Comparison of truncation and optimum contribution genomic selection in a small cattle population

JANA OBŠTETER
Janez JENKO
John HICKEY
Gregor GORJANC

EAAP 2019
Gent, Belgium, 26th August 2019

Agricultural Institute of Slovenia
University of Ljubljana Biotechnical Faculty
ROSLIN
geno

Introduction

- Small cattle populations - genomic selection not fully integrated
- How intensive can we go?
- Sustainable strategy?

J. Dairy Sci. TBC:1–12
https://doi.org/10.3168/jds.2019-16853

JDS16853

Efficient use of genomic information for sustainable genetic improvement in small cattle populations

J. Obšteter,[1]* J. Jenko,[1,2] J. M. Hickey,[3] and G. Gorjanc[3,4]
[1]Department of Animal Science, Agricultural Institute of Slovenia, Hacquetova ulica 17, 1000 Ljubljana, Slovenia
[2]Geno Breeding and A.I. Association, Storhamargata 44, 2317 Hamar, Norway
[3]The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush, Midlothian, EH25 9RG, United Kingdom
[4]Biotechnical Faculty, University of Ljubljana, Jamnikarjeva 101, 1000 Ljubljana, Slovenia

ABSTRACT

In this study, we compared genetic gain, genetic variation, and the efficiency of converting variation into gain under different genomic selection scenarios with truncation or optimum contribution selection in a small dairy population by simulation. Breeding programs have to maximize genetic gain but also ensure sustainability by maintaining genetic variation. Numerous studies have shown that genomic selection increases genetic gain. Although genomic selection is a well-established method, small populations still struggle with choosing the most sustainable strategy to adopt this type of selection. We developed a simulator of a dairy population and simulated a model after the Slovenian Brown Swiss population with ~10,500 cows. We compared different truncation selection scenarios by varying (1) the method of sire selection and their conversion efficiency. The largest conversion efficiency was achieved with the simultaneous use of genomically and progeny-tested sires that were used over several years. Compared with truncation selection, optimizing sire selection and their usage increased the conversion efficiency by achieving either comparable genetic gain for a smaller loss of genetic variation or higher genetic gain for a comparable loss of genetic variation. Our results will help breeding organizations implement sustainable genomic selection.

Key words: small population, sustainability, genomic selection, optimum contribution selection

INTRODUCTION

In this article, we compare genetic gain, genetic variation, and the efficiency of converting variation into gain under different genomic selection scenarios in a small

DRAFT

1) Genetic gain with truncation selection

2) Loss of genetic variation with truncation selection

3) Comparison of truncation and optimum contribution selection

Stochastic simulation

- Mimicked a realistic cattle population ~30,000 active animals
- 20 years burn-in + 20 years evaluation
- Python wrapper around
  - AlphaSim (Faux et al., 2012),
  - blupf90 (Misztal et al., 2002)
  - AlphaMate (Gorjanc and Hickey, 2018)

Truncation selection

PT

Progeny tested sires

GT-PT

Preselection on gEBV

GT

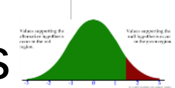
Genomically tested sires

Truncation selection

PT
Progeny tested sires

GT-PT
Preselection on gEBV

GT
Genomically tested sires

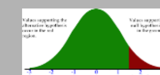
Scenarios	1. variable	2. variable
PT	PT sires	5 sires / 5 years
GT-PT	GT-PT sires	5 sires / 1 year
GT-BD	GT sires for Bull Dams	1 sire / 5 years 
GT	GT sires	

- Genetic gain
- N_e
- Genetic variability
- Conversion efficiency

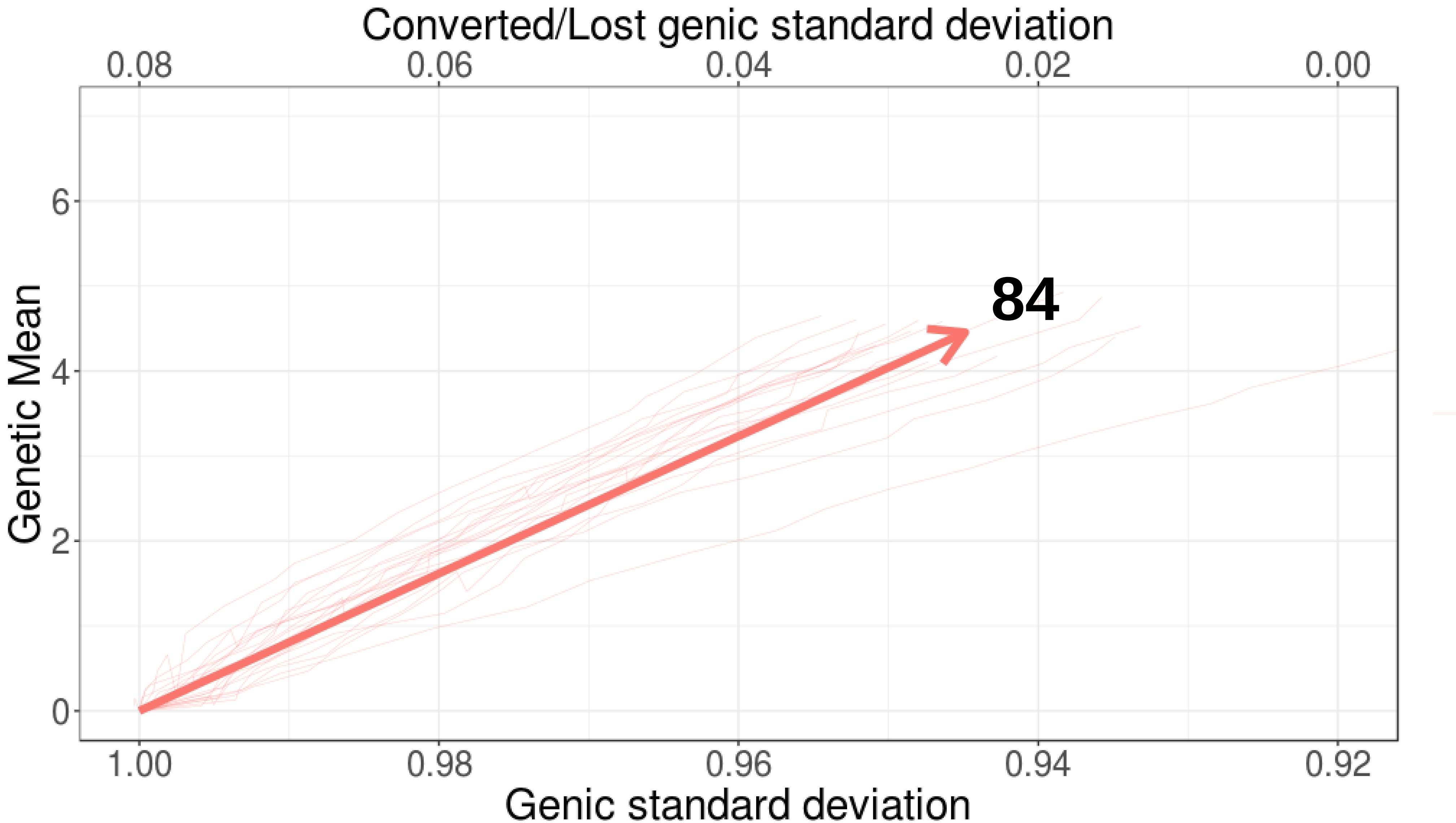
Genetic gain [sd] with truncation selection

	5 bulls / 5 years	5 bulls / 1 year	1 bull / 5 years 
PT	2.5	2.8	3.0
GT-PT	3.4	4.0	3.8
GT-BD	4.2	4.6	4.5
GT	4.8	6.0	5.6

Effective population size of truncation selection

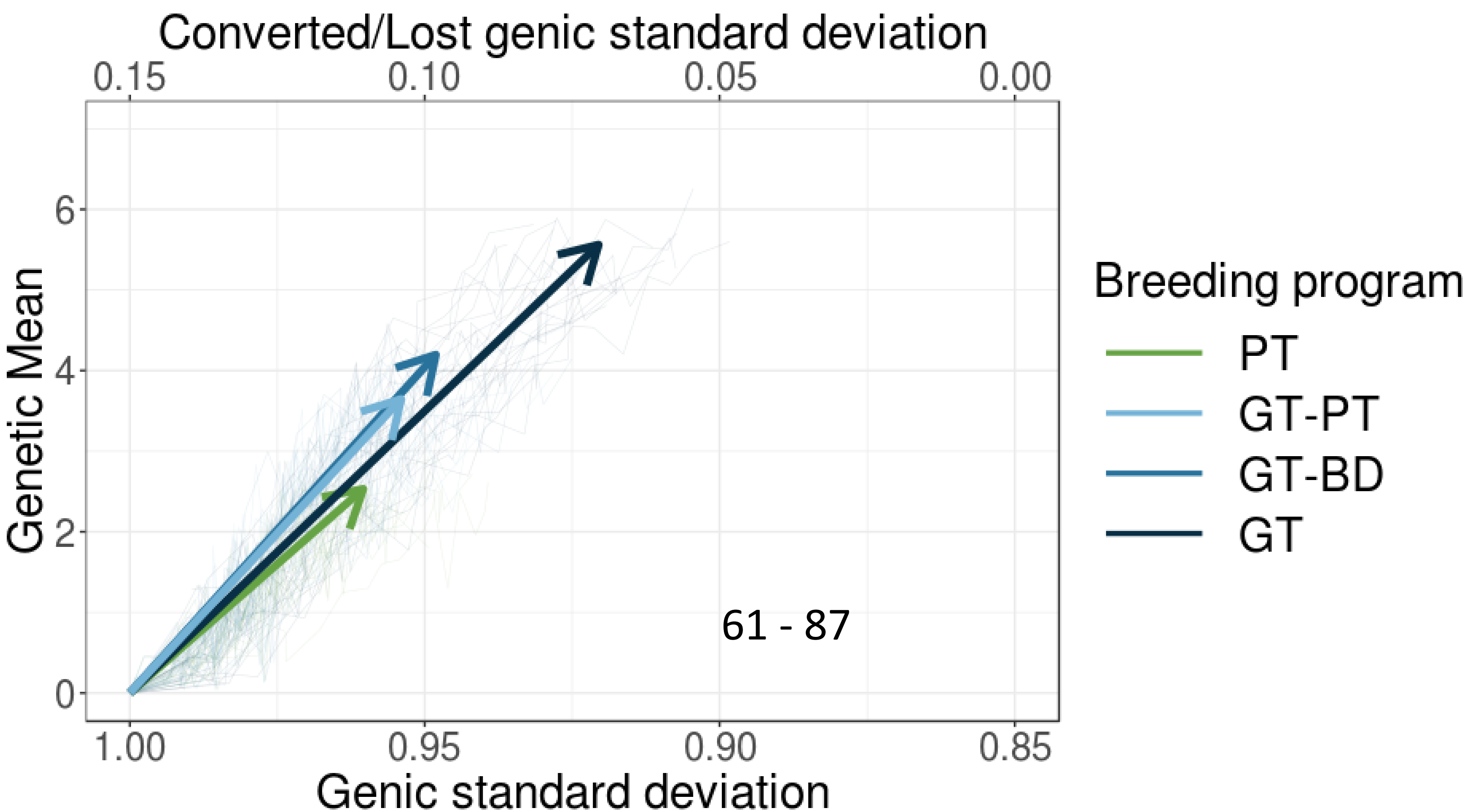
	5 bulls / 5 years	5 bulls / 1 year	1 bull / 5 year 
PT	172	184	96
GS-PS	159	146	99
GS-BD	119	113	93
GS	90	72	38

Conversion efficiency



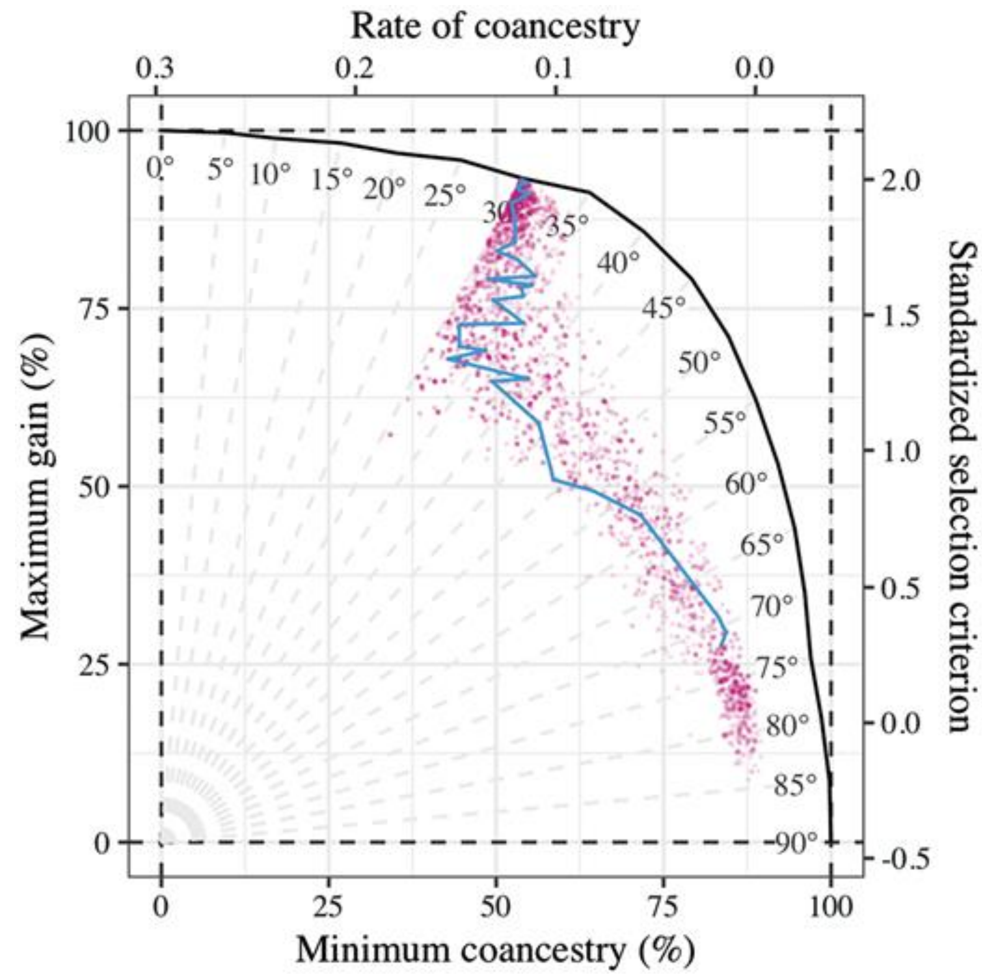
Conversion efficiency of truncation selection

5 sires/year, use 1 year

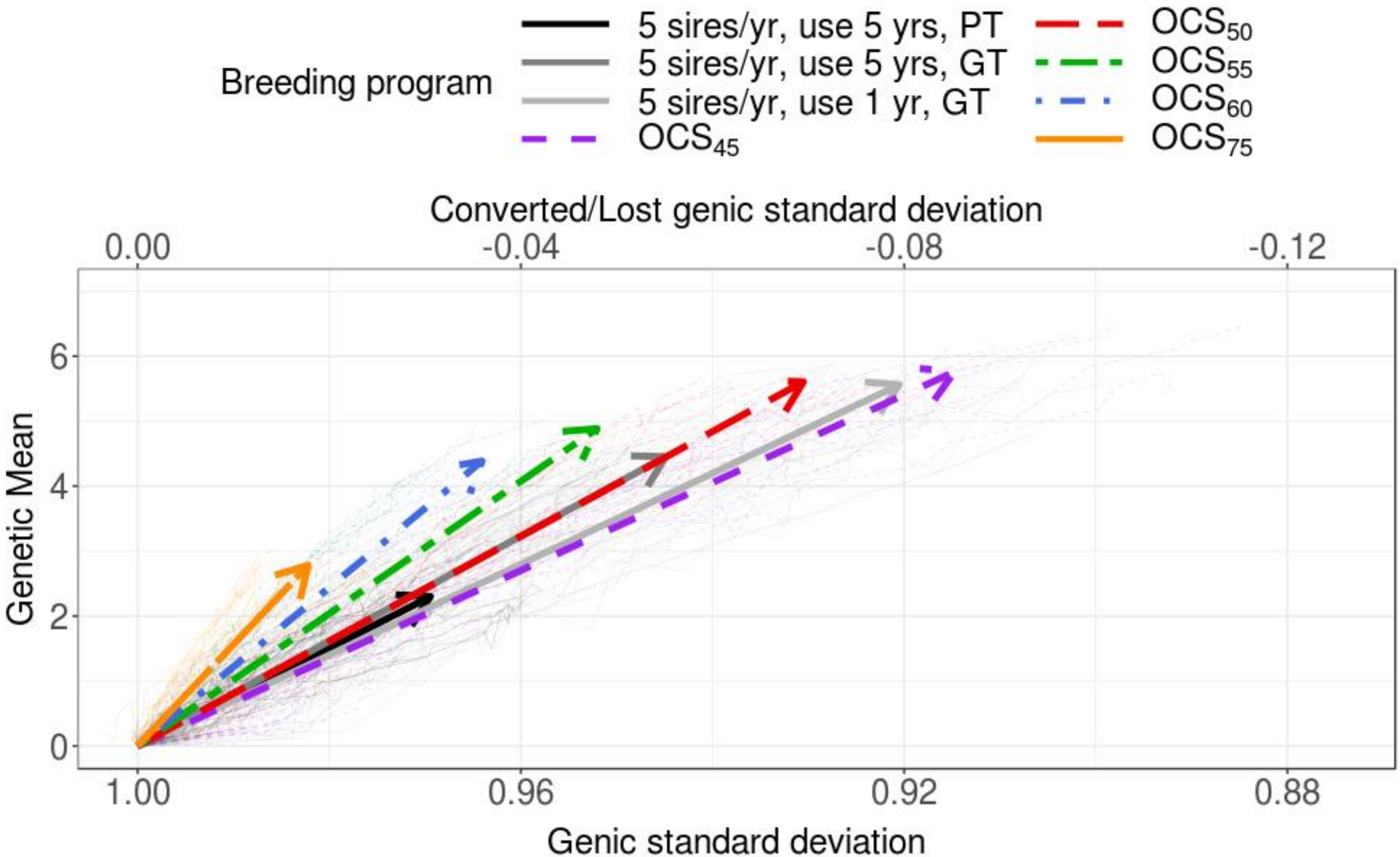


Truncation vs optimum contribution selection

- Optimized selection and use of sires
- Active bulls (PT, GT) + young candidates
- Target degrees:
  - 45
  - 50
  - 55
  - 60
  - 75



Truncation vs OCS



Conclusions

- Highest genetic gain?

  GT, faster turn-over of animals

- Highest N_e and conversion efficiency?

  Hybrid scenarios (PT, GT) and faster turnover

- To optimize, or not to optimize?

  Increases conversion efficiency of all scenarios

  More gain, same loss

  Same gain, less loss