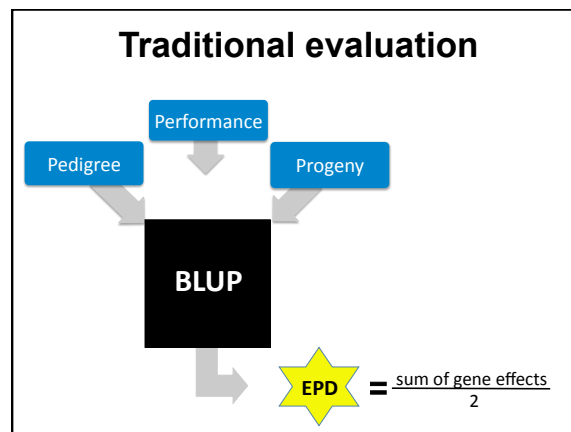
  
**The promise of  
genomics for beef  
improvement**

Daniela Lourenco  
Keith Bertrand

Heather Bradford, Steve Miller, Ignacy Misztal

BIF - Athens, GA - 06/01/2017



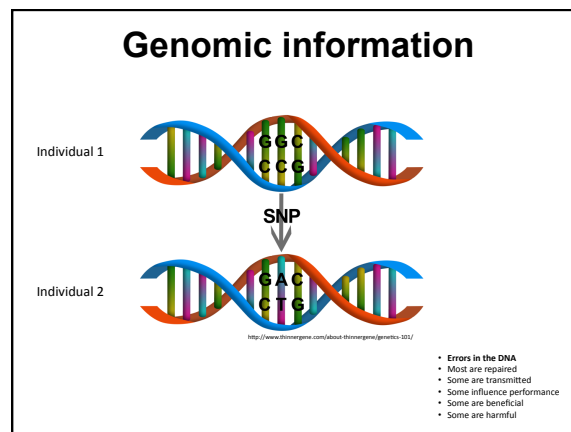
**What if we could know the  
genes that affect the traits?**

↓

**Could we have more accurate  
EPD?**


↓

**Genomics in livestock breeding**



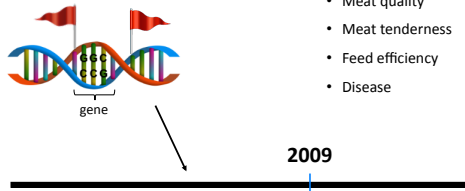
**Genomic information**

SNP used as markers  
for GENES  
or  
regions in the genome that contain genes = QTL



**Genomic information**

**"Marker Assisted  
Selection - MAS"**



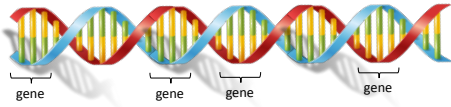
gene

2009

- Expensive!!!
- Few SNPs
- Meat quality
- Meat tenderness
- Feed efficiency
- Disease

## Why MAS did not quite work?

- Traits of interest are polygenic



Thousands of genes → Thousands of SNP

## What if we could use thousands of SNPs?

Meuwissen  
Hayes  
Goddard

2001

2009

## The promises...

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### Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps

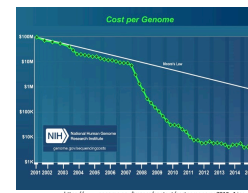
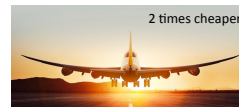
T. H. E. Meuwissen,<sup>a</sup> B. J. Hayes<sup>a</sup> and M. E. Goddard<sup>b,c</sup>

<sup>a</sup>Research Institute of Animal Science and Health, 8200 AB Lelystad, The Netherlands, <sup>b</sup>Victorian Institute of Animal Science, Attwood 3049, Victoria, Australia and <sup>c</sup>Institute of Land and Food Resources, University of Melbourne, Parkville 3052, Victoria, Australia  
Manuscript received August 17, 2000  
Accepted for publication January 17, 2001

- We can use thousands of SNPs
- Genotyping thousands of SNPs will become cheap
- We can calculate EPD based on SNPs (e.g., MBV)
  - Without own performance or progeny records
- Accuracy of predicting EPD more than double (0.40 vs. 0.85)
- Increase in accuracy for traits with low  $h^2$  and hard to measure
- We can select animals earlier (reducing generation interval)

## Cost of genotyping

What is 100,000 cheaper NOW than in 2001?



## Peak of excitement

Cheaper  
genotyping  
2009



Who would go first?

2009

## Dairy Industry

First genomic evaluation in  
2009



50K SNP + parent information  
No daughters with records

Net merit = \$792

7 bulls > \$700

Evaluation in 2012



Parent information +  
100s of daughters with records

## The promises...

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### Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps

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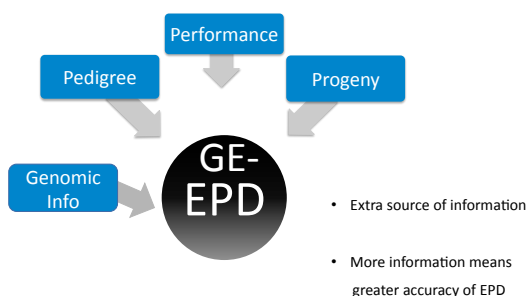
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## Genomics in beef cattle

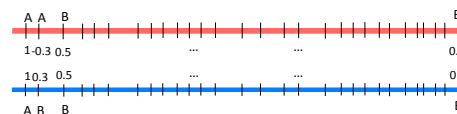
- 2009-2010: Angus
- 2012: Simmental, Hereford, Red Angus, Limousin
- 2013-2016: Charolais, Santa Gertrudis, Shorthorn, Brangus, Guelbvieh

## How is genomic incorporated?



## How is genomic incorporated?

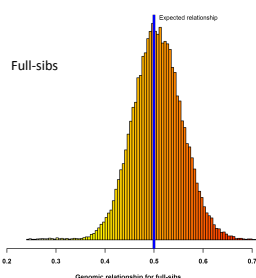
### 1. SNP effects



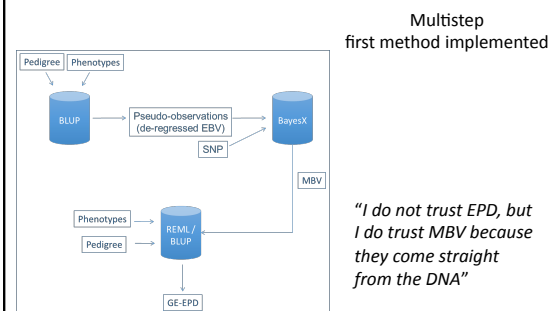
$$MBV = 1 + 1 - 0.3 + 0.3 + 0.5 + 0.5 + \dots + 0.6 + 0.6 = 5.7$$

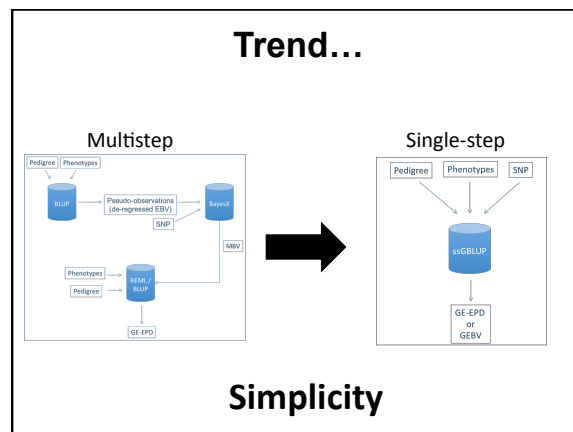
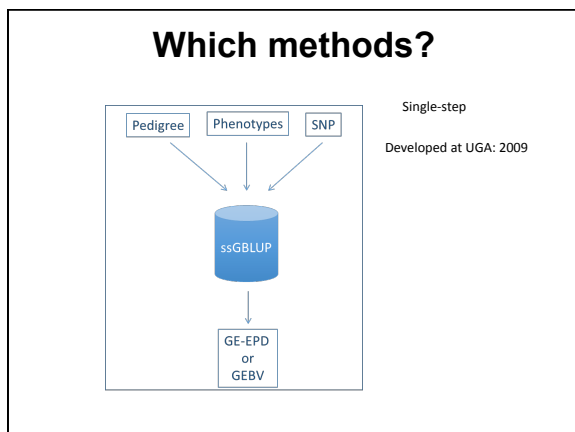
## How is genomic incorporated?

### 2. Better relationships




## Which methods?








### Which software to use for single-step?

UGA: blupf90 family      Theta Solutions: Bolt

  
Keith

  
Ignacy

  
Daniela

  
Bruce   Dorian   Daniel

### The biggest promise

Increase (double) accuracy of predicting EPD  
Meuwissen et al., 2001

➡

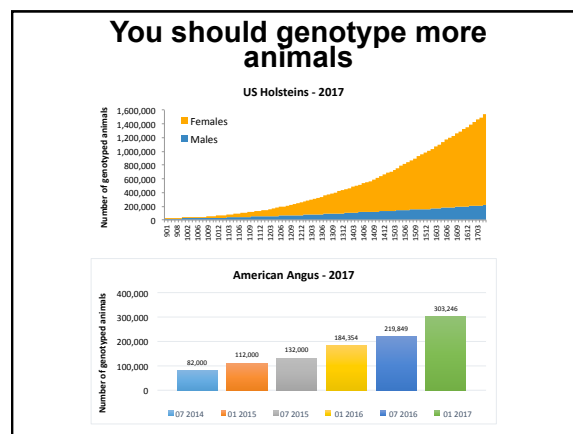
## Beef cattle?

### Accuracy gains in beef

Trait	Breed	number of genotyped animals	EPD accuracy	GE-EPD or MBV accuracy	Gain %	Author
Simulated	-	2,000	0.40	0.84	110	Meuwissen et al., 2001

Small gain due to small number of genotyped animals  
~ 2,000

"You should genotype more animals"



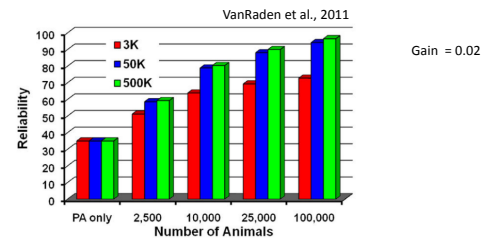
## Accuracy gains in beef

Trait	Breed	number of genotyped animals	EPD accuracy	GE-EPD or MBV accuracy	Gain %	Author
Simulated	-	2,000	0.40	0.84	110	Meuwissen et al., 2001
Growth	Angus	2,000	0.29	0.32	10	Lourenco et al., 2015
Growth	Angus	33,000	0.29	0.35	21	Lourenco et al., 2015

"You should genotype more animals" ✓

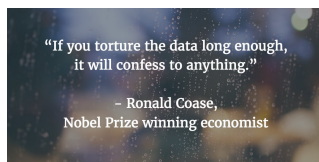
"You are using only 50k SNP... not enough... you should use over 300,000"

## Accuracy gains 50k vs. 500k



"You are using only 50k SNP... not enough... you should use over 300,000" ✗

## Sequence the whole genome



Sequence vs. genotyping

> 30M

50k

## Sequence information for predictions

### Overall gains in REL

Trait group	60K + 17K
Production	1.5
Health	2.5
Calving	3.3
Type	3.2
All traits	2.7

Interbull annual meeting, Puerto Varas, Chile – October 25, 2016 (18)

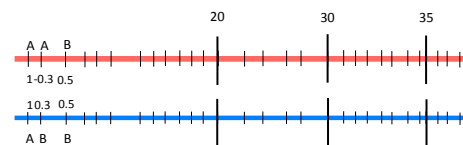
VanRaden et al., 2017

## Small gain with more SNP

- Better relationships: already accurate with 50k
- SNP effects: only more SNP to estimate effects without increasing phenotypes



## Why Meuwissen et al. (2001) got it, but we did not?



- Assumed SNP with large effect
- Large SNP explained large proportion of genetic variance

Traits of interest are polygenic: several genes with small effect

## The promises...

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### Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps

T. H. E. Meuwissen,<sup>a</sup> B. J. Hayes<sup>a</sup> and M. E. Goddard<sup>1,2</sup>

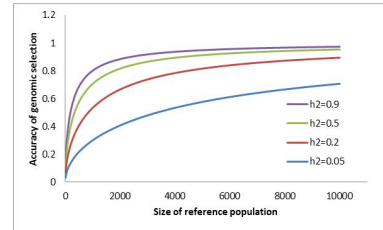
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- Increase in accuracy for traits with low  $h^2$  and hard to measure ✓
- We can select animals earlier (reducing generation interval) ✓

## Increase in accuracy for traits with low $h^2$ and hard to measure



Kor Oldenbroek and Liesbeth van der Waaij, 2015

- Increase is small
- Need more genotypes and phenotypes

## The promises...

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### Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps

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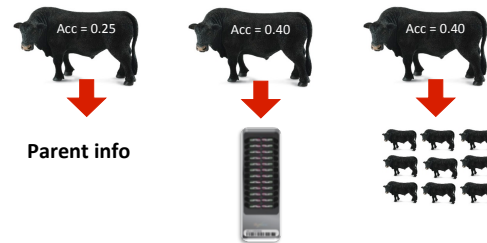
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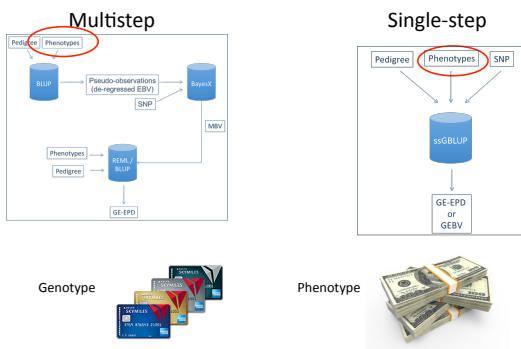
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## We can select animals earlier

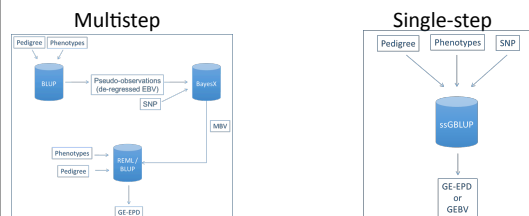


Does it mean we do not need to collect phenotypes?

## There is no magic here



## "I like GE-EPD, but I want to see MBV"



MBV = Sum of SNP effects

GE-EPD = MBV + Parent Average + Performance + Progeny

**More information = higher accuracy**

## Millions of genotyped animals How is it possible?

More information = higher accuracy



More genotypes, phenotypes, pedigree

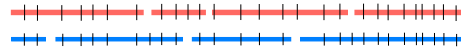


Challenge



## Millions of genotyped animals How is it possible?

- DNA inherited in blocks



- If we trace those blocks...few ancestors

4,000 blocks = 4,000 animals = 90% of variance

+10,000 blocks = +10,000 animals = 99% of variance

## Millions of genotyped animals How is it possible?

Single-step before  
2015




Max. load  
150,000

Single-step now




Max. load  
Keep genotyping...


## New single-step = single-step with APY

- American Angus 

- 300k genotyped animals
- 10M pedigree
- All traits

- US Holsteins 

- >250k genotyped animals
- Millions in pedigree
- Several traits

- USDA  US Holsteins
  - 760k genotyped animals
  - 23M pedigree
  - 37M phenotypes
  - Production traits

## Keep in mind

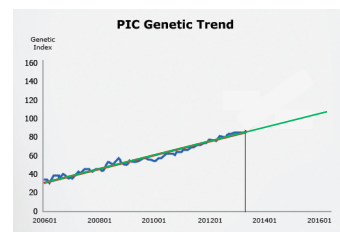
- Promises were higher than the realized
- We can use genomic information to better estimate EPD
- Accuracy of EPD increases (not astronomically)
- We can select animals earlier reducing generation interval
- Keep genotyping and phenotyping if you want more reliable GE-EPD

Genetic gain = (selection intensity \* accuracy \* genetic SD) / generation interval

$$\Delta G = \frac{i r \sigma_a}{L} x^{\delta}$$

How much you trust in  
the genetic advisor

## Keep in mind



Expected trend if no changes  
in 2013

