How Whole-Genome Sequencing Will Impact Selection Decisions

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Do not run through life
so fast that you forget
not only where you have been,
but also where you are going.
-from "Peace"

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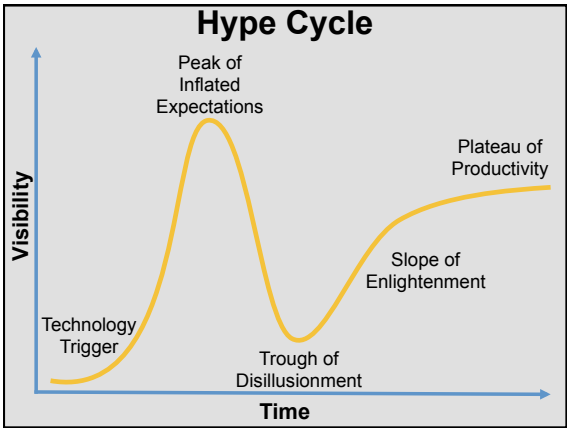
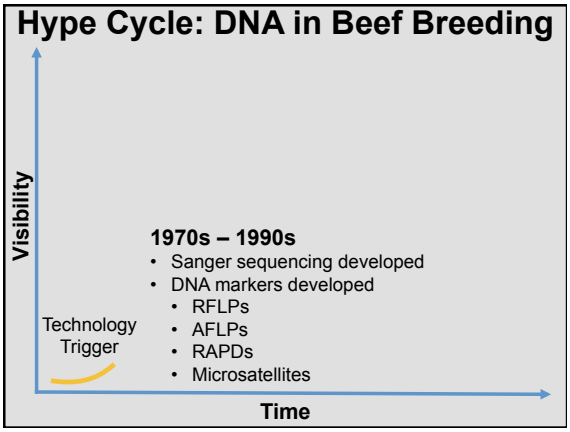
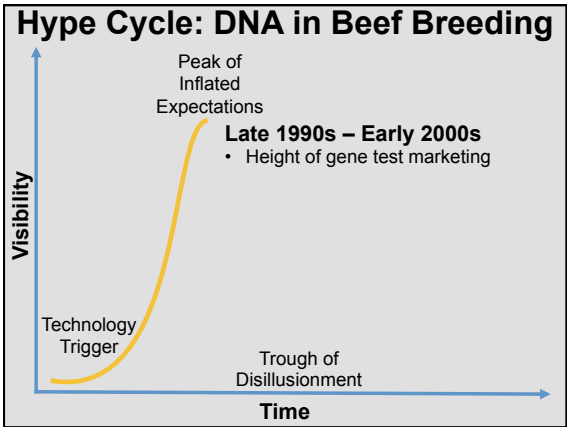
Hype Cycle



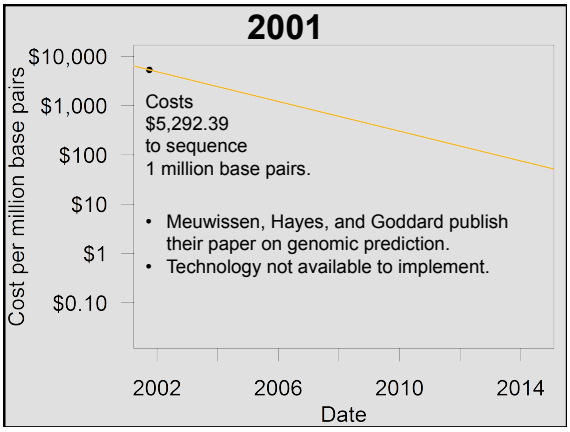
Hype Cycle: DNA in Beef Breeding

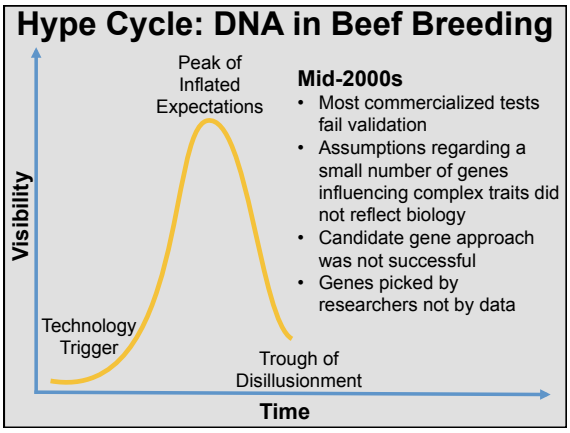


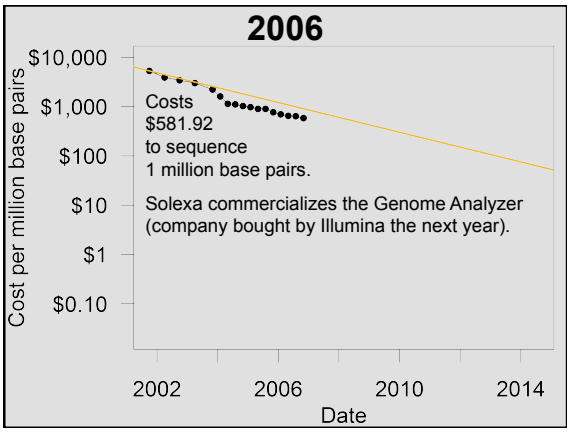
Hype Cycle: DNA in Beef Breeding

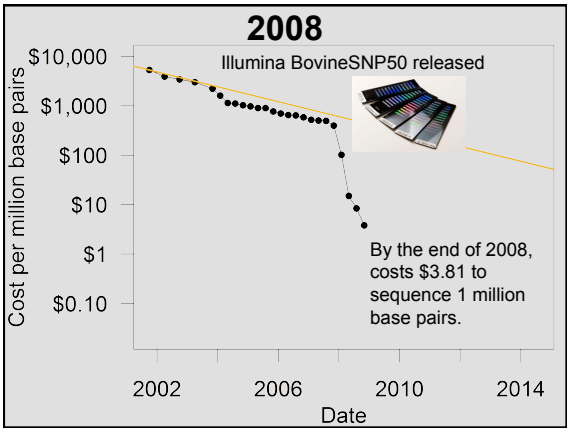


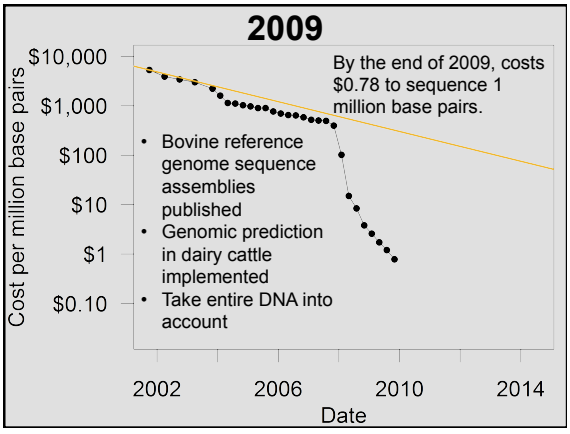
2001

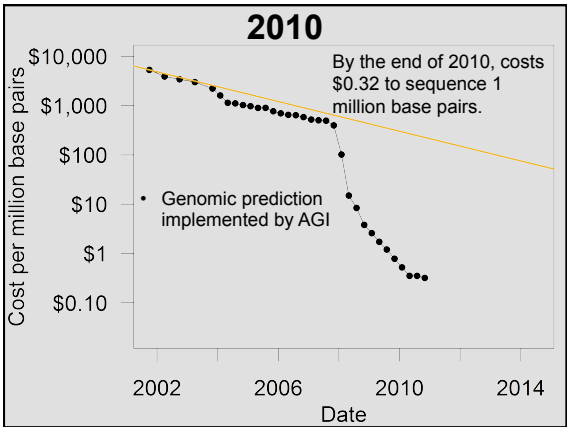


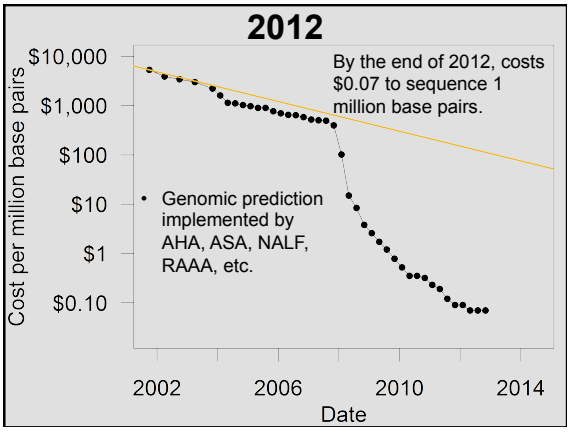

Hype Cycle: DNA in Beef Breeding
Peak of Inflated Expectations
Mid-2000s
• Most commercialized tests fail validation
• Assumptions regarding a small number of genes influencing complex traits did not reflect biology
• Candidate gene approach was not successful
• Genes picked by researchers not by data
Visibility
Technology Trigger
Trough of Disillusionment
Time

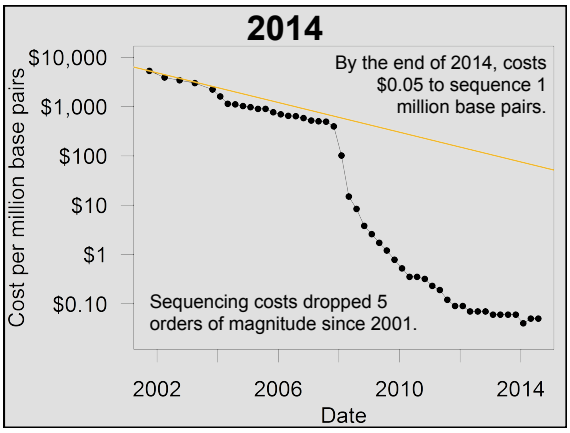

2006
Cost per million base pairs
$10,000
$1,000
$100
$10
$1
$0.10
Costs $581.92 to sequence 1 million base pairs.
Solexa commercializes the Genome Analyzer (company bought by Illumina the next year).
2002
2006
2010
2014
Date

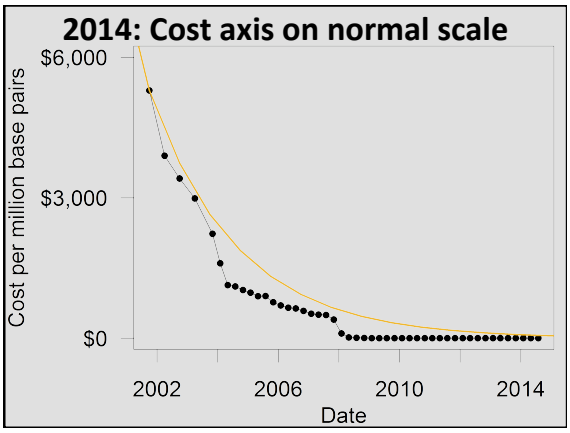

2008
Cost per million base pairs
$10,000
$1,000
$100
$10
$1
$0.10
Illumina BovineSNP50 released
By the end of 2008, costs $3.81 to sequence 1 million base pairs.
2002
2006
2010
2014
Date


2009
Cost per million base pairs
$10,000
$1,000
$100
$10
$1
$0.10
By the end of 2009, costs $0.78 to sequence 1 million base pairs.
• Bovine reference genome sequence assemblies published
• Genomic prediction in dairy cattle implemented
• Take entire DNA into account
2002
2006
2010
2014
Date


2010
Cost per million base pairs
$10,000
$1,000
$100
$10
$1
$0.10
By the end of 2010, costs $0.32 to sequence 1 million base pairs.
• Genomic prediction implemented by AGI
2002
2006
2010
2014
Date


2012
Cost per million base pairs
$10,000
$1,000
$100
$10
$1
$0.10
By the end of 2012, costs $0.07 to sequence 1 million base pairs.
• Genomic prediction implemented by AHA, ASA, NALF, RAAA, etc.
2002
2006
2010
2014
Date





Where are we going next?

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Where are we going next?

- Sequencing lots of animals!
  - Mostly influential sires
- 1000 Bull Consortium
- Individual groups
  - Support from breed associations

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Where are we going next?

- Imputation

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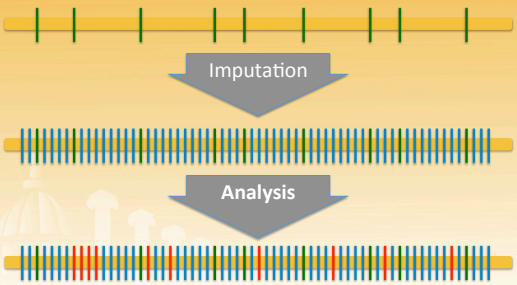
Where are we going next?



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Where are we going next?

- More types of SNP chips/panels
- Higher density panels focusing on functional variants for research
- Lower density panels focusing on functional variants for prediction
- Functional variants -> variants that influence protein sequence or abundance

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Where are we going next?

- Then genomic predictions would be based on causal variants or closely linked variants
- Fewer variants on prediction panels leads to lower cost?
- Hope for multiple breed predictions?
- More precise predictions based using causal/ closely linked

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Where are we going next?

- Back to causal variants
- Led to genes by data not researchers opinion
- Continue to take very large numbers of genes and genomic regions into account

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Where are we going next?

- Genomic "surveillance" of influential sires
- Breed associations sequences a sire when it reaches a certain number of progeny equivalents
  - 10,000?
  - 5% of annual registrations?
- Progeny equivalents
  - Progeny are 1 points
  - Grand progeny are 0.5 points
  - Great-grand progeny are 0.25 points

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Where are we going next?

- Genomic "surveillance" of influential sires
- Early identification of possible functional variants
- Good and bad
- Variants responsible for embryonic lethals

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Where are we going next?

- Manage inbreeding based on shared detrimental variants

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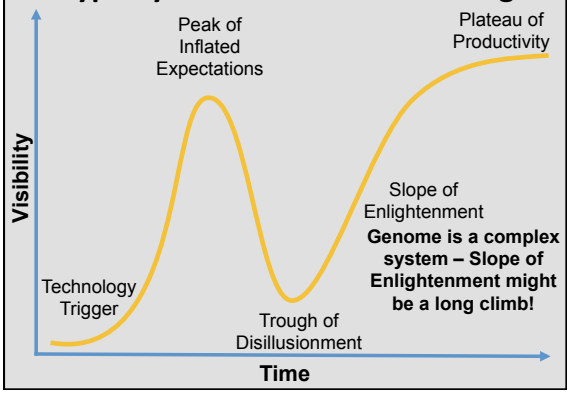
Hype Cycle: DNA in Beef Breeding



Questions?

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