Predicted response of genomic selection for new traits using combined cow and bull reference populations Mario Calus

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Develop innovative and practical breeding tools for improved dairy products from more robust dairy cows



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## **Introduction**

#### Genomic selection:

- Beneficial for dairy cattle breeding programs
  - Reduces generation interval
  - Cheaply increases selection intensity
- Allows selection for 'new' traits
  - Relaxes requirement (daughter) performance recording
  - Expensive or hard to measure
- New traits:
  - Progesterone; Energy balance; Methane emission

# $\rightarrow$ How promising is this?



# Objective

Investigate for a new trait measured on a limited number of cows only (e.g. methane emission):

### DGV reliability:

- Using cows only
- When adding sires with known DGV for correlated trait

#### The selection response



# **Deterministic simulation**

Reliabilities predicted (Daetwyler et al., 2009)

- For cows and bulls separately
- Blended using 'information source method' (Harris & Johnson, 1998)

 Selection response predicted using SelAction (Rutten et al., 2002)

• 4 selection pathways with different generation intervals

### Simultaneous selection of new trait and index



#### Parameters

# Cows: 0 - 4000
# Bulls: 0, 200, 500, 2000, 5000, 20,000

Trait	h²	DGV reliability	Economic value
Index	0.3	0.64	1
New trait	0.3	0.0 - 0.64	1

 $r_{q}(index, new trait) = -0.5, 0, or 0.5$ 

Breeding program with 1-stage genomic selection



## Results: DGV reliabilities – cows only





## Results: DGV reliabilities – cows only





# Results: DGV reliabilities – bulls added

 $r_g(index, new) = 0.5$ 





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# Results: selection response





# Results: selection response





# Results: selection response





# Summarized – impact 2,000 cow reference pop.

#### $\rightarrow$ DGV reliability = 0.3

# Compared to no selection for new trait

r <sub>g</sub> (index, new trait)	Response (gen. SD / yr)	Increase response (gen. SD / yr)
0.5	0.1	0.02
0.0	0.06	0.06
-0.5	0.0	0.08
	Negative trend broken	



# **Conclusions**

- Combining cow and bull reference populations can increase reliability DGV of new traits
  - When  $r_q$ (index, new trait)  $\neq 0$
  - Reduces the required size of cow reference population

 Genomic selection for new traits is beneficial, even with a small cow reference population
 Low DGV reliability is offset by decrease of generation

interval





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