

Using genomics to manage progress and diversity: an industry perspective

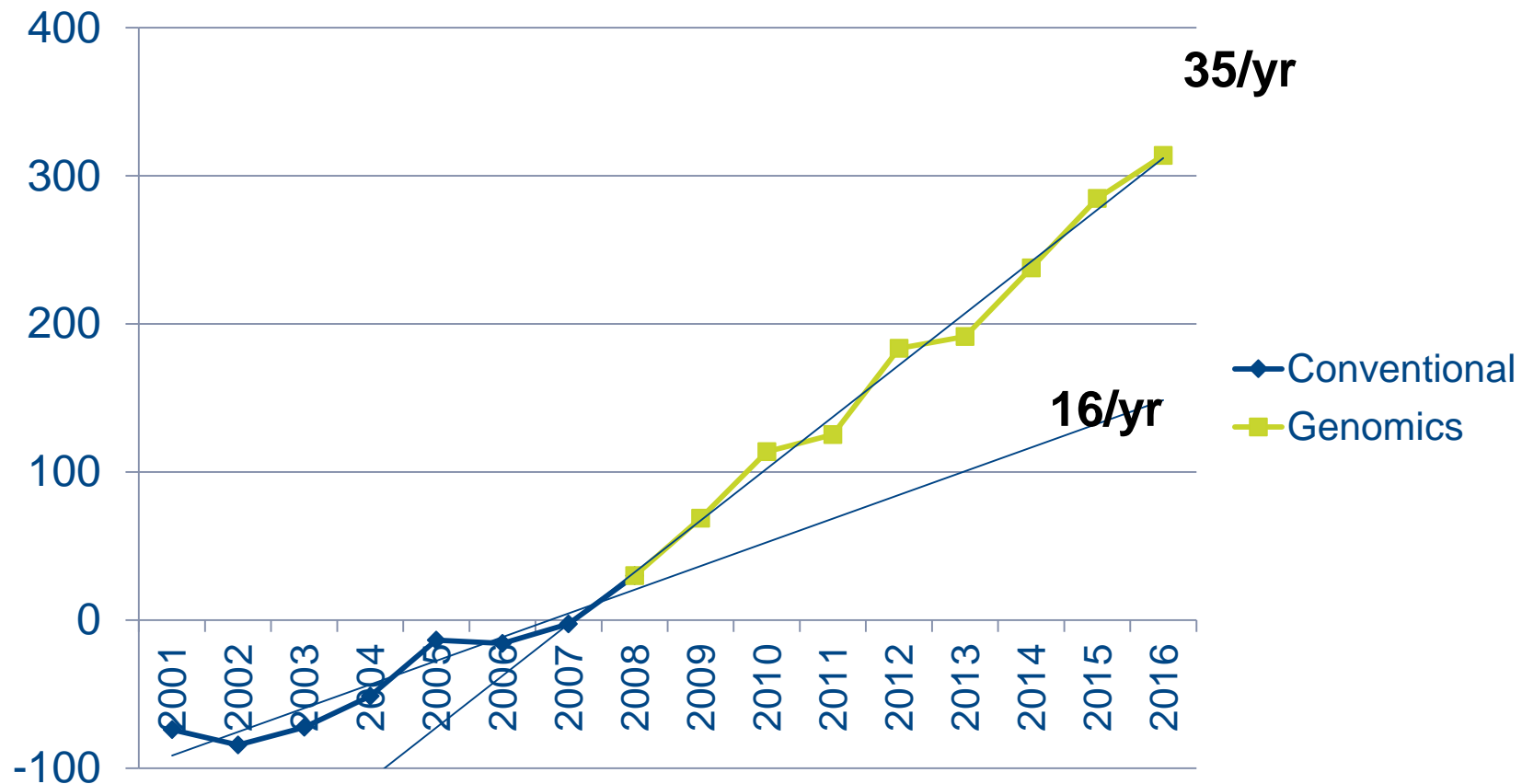
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SAFE VERSION OF MY TALK

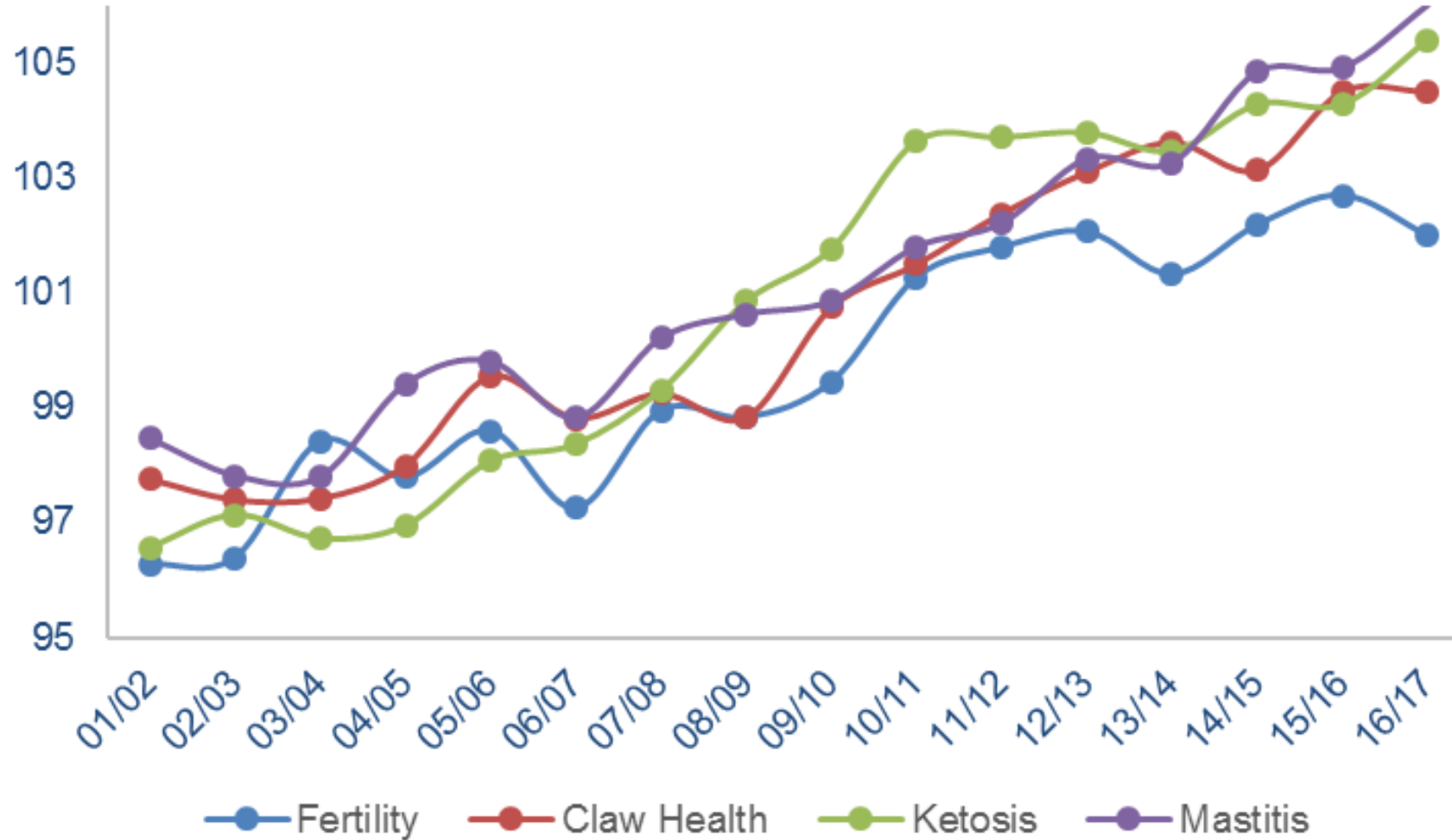
- Genomic selection did double genetic gain
- We expected genomics would also make it easier to balance progress & diversity
- So we did not anticipate the increase in inbreeding we see in the last years
- But, now we are aware, and will forcefully use genomic relationships and genomic inbreeding in our breeding programs and in the tools we use to support our customers



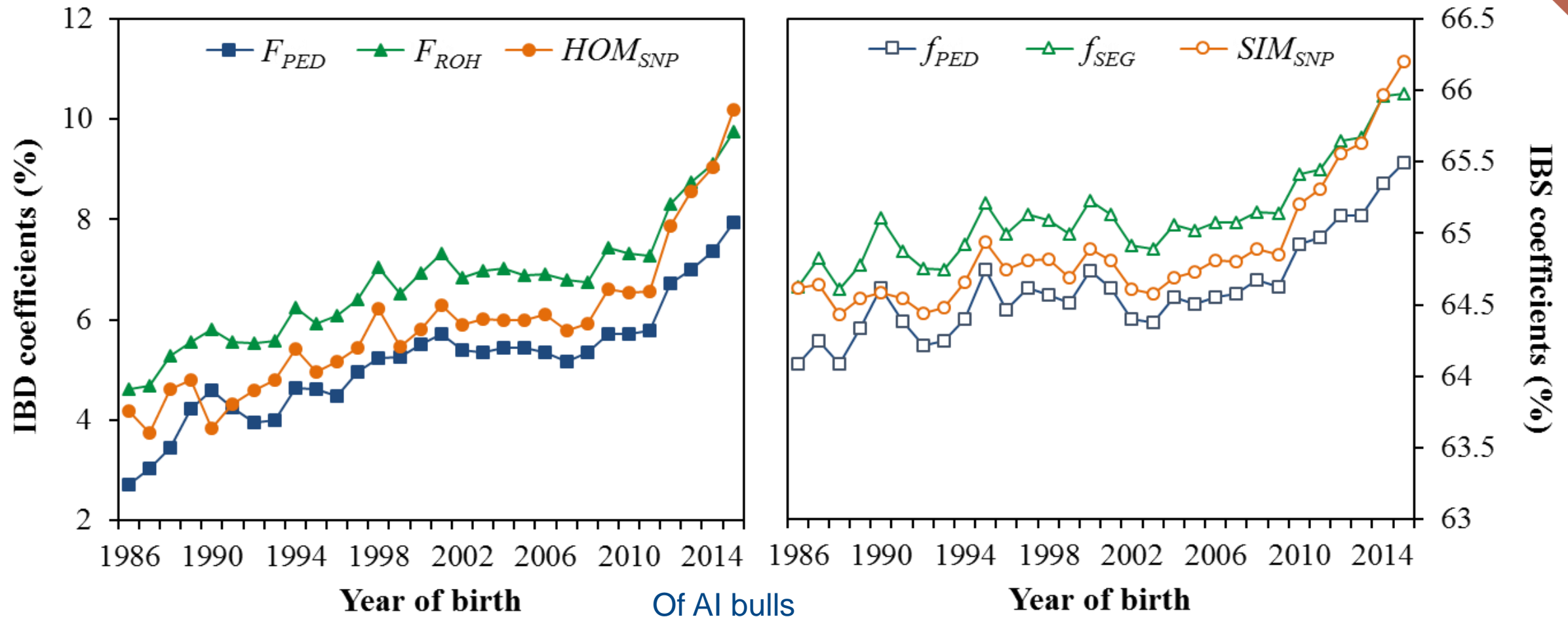
The Dairy Cattle breeding industry has been extremely successful in using genomics to drive genetic progress



The progress is of high quality



But in the same time, rate of inbreeding is increasing



We have been here before

For birth-year 1990:

5 sires were responsible for

50% of the

5000 bulls from 18 countries evaluated by Interbull

(Wickham & Banos, 1998)




Characteristics of Optimum breeding schemes

(Bijma, 2000)

- No Truncation Selection
- More focus on progeny testing, less on sib information
- Increased generation intervals
- Increased accuracy at the expense of selection intensity
- A mating strategy that accelerates the mixing of ancestral lines within the population



Segmentation



Expected success in 5
different market segments

Relatedness

Proportion of cow population
a bull can be mated to

The background image is a blurred pedigree chart or relationship matrix. It consists of a grid of cells, each containing a numerical value representing genetic relatedness. A green circle highlights a specific cell in the upper right quadrant. A yellow arrow points from this cell towards the text box on the right. The text box contains the text 'Proportion of cow population a bull can be mated to'. The overall image is out of focus, with the text and arrow being the primary elements of interest.

Proportion of the cow population a bull can be mated to

- Simulate future cow population based on current population and current sire use
- Use inbreeding rules of CRV mating program
- Compute for each bull the proportion of the cow population the bull can be mated to without running into inbreeding problems

WE ARE ALL TRUNCATERS!

- Interbull
- Herdbooks
- AI organisations
- Scientists
- Press
- Maybe farmers are the exception

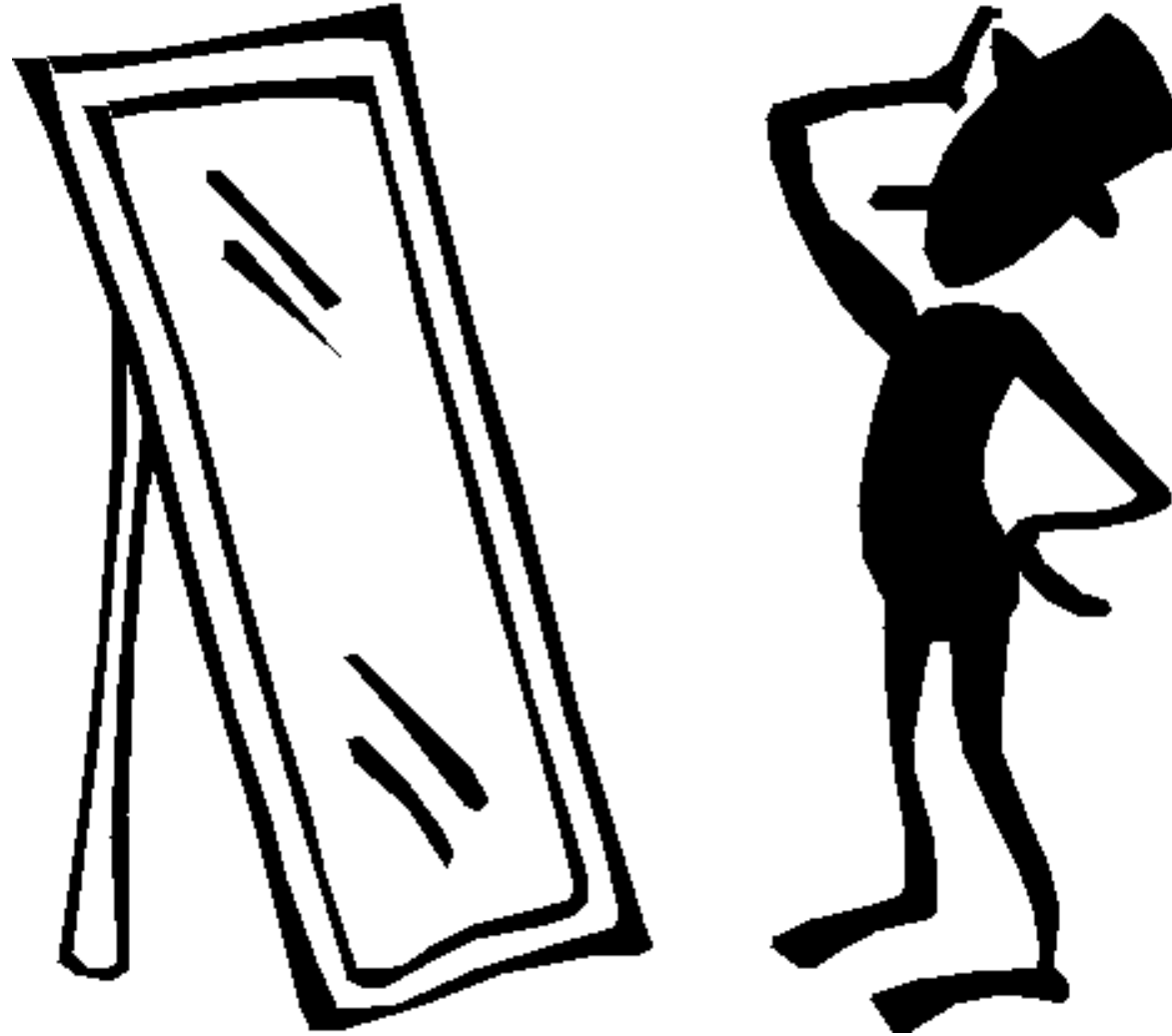
More focus on progeny testing, less on sib information

- Underexplored territory under genomics
- Gut-feeling: no focus on new Mendelian Sampling
All focus is on “best” haplotypes from reference population
- Haplotypes from outcross pedigrees never selected as “best”
- Rethink how we design cow reference populations
- Rethink how we analyse cow reference populations
- Investigate how we can detect and propagate new Mendelian sampling

Increased generation interval

- I.e. favouring animals that have expressed their Mendelian Sampling
- Genotyping exceptional cows
- Re-use the best progeny tested bulls
-

Increased accuracy at the expense of selection intensity



A mating strategy that accelerates the mixing of ancestral lines within the population

- Mate every mating sire to every bull dam [exploit IVP]

- Deliberately mate super elite cows to outcross bulls



Selection & mating at farm level

- As an industry, we should educate ourselves and farmers that with genomic inbreeding new rules are required [inbreeding < 0.0625 no longer possible]
- Show farmers inbreeding trends and genetic make-up of herd
- Show farmers relatedness of bulls to enable proper bull selection
- Then apply genomic mating

THIS TALK

- Genomic selection did double genetic gain
- We expected genomics would also make it easier to balance progress & diversity
- So we did not anticipate the increase in inbreeding we see
- We have to upgrade our tools to support selection and mating decisions of our customers
- But more importantly, as an industry we have to rethink how to balance progress and diversity in our breeding programs



THANK YOU!