

Use of genomic tests and sexed semen increase genetic level within herd

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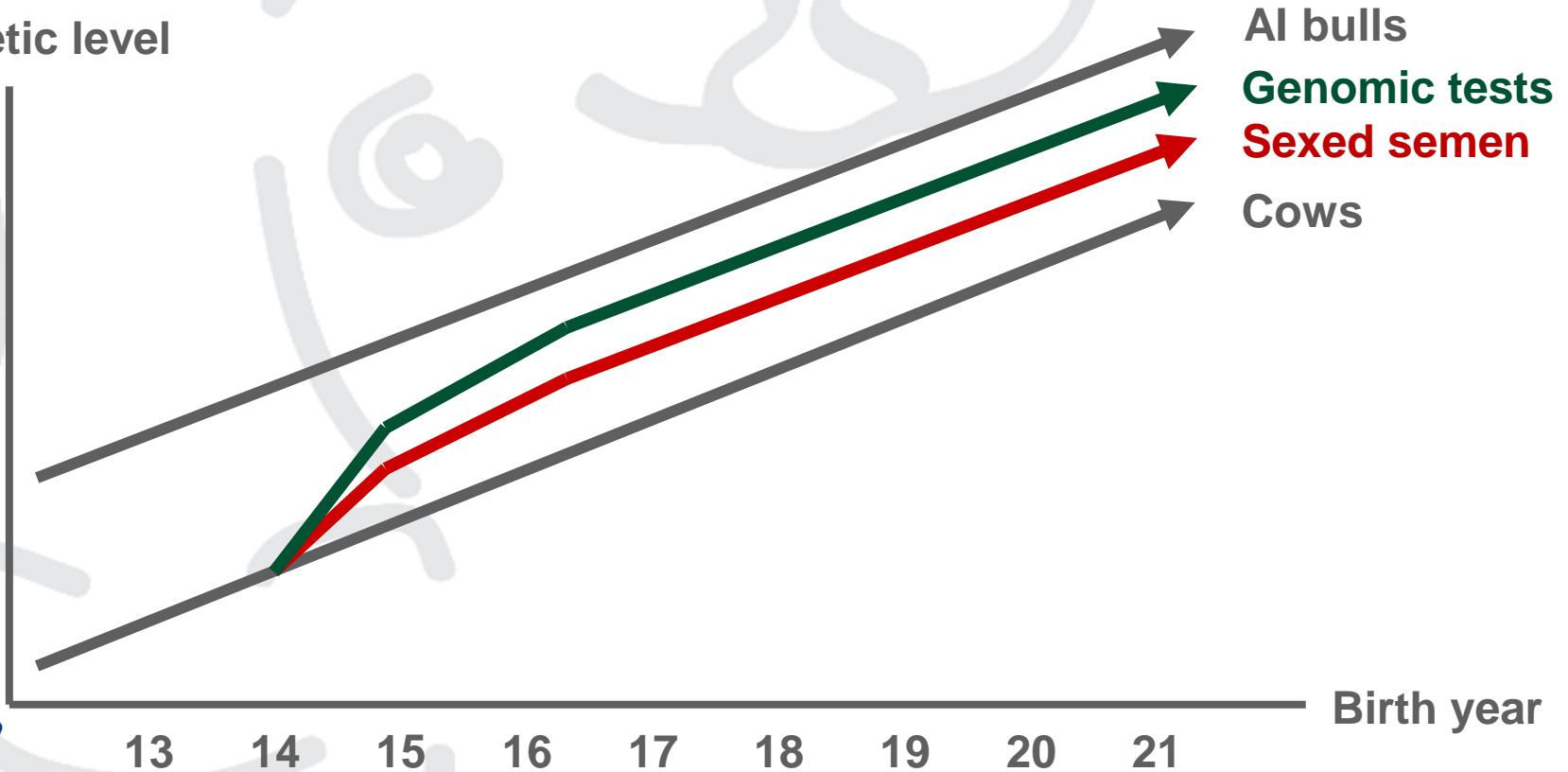
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STØTTET AF
mælkeafgiftsfonden

Sexed semen and genomic tests reduce genetic lag

Genetic level



AI bulls
Genomic tests
Sexed semen
Cows

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13 14 15 16 17 18 19 20 21 Birth year



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Aim and method

- How many NTM units will the genetic level increase if sexed semen and genomic tests are used?
- Simulation study
 - SimHerd
 - ADAM

Percentage of females inseminated with sexed semen

	Sexed semen scenarios				
Heifers, %	0	60	80	60	60
Cows, %	0	0	0	20	40

Percentage of heifers with genomic tests (GT)

		Sexed semen scenarios				
	Heifers, %	0	60	80	60	60
	Cows, %	0	0	0	20	40
Scenarios with GT	None					
	50 % best					
	All					

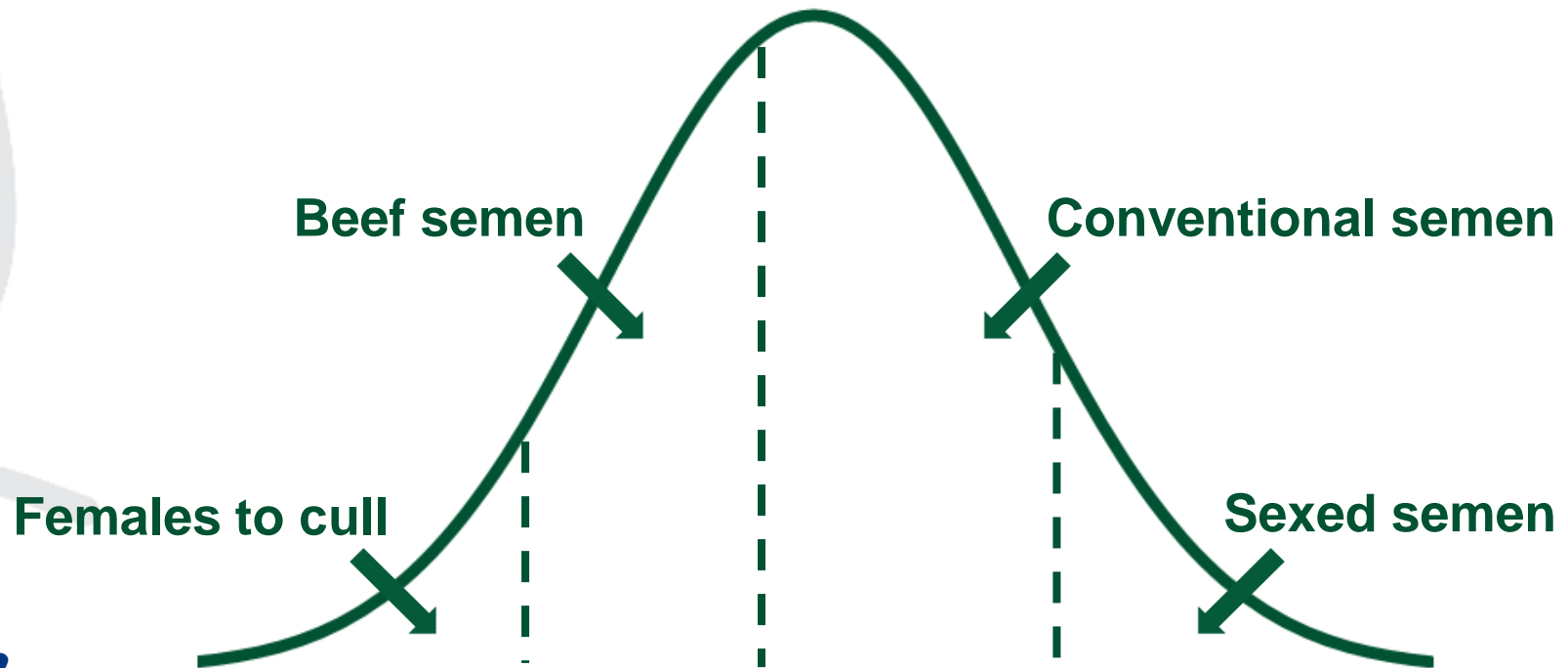
General assumptions

- **No surplus of heifers**
 - **Crossbred calves to beef production**
- **Holstein situation:**
 - **Reliability DGV(NTM): 50 %**
- **Herd size: 210 cows**
- **Danish average management level**
- **Investigated at equilibrium – no discounting**

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Genetic response from selection among females



Price assumptions, €

- Purebred bull calf: 81
- Crossbred bull calf: 178
- Crossbred heifer calf: 87
- Springing heifer: 1,340
- Genomic test: 50
- Conventional semen, including service: 24
- Sexed semen, including service: 40
- Beef semen, including service: 25

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Percentage of cows inseminated with beef semen

	Sexed semen scenarios				
Heifers, %	0	60	80	60	60
Cows, %	0	0	0	20	40
	0	25	32	29	32

- Replacement rate: 41 %

Reduced genetic lag in NTM units

		Sexed semen scenarios				
	Heifers, %	0	60	80	60	60
	Cows, %	0	0	0	20	40
Scenarios with GT	None	0	1.2	1.2	1.3	1.5
	50 % best					
	All					

Reduced genetic lag in NTM units

		Sexed semen scenarios				
	Heifers, %	0	60	80	60	60
	Cows, %	0	0	0	20	40
Scenarios with GT	None	0	1.2	1.2	1.3	1.5
	50 % best	0.5				
	All	0.9				

Reduced genetic lag in NTM units

		Sexed semen scenarios				
	Heifers, %	0	60	80	60	60
	Cows, %	0	0	0	20	40
Scenarios with GT	None	0	1.2	1.2	1.3	1.5
	50 % best	0.5	1.9	1.9	2.0	2.3
	All	0.9	2.3	2.3	2.6	2.8

Interactions between use of sexed semen and GT in NTM units

		Sexed semen scenarios				
	Heifers, %	0	60	80	60	60
	Cows, %	0	0	0	20	40
Scenarios with GT	None	0	0	0	0	0
	50 % best	0	0.2	0.2	0.2	0.3
	All	0	0.2	0.2	0.4	0.4

Break-even prices for a genomic test in €

		Sexed semen scenarios				
		0	60	80	60	60
Heifers, %		0	60	80	60	60
Cows, %		0	0	0	20	40
Scenarios with GT	None	-	-	-	-	-
	50 % best	22.0	32.0	35.5	33.5	38.5
	All	21.0	27.5	28.0	32.5	32.0

Conclusion

- How many NTM units can the genetic level potentially increase
 - if sexed semen is used: 1.5
 - if genomic tests are used: 0.9
 - if both sexed semen and genomic tests are used: 2.8
- The scenario with the highest genetic level does not correspond to the scenario with the **NAV** highest break-even price for a genomic test

Comparison between this study and other studies

- **EAAP 2013**
 - **Calus et al.**
 - **Boichard et al.**
- **Both studies are based on a different set-up**

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Assumptions – Calus et al.

- **Commercial herd**
 - 100 cows
 - Number of heifers available = 15 - 40
 - • Replacement rate 15 - 30%
 - Survival female calves = 80%
 - Use of conventional or sexed semen (SS)
 - • SS doubles number of heifers available (30 – 80)
 - Proportion of heifers genotyped
 - All or pre-selection based on parent average (PA)

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Assumptions – Calus et al.

- $R = i \times \rho \times \sigma_H$
 - R = response in Euros
 - i = selection intensity
 - ρ = accuracy of selection
 - $\rho_{PA} = 0.15$; $\rho_{GS} = 0.7$
 - $\sigma_H = \text{SD breeding goal} = 300 \text{ Euro (de Roos, 2011)}$
 - 100 Euro per SD per lactation x 3 lactations
- Additional response:

NAV $R = i \times (\rho_{GS} - \rho_{PA}) \times \sigma_H$



Assumptions – Boichard et al.

- Assuming sexing and no female selection on pedigree
- Additional genetic gain
 - ➔ • $p = 0.5 \Rightarrow i = 0.8$
 - ➔ • $\rho_{GS}^2 = 0.7 \Rightarrow \rho_{GS} = 0.85$
 - Do not compare with pedigree index ($\rho_{PA} = 0$)
 - $\sigma_H = 100 \text{ €}$

Conclusion

- **Calus and Boichard assume**
 - Different set-up
 - Higher selection intensity
 - Larger increase in accuracy of selection
- Higher additional response that can pay for the genomic tests =>
- Higher break-even prices

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