Increasing genetic gain without compromising diversity by selecting matings

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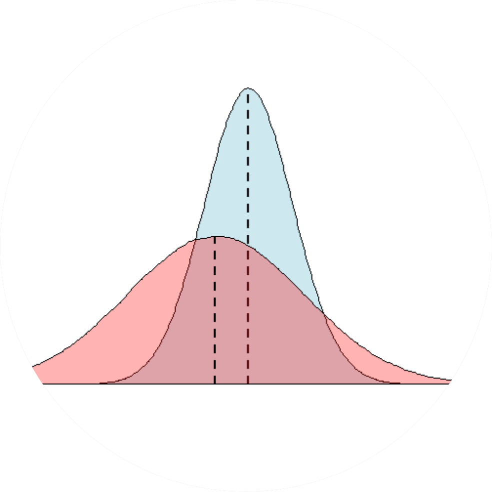

```
 cohorts = tail(get.cohorts(pop),
rder(bvm, decreasing = T)[1:n.sel.males]]
 = pop, cohorts = tail(get.cohorts(pop),1), use
[[2]]
sef[order(bvf, decreasing = T)[1:n.sel.females]])

n(c(bvm, bvf)))
v_best, mean(c(rev(sort(bvm))[1:n.sel.males], rev(sort(

minimum_coancestry"){
oanc.mating(population = pop,
            n.offspring = breeding.size,
            id_m = id_m, id_f = id_f,
            avoid_sibmating = FALSE,
            depth.pedigree = 7)

oid(pop,
    fixed.breeding = mate.plan,
    verbose = F,
    delete.same.origin = T



      = F,
        origin = T,
```

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New selection criterion

- Genetic gain vs diversity
- Diversity is needed for future progress

We want to be better in one aspect without compromising the other

New selection criterion

Is there a better selection criterion than breeding values?

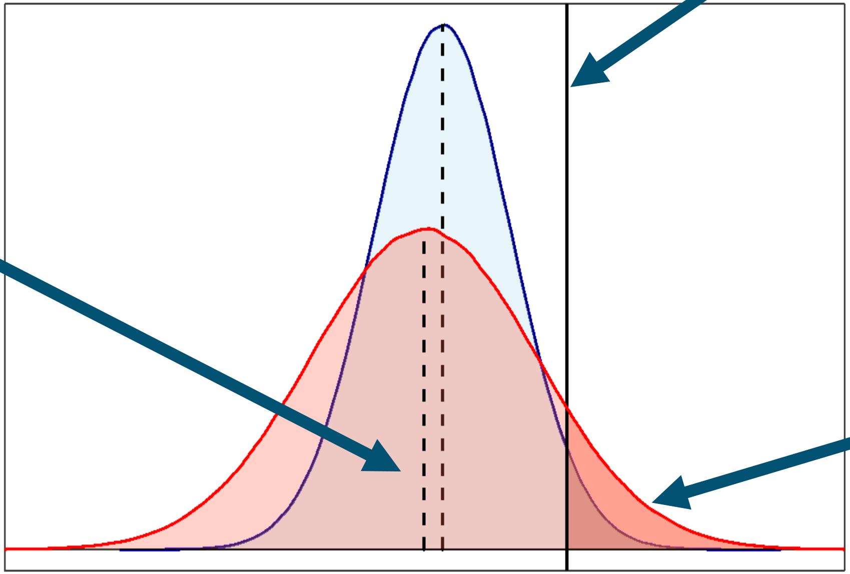
Answer: Yes, the probability to select top genotypes in the next generation (e.g., Bijma et al. 2020)

- Can we do even better?

  ...without compromising short-term gain

Objective: develop new selection criterion

Selecting matings



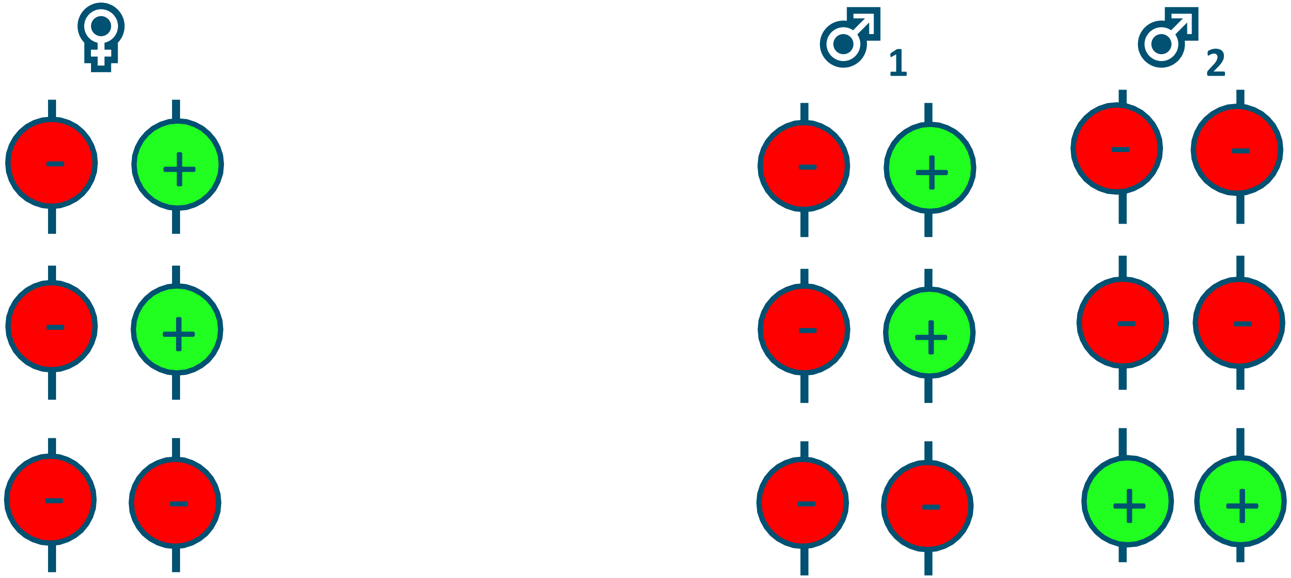
Selection threshold

Parent average of **red** family is lower

Red family produces more very good animals

Selecting matings

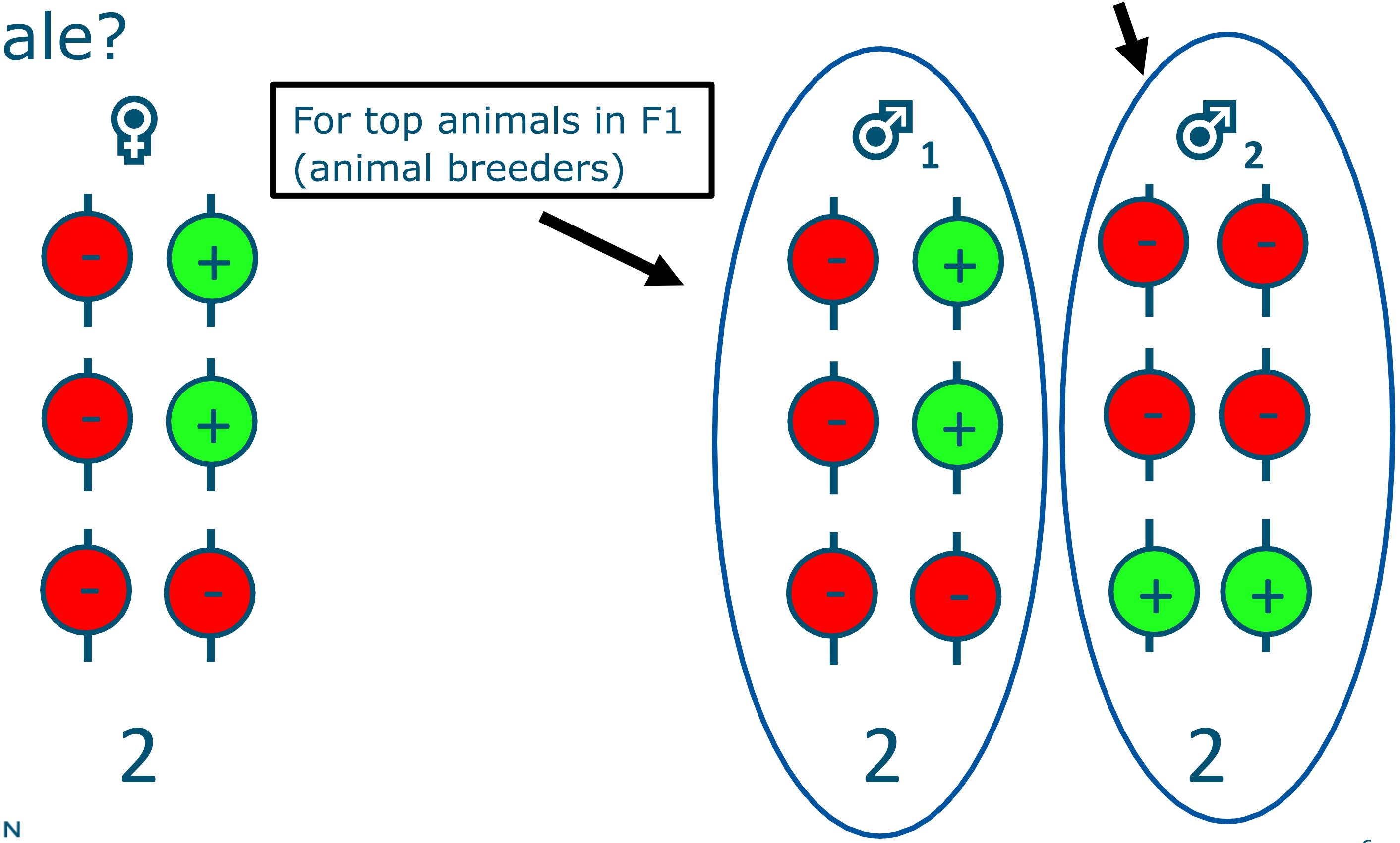
- Which male?



BV: 2 2 2

Selecting matings

Which male?



For top animals in F1 (animal breeders)

For top animals in F2 (plant breeders)

BV: 2 2 2

Mate selection

- What is the difference between the choices?

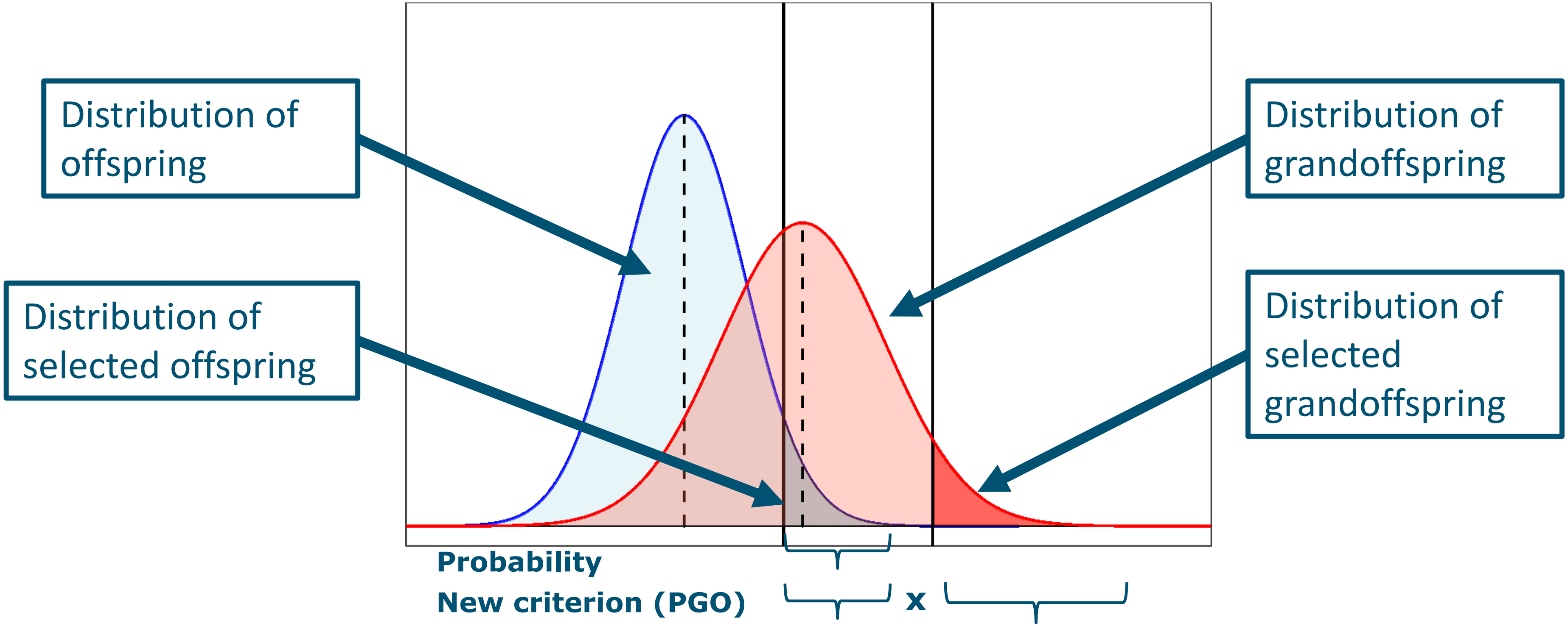
- Choice 1:
  - High variance in F1
- Choice 2:
  - High variance in F2

- Solution:

Express quality assuming selected offspring known

$$ProbGO = Prob_{offspring} * Prob(Grandoffspring|selected\ offspring)$$

New criterion PGO



Distribution of offspring

Distribution of selected offspring

Distribution of grandoffspring

Distribution of selected grandoffspring

Probability

New criterion (PGO)

$$ProbGO = Prob_{offspring} * Prob(Grandoffspring|selected\ offspring)$$

Simulation study

Mate selection in recurrent selection

- 20 generations
- Cattle genome
- 20 sires, 20 dams every generation
- Population size 4000 → 1% are selected
- QTL effects and haplotypes assumed known

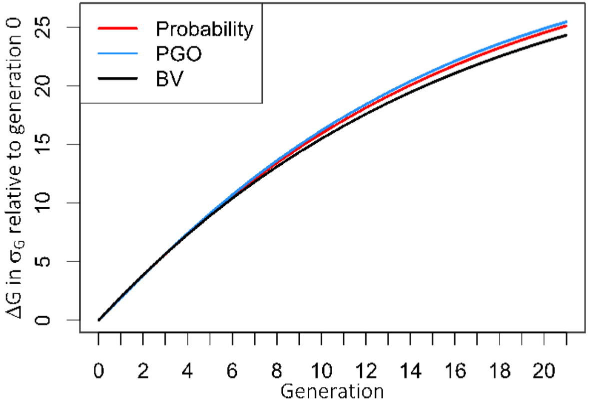
- Maximum number of offspring per mating: 40

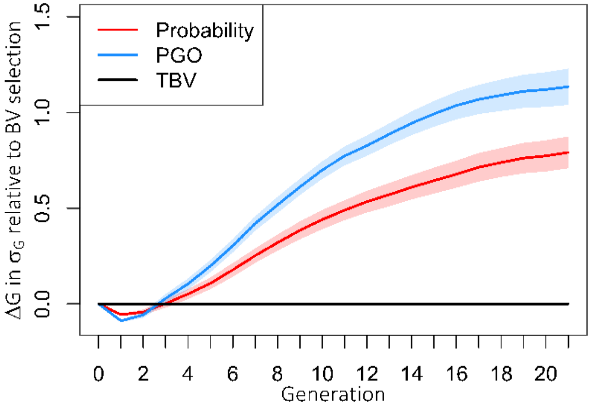
Mate selection in recurrent selection

Genetic level in genetic sd

Genetic level relative to BV selection

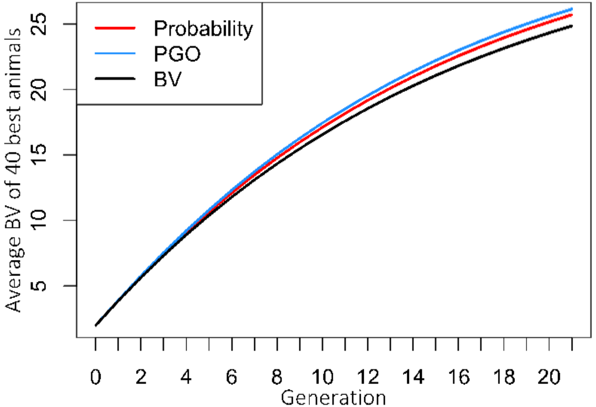
Population average BV

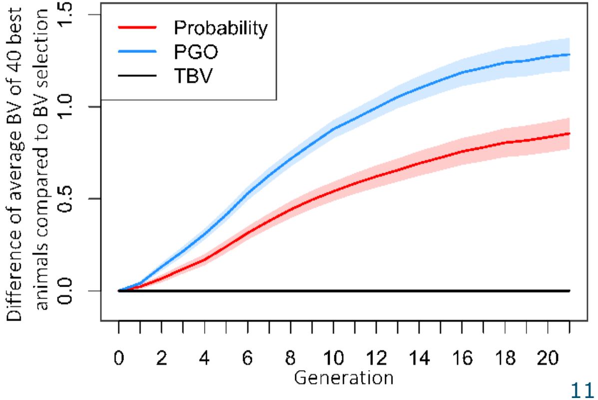




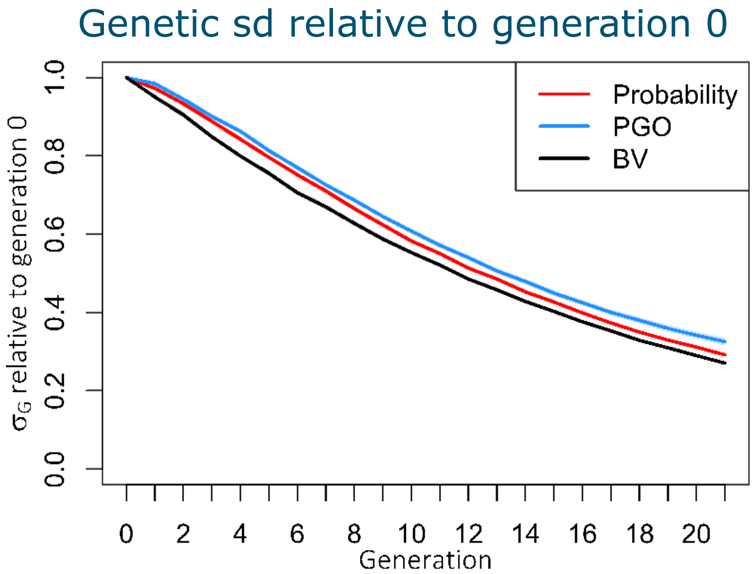
BV of best animals

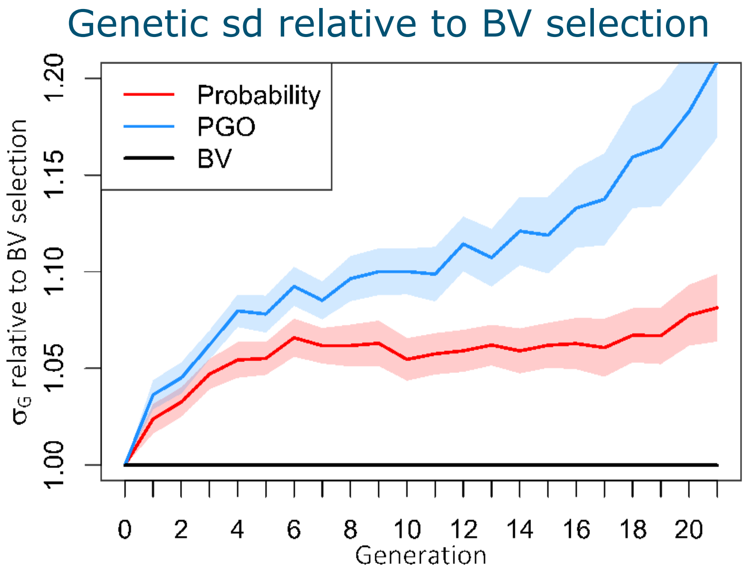
	Gen5
BV	100%
Prob	103.3%
PGO (mine)	105.1%





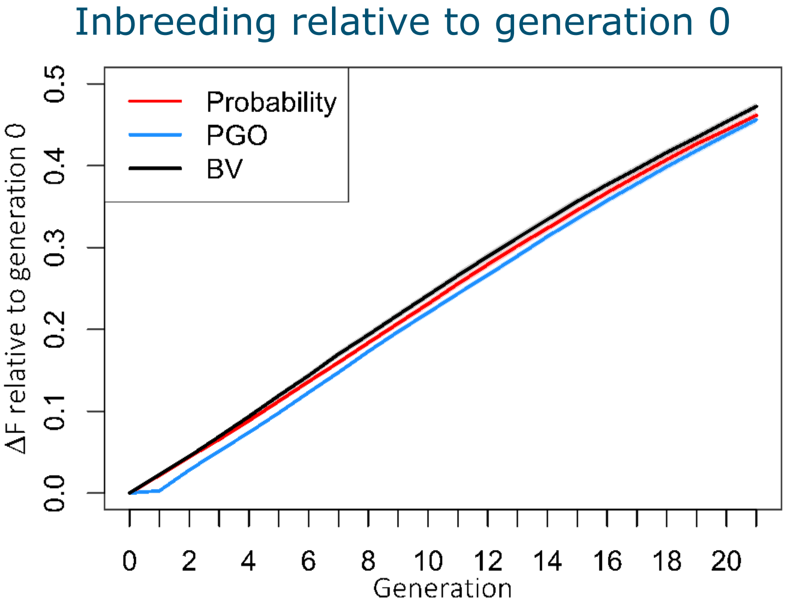
Mate selection in recurrent selection

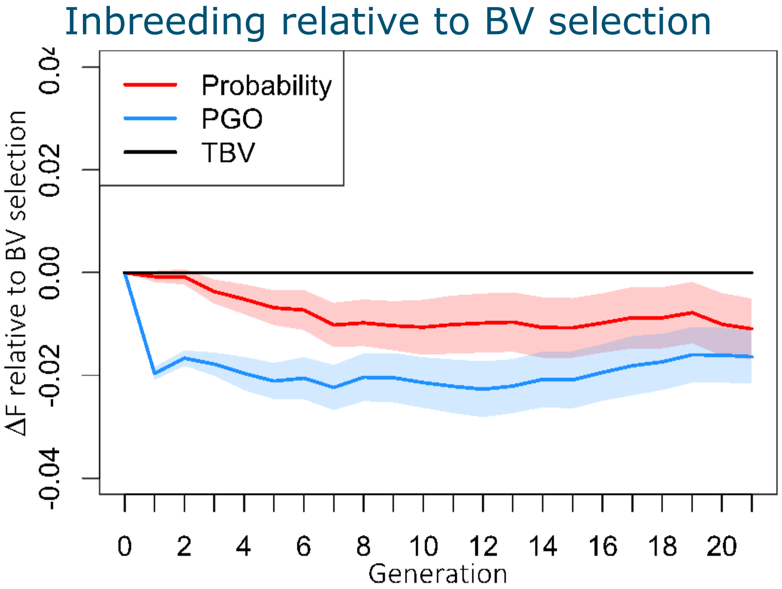

Genetic sd relative to generation 0


Genetic sd relative to BV selection

	Gen5
BV	100%
Prob	105.4%
PGO (mine)	111.9%

Mate selection in recurrent selection





	Gen5
BV	100%
Prob	93.7%
PGO (mine)	80.6%

Conclusion

- Faster genetic progress

… with higher genetic variance

… and lower inbreeding level

… without compromising short-term gain

… at no additional costs

Other sessions

- Enhancing long-term genetic gain through a Mendelian sampling-based similarity matrix
    - Abdulraheem Musa, session 69

- Strategies to improve selection compared to selection based on estimated breeding values
    - Torsten Pook, session 27

Thanks for your attention!

- Mario Calus
- Jan ten Napel
- Piter Bijma
- Yvonne Wientjes
- Torsten Pook
- Bernadett Hegedűs

BREED4FOOD

Cobb

HENDRIX GENETICS

CRV
BETTER COWS > BETTER LIFE

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