Stochastic simulation of breeding plans in mink (*Neovison vison*): Evaluation of genomic selection

Kristian Meier
Mogens S. Lund
A. Christian Sørensen

Genomic selection should improve mink breeding

”Difficult” traits

- **Litter size**
- **Skin quality**

Challenges

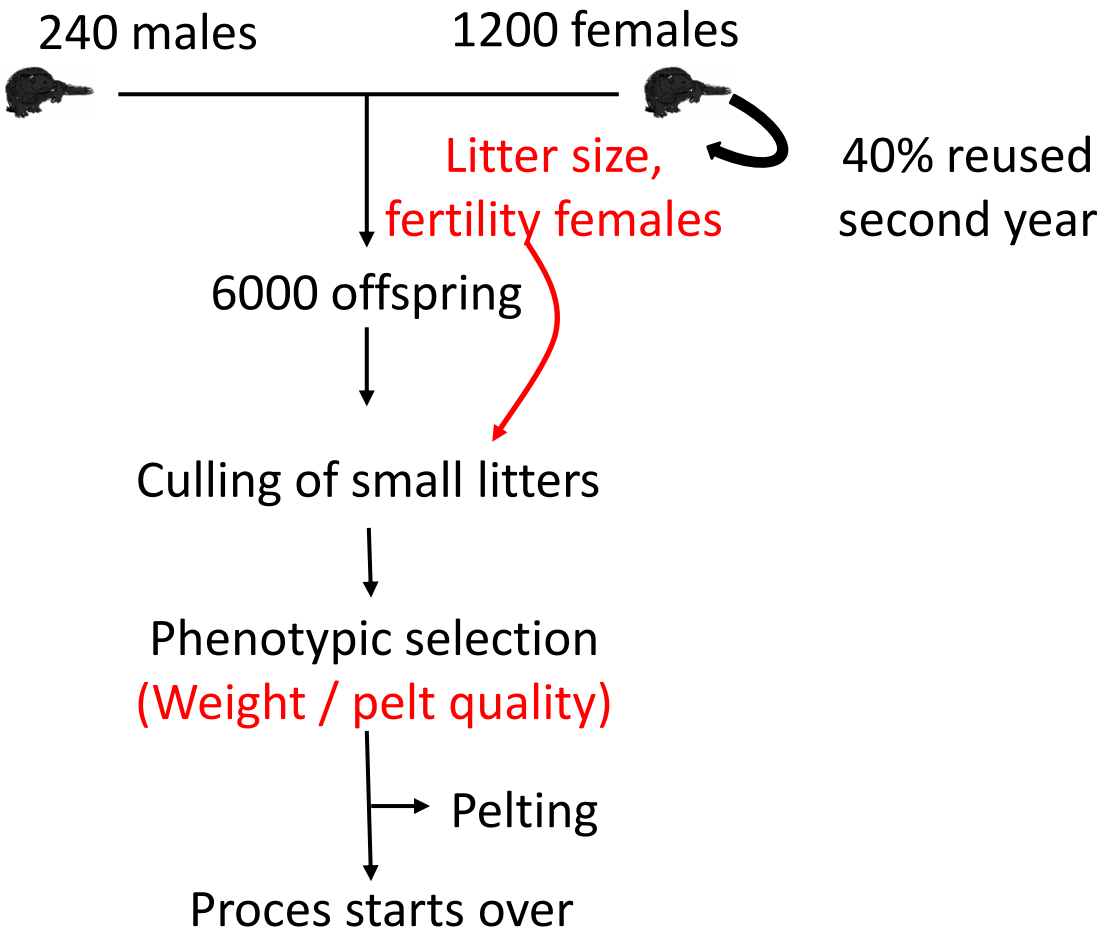
Limited reproductive capacity of males and females

‘Weak’ infrastructure

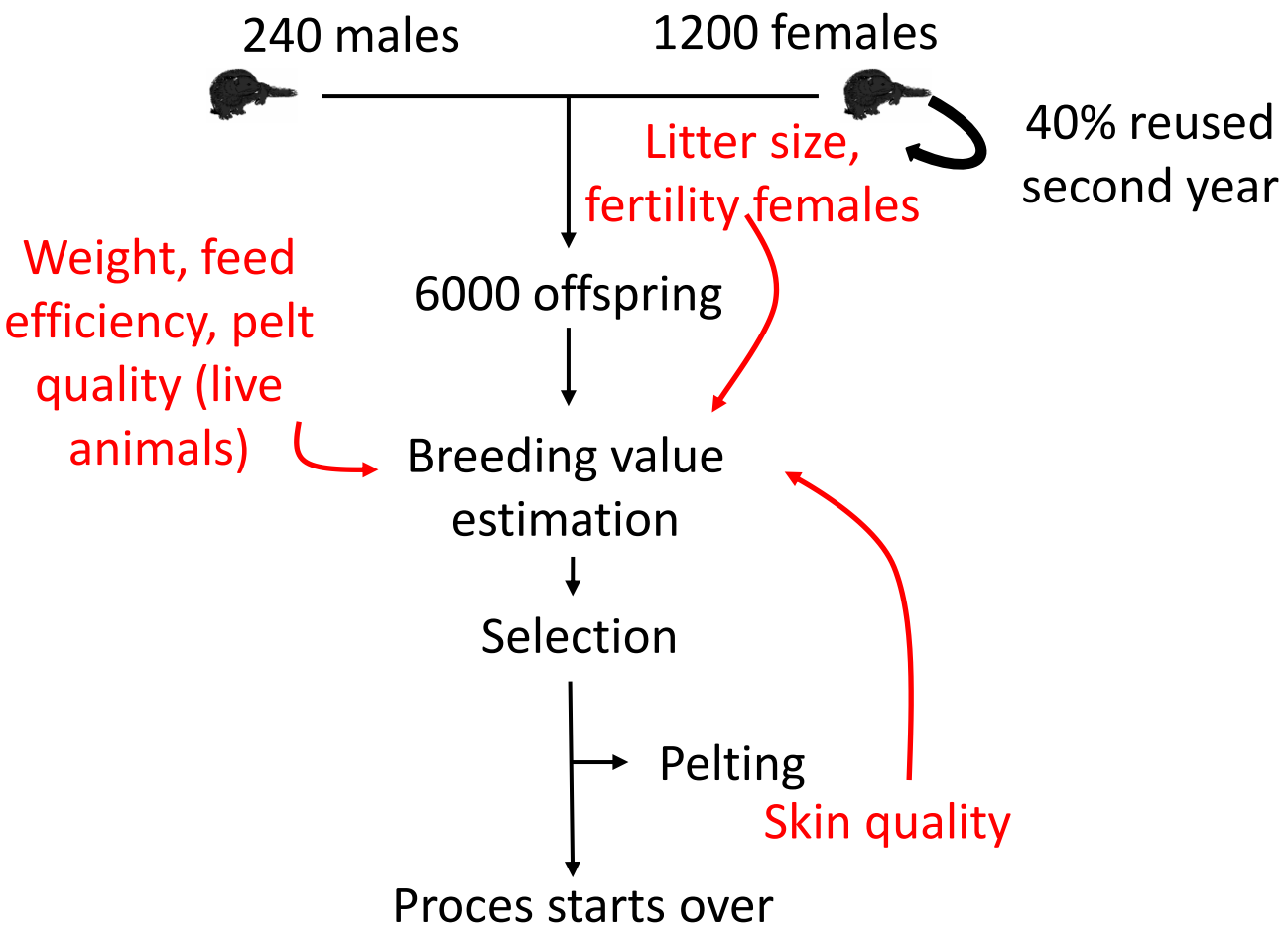
Individual farmers with own ‘breeding programs’

‘Private’ breeding goals

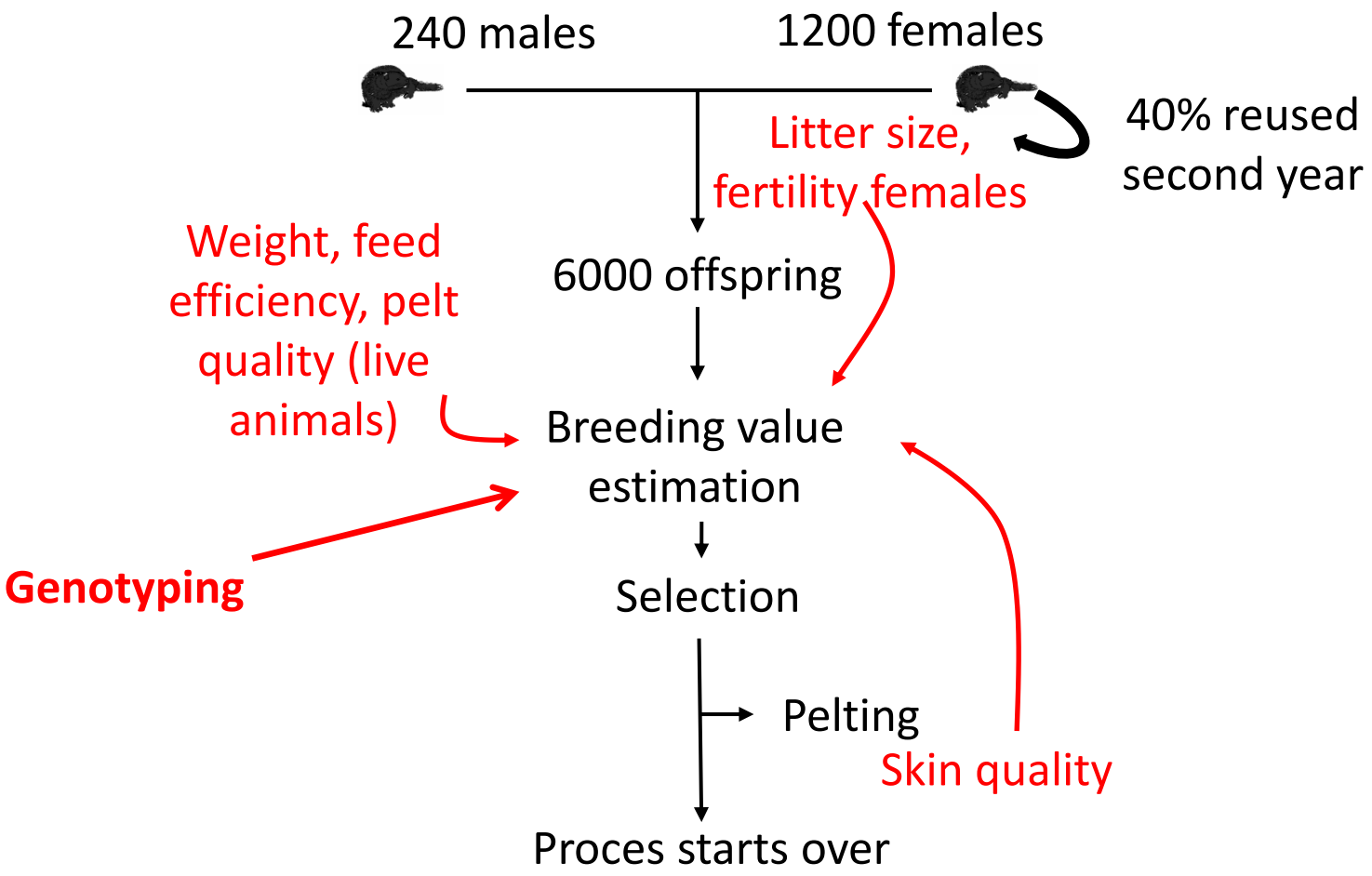
Many farmers still use phenotypic selection



A group of farmers use selection index



Potential use of genomic selection



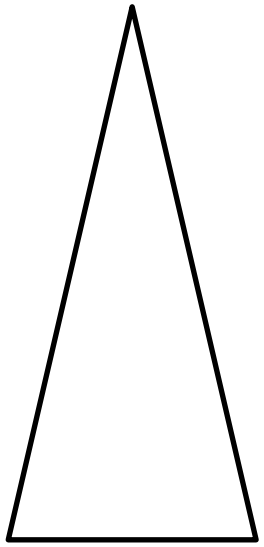
Total economic gain

	ΔG			
Phen	€6.1			
ST BLUP	€10.6			
MT BLUP	€13.0			
GS low	€14.0			
GS high	€23.3			

Contribution (%) to the total economic gain

	ΔG			
		Litter size	Weight	Pelt quality
Phen	€6.1	-21	100	-14
ST BLUP	€10.6	4	59	-10
MT BLUP	€13.0	32	18	8
GS low	€14.0	33	17	7
GS high	€23.3	50	9	2

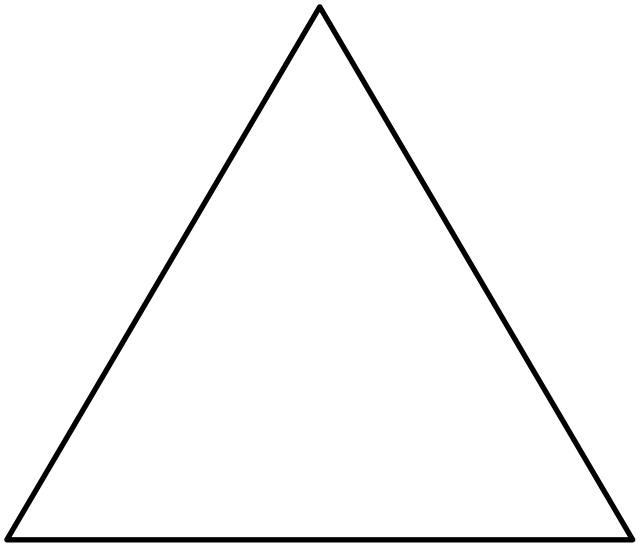
Dissemination



Nucleus

Multiplier

Production



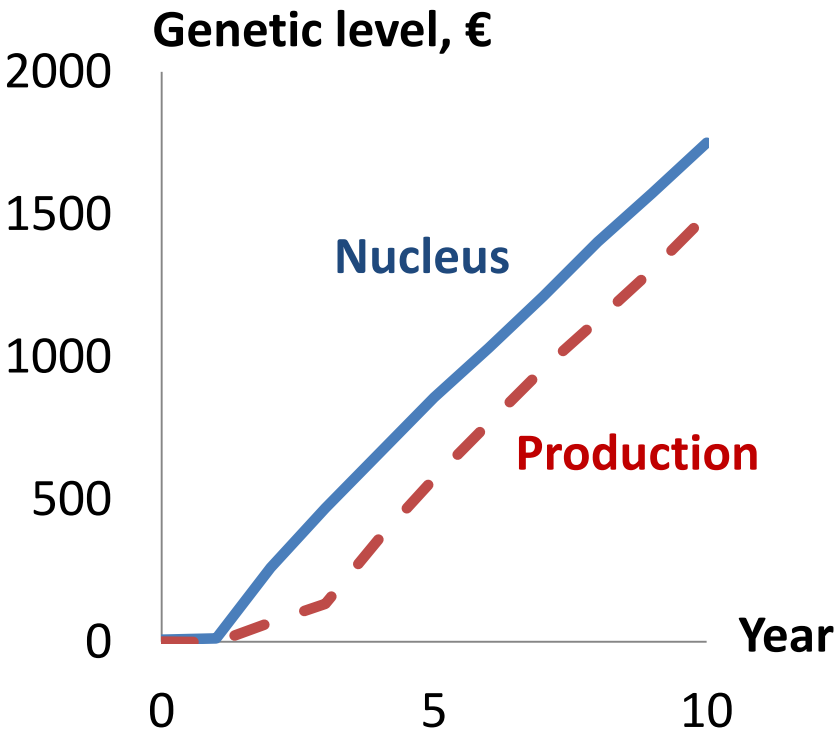
‘Narrow’

‘Wide’

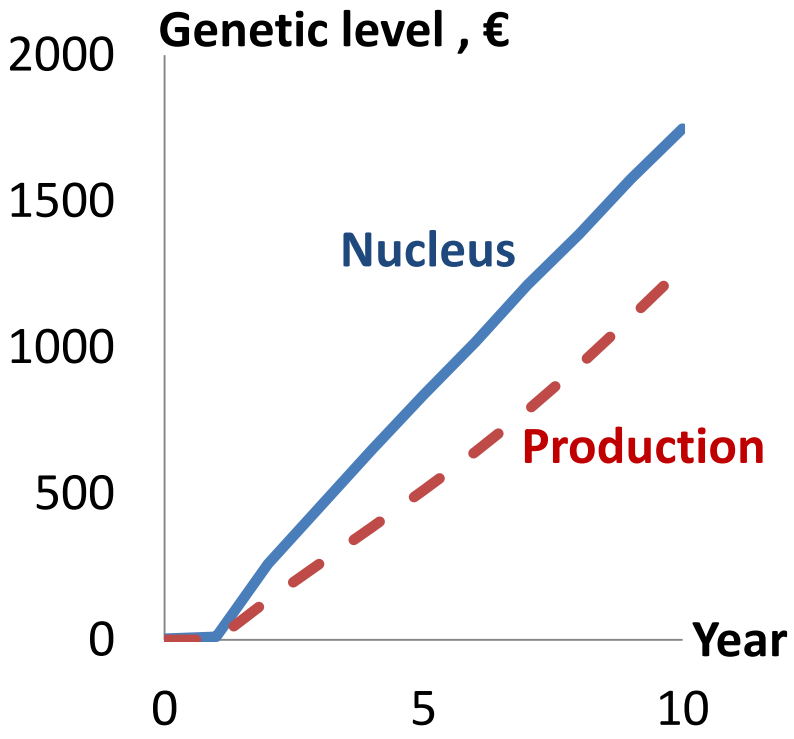
Complete replacement of females

Internal recruitment of females

Genetic trend and genetic lag



‘Narrow’



‘Wide’

Genetig lag, years

	‘Narrow’	‘Wide’
Low accuracy	-1.4	0.1
High accuracy	-1.4	-2.6

Low: Multiplier makes more genetic gain in ‘wide’

High: The ‘narrow’ structure disseminates gain effectively

Genomic selection increases total economic gain

Increased genetic gain for litter size

Best dissemination structure depends on the rate of genetic gain

Genomic selection should improve mink breeding