parent genotyped, sire known	129,985
No parent genotyped, unknown sire	80,566
Both parents genotyped	73,945
Dam also genotyped sire known	21,170
Dam also genotyped, unknown sire	7,761

Category by sex	Count
AI sire	4,133
Males with progeny	45,064
Male with NO progeny	62,963
Female with progeny	303,358
Female with NO progeny	117,572

Approach to Genomic Evaluations

- Mix99 software used at ICBF since 2008.
- Preference to develop Single step evaluation
  - Convergence issues for some traits, memory and disk space
- "Hard" deadline of August 2016 for delivery of "official" genomic evaluations. Expectation of genomics for all traits
- **Farmers needed genomic evaluations to make decisions ahead of 2018 and 2020 BDGP scheme deadlines.**
- Decision in May 2016 to proceed with 2-step, NOT 1-step.
- Two step GBLUP applied successfully for Irish dairy cattle since 2009.

2-Step Genomic Evaluation (Mix99)



Blending using selection index methodology

(Van Raden et al. 2009)

Informative animals by trait

	Effective record contribution distribution (ERCs) for genotyped animals					
Trait	Total	1 - 5	5 - 10	10 - 20	20 - 50	> 50
calving difficulty	330,510	297,554	10,398	10,809	8,906	2,843
calf mortality	291,315	260,122	13,019	10,322	5,506	2,346
maternal calving difficulty	335,371	201,929	117,594	12,832	963	2,053
gestation	80,928	77,107	1,147	658	794	1,222
carcass fat	53,308	39,548	5,744	4,880	2,001	1,135
carcass conformation	49,087	35,614	5,798	4,721	1,843	1,111
carcass weight	43,298	30,337	5,816	4,507	1,576	1,062
cow survival	234,740	184,410	44,703	4,278	607	742
cull cow weight	29,861	27,633	587	473	525	643
calving interval	210,767	191,053	17,466	1,200	445	603
cow live weight	16,727	13,688	1,648	707	406	278
cow milk score	234,597	218,721	15,062	375	200	239
docility	47,478	42,746	3,006	1,206	295	225
age 1st calving	49,386	48,246	476	262	215	187
maternal wean wt	81,564	64,317	14,321	2,585	171	170
feed intake	444	435	9			

Validation carcass wt AI sires

- AI sires (n = 524) with first progeny born in 2012 had all their progeny phenotypes

	Validation category		
	Holstein	ALL Beef breeds	Charolais
Current Reliability	>95%	>95%	>85%
N	36	49	16
	Correlation with current deregressed univariate ebv		
EBV uni validation	0.750	0.891	0.590
EBV multi validation	0.719	0.899	0.584
DGV validation	0.790	0.910	0.628
GEBV validation	0.788	0.893	0.674
% of bulls whose sires were in SNP BLUP	100%	49%	56%

Next steps

- Validation for different selection candidates
  - AI sires, young pedigree males, commercial females
- Single step solution with research partners
  - LUKE, WUR, Iowa State
- Genetic disease reporting and sire advice
  - 86 genetic diseases/traits on IDBV3.
- Tag solution to allow both health screening (compulsory for BVD) and genomic selection from single sample at birth (currently separate tissue tag)
- Whole Genome Sequencing to identify potential new SNPs on next version of IDB chip


Thanks for listening!