Selection for novel traits: an international genomics perspective
(Experience from dairy)

Donagh Berry

Teagasc, Moorepark, Ireland.

BIF Conference, Nebraska, June 2014

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Molecular genetics 101

- DNA is the building blocks of genes
- Genes (+management) determine performance
- Everyone's DNA is (subtlety) different
  - Except twins
- The DNA you're born is what you die with
- DNA in your big toe is the same as your eye
  - or in the follicles of your hair

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So….

- If we knew the effect of each piece of DNA on performance then….
- DNA from the hair sample of a calf could predict future performance!

- Simple???
  - Cattle have ~3 billion pieces of DNA
  - Many million differ between individuals
  - …and they interact!!!

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Problem

- Need HUGE datasets to quantify the "effect" of each DNA variant on performance
  - Collaboration

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Analogy

Feed 1   Feed 2   Feed 3   Feed 36,900,000

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Problem

- Need HUGE datasets to quantify the "effect" of each DNA variant on performance
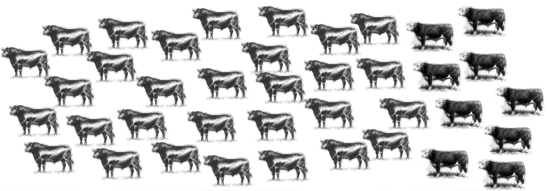 - Collaboration
- Costs a lot of money to generate genotypes
  - Collaboration
- Costs even more money to generate field data (phenotypes) especially for novel traits
  - Collaboration
- Algorithms, breeding schemes, chip design….
  - Collaboration

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Size matters!!

h² 0.03 (fertility)
h² 0.20 (dystocia)
h² 0.40 (carcass)
h² 0.90 (AI bulls)
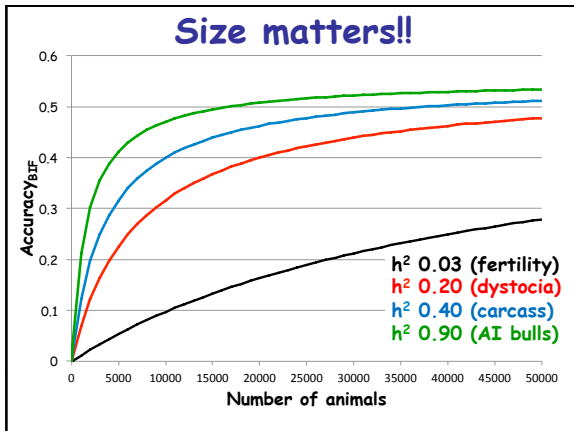
Genomic selection in dairy

- **Launched in several countries in 2009**
- **~60% of semen sold is from genomic bulls**

- **Retrospective analysis across (almost all) countries shows that it works**
  - **Up to 30% more accurate that traditional evaluations**
  - **Seems to be over-estimation of proofs for genomically tested animals**

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Why less uptake in beef?

1. Breed(s)
2. Effective population size
3. AI usage
4. Data recording
5. International genetic evaluations

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Breed(s)

- **Holstein-Friesian predominates temperate dairy populations**
- **DNA effects can differ between breeds**

Holstein   Dystocia   Charolais

Purfield et al., (2014)

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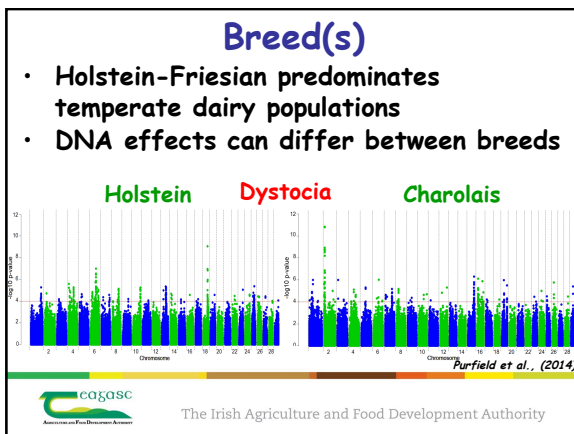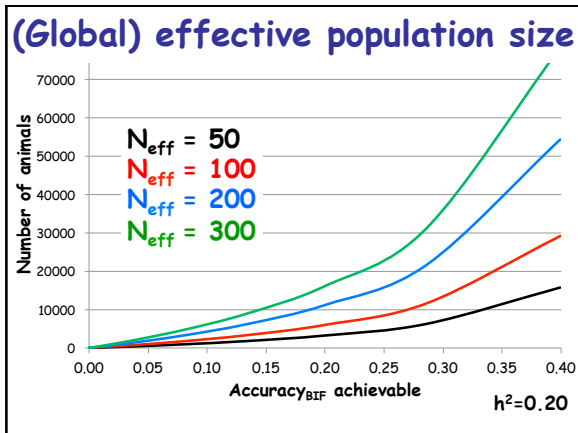
Why less update in beef

1. Breed(s)
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(Global) effective population size

N_{eff} = 50
N_{eff} = 100
N_{eff} = 200
N_{eff} = 300

Number of animals

Accuracy$_{BIF}$ achievable

h^2=0.20

Why less uptake in beef?

1. Breed(s)
2. Effective population size
3. **AI usage**
4. Data recording
5. International genetic evaluations

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Accuracy of genomic evaluations

Sires

Accuracy$_{BIF}$

h^2 0.03 (fertility)
h^2 0.20 (dystocia)
h^2 0.40 (carcass)
h^2 0.90 (AI bulls)

Ireland (>year 1985)
4160 dairy AI sires
(2374 high reliability)
2640 beef AI sires
749 high reliability

Number of animals

Why less update in beef

1. Breed(s)
2. Effective population size
3. AI usage
4. **Data recording**
5. International genetic evaluations

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Data recording

"In the age of the genotype the phenotype is king!!"
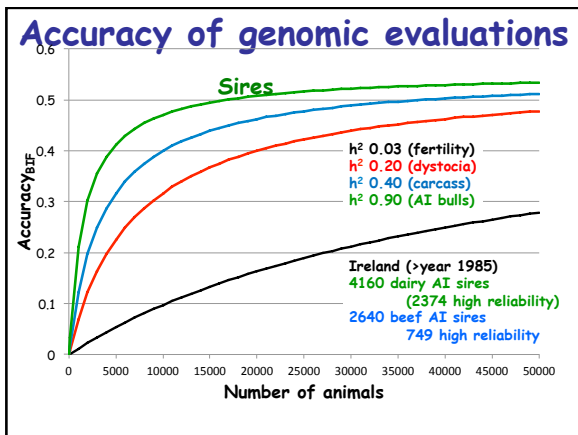
Mike Coffey, SRUC

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Why less uptake in beef?

1. Breed(s)
2. Effective population size
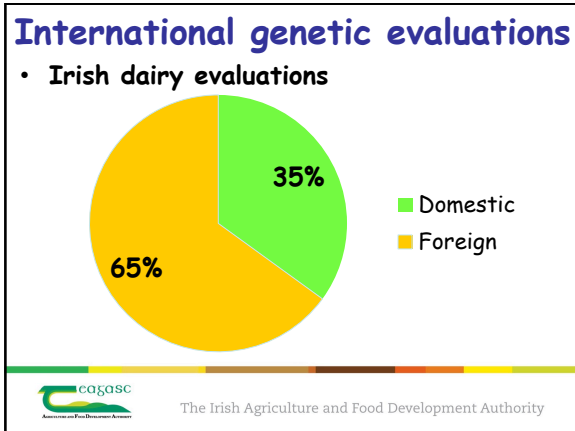3. AI usage
4. Data recording
5. **International genetic evaluations**

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International genetic evaluations

- **Irish dairy evaluations**

35%

65%

■ Domestic
■ Foreign

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Solution??

- **Collaboration!**
    1. Share information on animals genotyped/have DNA
    2. Share genotypes
    3. Share phenotypes
    4. Share genomic keys
    5. Pan-global list of bulls
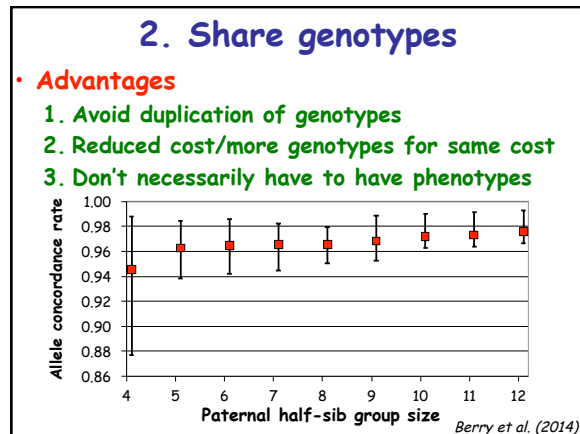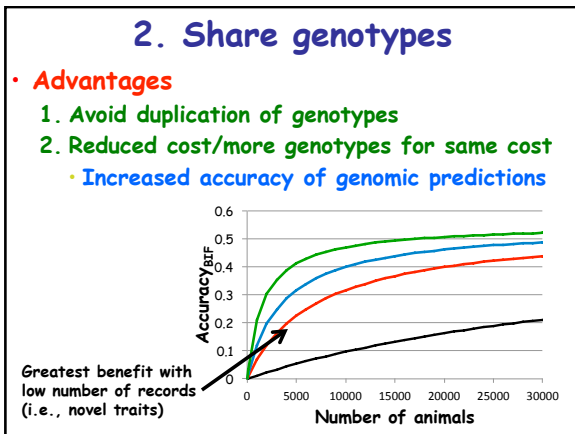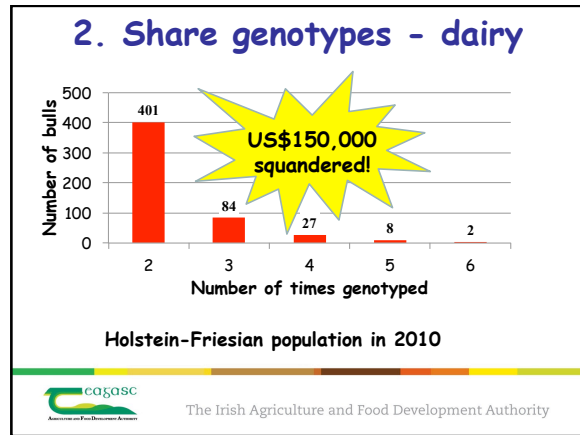
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1. Information on genotyped animals

ANIMAL_NAME	ID	DOB	Brd	IRL	UK	FRA
BLUEBELL AIGLON	CHLFRAM007185101623	24/01/1985	CH	Want		
COMMANDEUR	CHLFRAM007187126401	01/01/1987	CH	Have DNA		
BANDIT	LMSFRAM008786003322	14/02/1986	LM	Want		Illumina_54K
TANHILL RUMPUS	LMSIRLM000000FBR092	24/04/1980	LM		Illumina_HD	
ESPOIR	LMSFRAM008789003720	02/03/1989	LM			
HIGHLANDER	LMSFRAM001692111209	01/01/1992	LM	Illumina_HD		Illumina_54K
OMAR	LMSFRAM001930098242	24/12/1998	LM	Illumina_HD		Illumina_54K
KILKELLY DUKE	AANIRLM272061330257	01/03/2007	AA	Illumina_HD		
DELFUR T-BONE	SIM6BRM523461601799	09/04/2006	SI	Illumina_HD		

Email: donagh.berry@teagasc.ie

- **Advantages**
    1. Engage with owners of genotyped animals
        - No competitive advantage of genotyping a animal twice
- **Disadvantages**
    1. Can't think of any!!!
    2. US dairy genotypes (https://www.cdcb.us/eval.htm)

2. Share genotypes - dairy

US$150,000 squandered!

401

84

27

8

2

Number of bulls

Number of times genotyped

Holstein-Friesian population in 2010

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2. Share genotypes

- **Advantages**
    1. Avoid duplication of genotypes
    2. Reduced cost/more genotypes for same cost
        - Increased accuracy of genomic predictions

Accuracy$_{BIF}$

Number of animals

Greatest benefit with low number of records (i.e., novel traits)

2. Share genotypes

- **Advantages**
    1. Avoid duplication of genotypes
    2. Reduced cost/more genotypes for same cost
    3. Don't necessarily have to have phenotypes

Allele concordance rate

Paternal half-sib group size

Berry et al. (2014)

2. Share genotypes

- **Advantages**
  1. Avoid duplication of genotypes
  2. Reduce cost/increase ~ same cost
  3. ...
  4. Inter...
     - SNPchip ...
     - Genotype-by-sequencing (GBS)
  5. Conversion from microsatellites to SNPs for parentage

Precedence already there with sequence

2. Share genotypes

- **Disadvantages**
  1. Little to gain in large populations???

Hands up who's here??

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2. Share genotypes

- **Disadvantages**
  1. Little to gain in large populations???
  2. Cost a lot of money
     - Cost others the same money!
     - Equal genotype contributions/monetary contribution
  3. Should be related to the candidate population

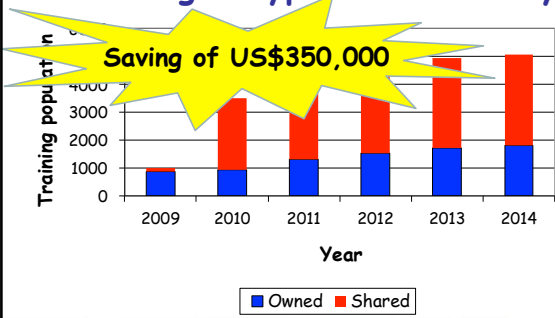The Irish Agriculture and Food Development Authority

2. Share genotypes

- **Set the record straight!**
  - (Untrue) perception that sharing only benefits the smaller population
- **Accuracy of genomic predictions**
  a) Size of reference population
  b) Effective population size
  c) Heritability
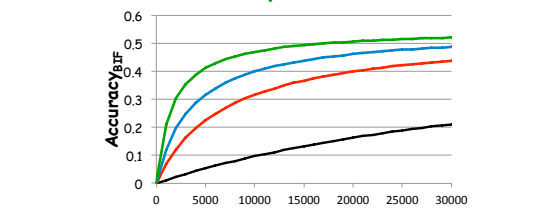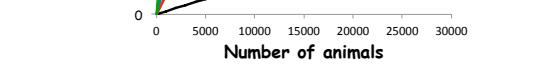 d) Relationships between reference and candidate population

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2. Share genotypes – Irish dairy

Saving of US$350,000

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3. Share phenotypes

- **Advantages**
  1. Larger reference population
  2. Particularly important for novel traits
  3. Precedence there with INTERBULL/ INTERBEEF/Breedplan

3. Share phenotypes

- **Disadvantages**
  1. **Very costly to generate (novel) phenotypes**
  2. **Forgoing competitive advantage**
     - **Is there much competitive advantage with a Accuracy$_{BIF}$ of 0.05??**
     - **Agreements could be based on equal contribution/monetary contribution**
       - **Value dependent on current population size**
     - **INTERBULL in dairy (no issue!)**
     - **INTERBEEF/Breedplan in beef**

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4. Share genomic keys

- **Genomic key is the SNP effects**

SNP	Dystocia	Birth wt.	Yearling wt.	Carcass
1	+0.02	+0.02	+0.02	+0.53
2	-0.03	+0.19	-0.07	-0.09
3	+0.12	+0.02	+0.02	+0.02
4	+0.23	+0.13	+0.05	+0.07
5	-0.09	+0.19	-0.09	+0.19
6	+0.19	+0.03	+0.02	+0.02
7	+0.05	+0.02	+0.02	+0.00

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4. Share genomic keys

- **Advantages**
  1. **Quantify robustness across different systems/populations**
  2. **Aid in refining (i.e., more supervised) genomic regions of importance**
     - **Different datasets – breeds, systems**
     - **Different statistical approaches**
     - **Should be validated in other population**
- **Disadvantages**
  1. **Cost money to generate**
     - **Key will soon be obsolete**

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5. Pan global bull list

- **Genetic connectedness is paramount to estimation of genetic correlations between environments**
  - **Genotype-by-environment**
  - **Issue even in dairy**
- **Could identify a pan-global bull list per breed**
  - **Not every population must use every bull**
  - **Can use algorithms developed in sheep**

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5. Pan global bull list

- **Advantages**
  1. **Improved genetic connectedness**
     - **Especially important for novel traits**
     - **Important if using multi-country genetic/ genomic evaluations**

- **Disadvantages**
  1. **Reaching a consensus on bull list**

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Case study – dairy feed intake

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Data

International genetic evaluations for feed intake in dairy cattle through the collation of data from multiple sources

D. P. Berry,*[1] M. P. Coffey,† Z. Wang,¶ D. Spurlock,** K.

- **224,174 feed intake records**
  - **10,061 parity 1 to 5 records**
  - **6,953 cows**
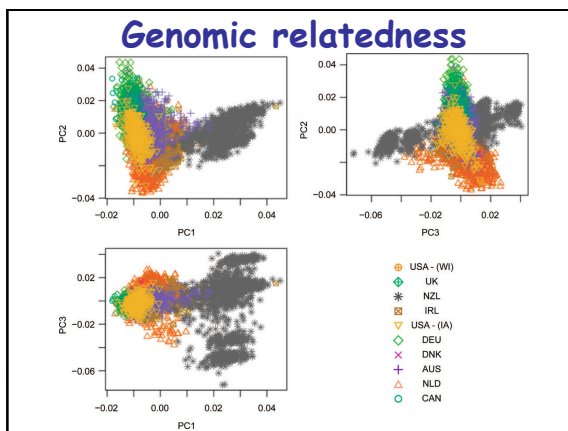 - **+1,784 growing heifers**
  - **9 countries**

Imputation of genotypes from low density (50,000 markers) to high density (700,000 markers) of cows from research herds in Europe, North America, and Australasia using 2 reference populations

J. E. Pryce,*†‡[1] J. Johnston,§ B. J. Hayes,*†‡ G. Sahana,# K. A. Weigel,ǁ S. McParland,¶ D. Spurlock,** N. Krattenmacher,†† R. J. Spelman,‡‡ E. Wall,§§ and M. P. L. Calus##

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Genomic relatedness

Legend:
- ⊕ USA - (WI)
- ⊕ UK
- ✳ NZL
- ⊠ IRL
- ▽ USA - (IA)
- ◇ DEU
- ✕ DNK
- + AUS
- △ NLD
- ○ CAN

Genetic parameters

Country	N	Mean (kg DM/d)	Heritability
Cows			
All	10,641	19.7	0.34 (0.03)
Canada	411	22.2	0.19 (0.14)
Denmark	668	22.1	0.52 (0.12)
Germany	1141	20.2	0.08 (0.06)
Iowa	398	23.5	0.41 (0.14)
Ireland	1677	16.7	0.41 (0.10)
NLD	2956	21.4	0.39 (0.05)
UK	2840	17.4	0.31 (0.06)
Wisconsin	447	24.9	0.24 (0.16)
Heifers			
Australia	843	8.3	0.20 (0.11)
New Zeal.	941	7.6	0.34 (0.12)

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Genetic correlations

Region	North-America	EU high-input	EU low-input
North-America			
EU high-input	0.76 (0.21)		
EU low-input	0.79 (0.38)	0.84 (0.14)	
Grazing	0.14 (0.43)	0.33 (0.20)	0.57 (0.43)

- **Similar variance components across countries**
- **GxE seems to be an issue with grazing**

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Conclusions

- **(Almost) everyone can undertake genomic selection on their own**
- **But will it be any good??**

- **Collaboration is the best approach to achieve more rapid genetic gain**
- **Is there currently fear of an international "take-over"**
  - **Why should genomics change this?**

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