

GS and the design of breeding programs

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Introduction

- GEBV are available in many countries
 - GBLUP (1step or blended GBLUP-TBLUP)
 - Bayes(A)/B/C
- Expectations high: accurate GEBV for:
 - Young genotyped animals
 - Nonrecorded animals (trait nor pedigree)
 - Difficult /costly traits
 - Animals living in a different environment (GxE)
 - Low heritability traits

AIM:

- Develop and compare alternative GS-breeding designs
- Demonstrate their results in computer simulations
 - accuracy of GEBV is result of the design

General Methods (1): simulation of (cattle) base population

- $N_e=200$ (Fisher-Wright idealised pop.)
- 2,000 ($=N_e * 10$) discrete generations
- 30 chroms of 1 Morgan each (10^6 bp)
- Mutation $10^{-8}/\text{bp}$ (infinite sites mutation mod)
- Recombination $10^{-8}/\text{bp}$
- 3,000 random SNPs => QTL
 - QTL effects from double exponential distrib.
- 15,000 SNPs with $MAF \sim 0.05$
 - Marker \neq QTL

Use same base population
for all alternative schemes

Simulation of breeding scheme

- Not possible to simulate entire cattle/pig/fish pop.
- Reduced size of simulated population
 - Number of selected males the same (in SD and SS)
 - Selected selection intensities identical
 - Conventional scheme: similar ΔG and ΔF
 - progeny test: keep test population outside breeding pop
 - Simulate progeny test results by DYDs:

$$DYD_i = \frac{1}{2}TBV_i + \sqrt{\frac{\frac{3}{4}V_g + V_e}{N_{dghtrs}}} * r_i$$

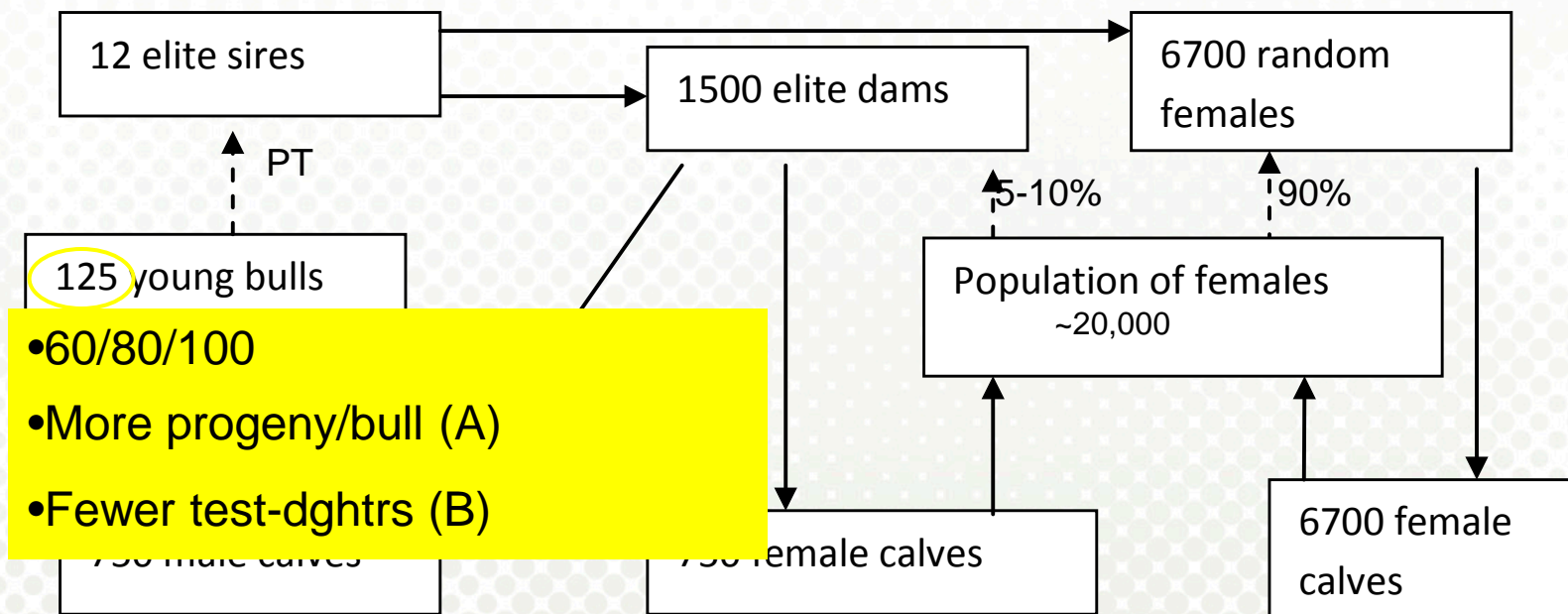
GS in cattle breeding schemes



Dairy cattle are ideal for GS:

- Progeny testing scheme:
 - Expensive
 - Slow (generation turn-over of 5-6 generations)
- Schaeffer (2006): ΔG^*2 and costs reduced
- N_e is small: big chromosome segments
- Bulls with known reliable DYDs
 - Large (across country) reference population
 - Bulls are valuable (spending 200 € is ok)

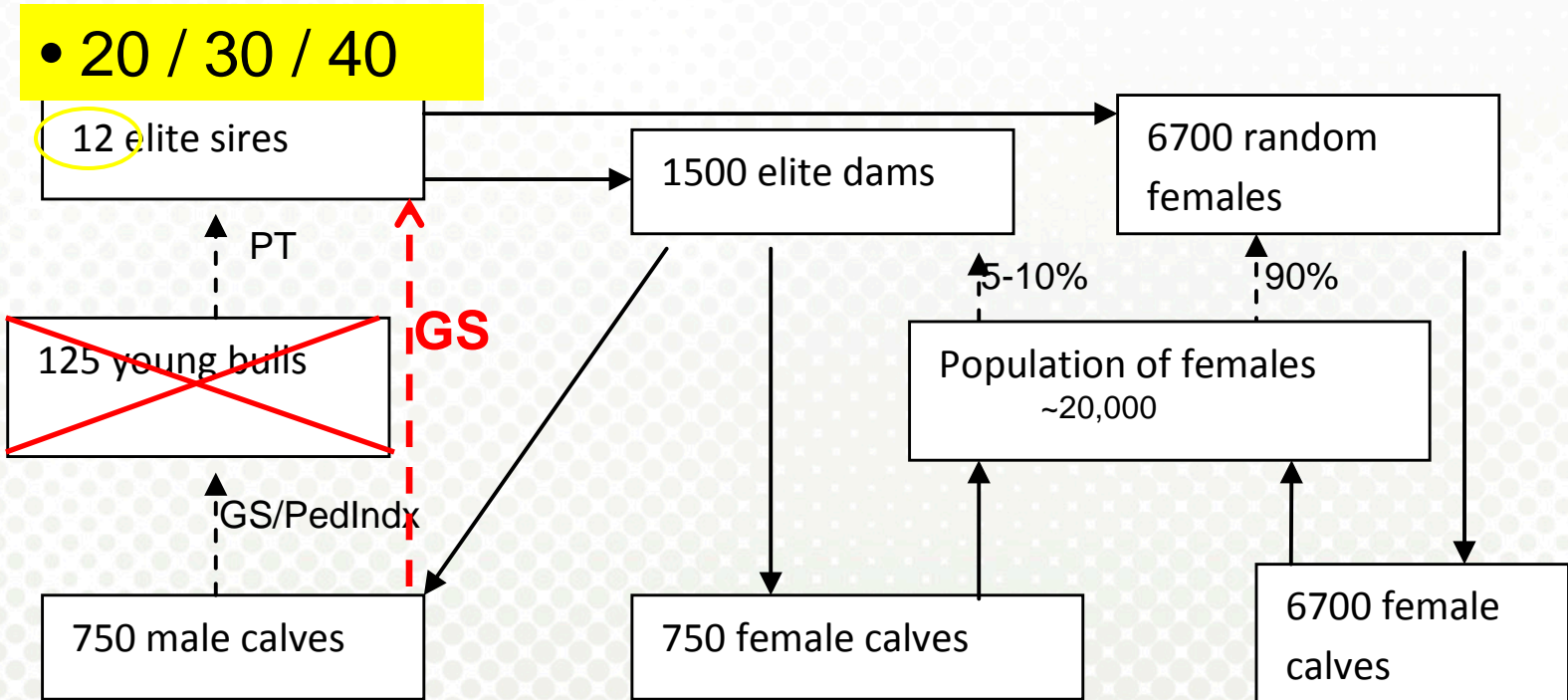
Preselection of young bulls in NRF (PS)



- 60/80/100
- More progeny/bull (A)
- Fewer test-dghtrs (B)

-----> Selection (TBLUP, unless stated otherwise)

Full genomic selection scheme (GS)



-----> Selection (TBLUP, unless stated otherwise)

Traits & GEBV

$$TBV_i = \sum_{j=1}^{3000} x_{ij1} g_{j1} + x_{ij2} g_{j2}$$

- $Y_i = TBV_i + e_i$
- $e_i \sim N(0, V_e)$
- V_e is adjusted so that h^2 is .1, **.15** or .30
- Trait recording: at 2-yr-old females (gen.interv. = 3yr)
- Progeny test: 5-yr-old sires (gen.interv. = 6yr)
- GS: only applied to young-bulls;
 - GBLUP (BLUP of marker effects; no blending):

$$y_i = \mu + \sum_{j=1}^n X_{ij} a_j + e_i$$

$$GEBV_i = \sum_{j=1}^n x_{ij} a_j$$

Results: preselection schemes

	ΔG	ΔF	Acc
Conv	1	1	xx
PS_125	1.13	0.67	0.7
PS_60A	1.13	0.68	0.68
PS_60B	1.11	0.63	0.66

Conv: $\Delta G=0.22 \sigma_g/\text{yr}$; $\Delta F=.0025/\text{yr}$

Lillehammer et al, 2011

Full GS schemes

	ΔG	ΔF	Acc
Conv	1	1	xx
GS_12	1.33	0.98	0.61
GS_30	1.25	0.47	0.63
GS_40	1.2	0.36	0.63

Conv: $\Delta G=0.22 \sigma_g/\text{yr}$; $\Delta F=.0025/\text{yr}$

Lillehammer et al, 2011

Effect of h^2 on ΔG

	ΔG		ΔF	
h^2	0.1	0.3	0.1	0.3
Conv	1	1	1	1
PS_125	1.15	1.11	0.69	0.57
GS_12	1.4	1.29	0.93	1.14
GS_40	1.25	1.17	0.33	0.35

Including females

- For selection:
 - Reduce generation interval in DS path
 - Avoids preferential treatment problem
- For training:
 - Need large numbers
 - $h^2 = .15 \Rightarrow$ 6 times as many as proven bulls
- Accross country/breed GS
 - see thesis Rasmus Brøndum

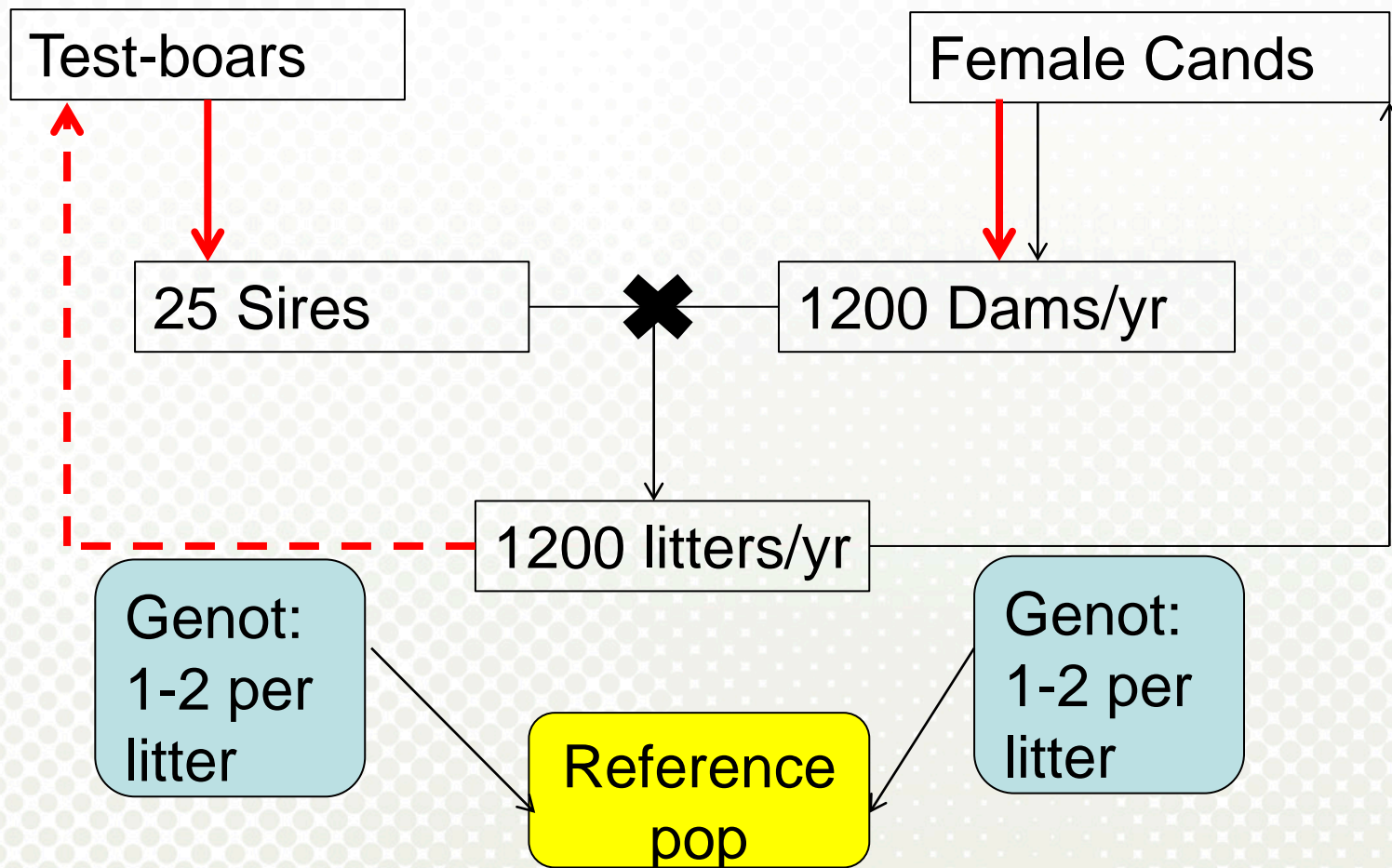
Pig breeding schemes



Opportunities for GS in pig breeding

- 1) Sow-lines: maternal traits are not recorded in boar test
- 2) Slaughter quality traits
- 3) GxG: crossbred \neq purebred performance
 - Estimate SNP effect in crossbreds
- 4) GxE: Enucleus \neq Epractice
 - Estimate SNP effects in practice
- 5) Selection further down in production pyramid

Breeding design



Results ($r_g(\text{product};\text{matern}) = -0.3$)

	ΔG	ΔF	Mat%
CONV	0.62	0.88 %	18
GS1200	0.79	0.48 %	26
GS2400	0.87	0.40 %	32
WL1200	0.88	0.57 %	27
WL2400	0.96	0.45 %	33

Lillehammer et al., 2013a

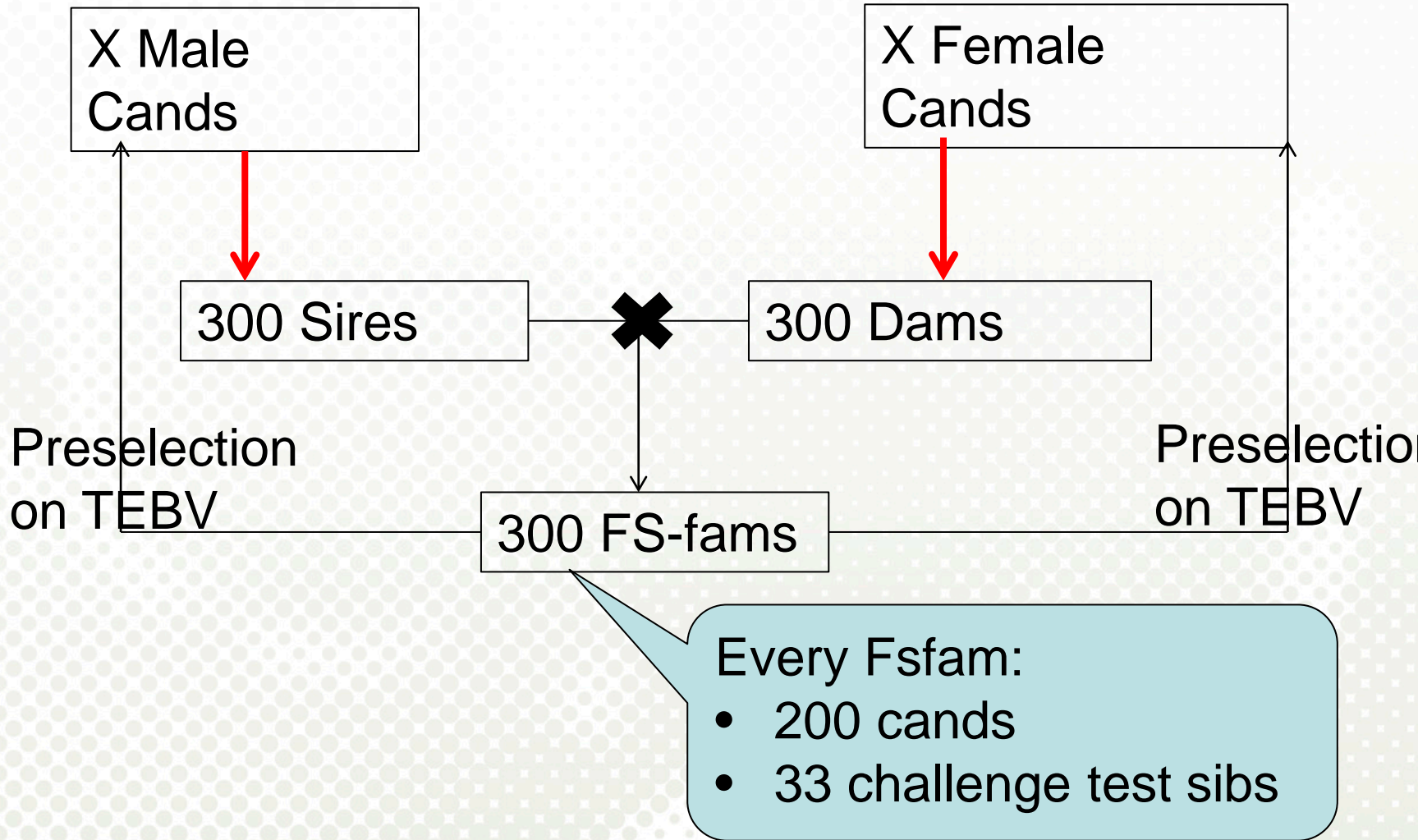
GS in Fish Breeding



Lots of opportunities, but...

- Big full sib families
- Growth: easy
- Disease traits : challenge tests
 - Outside of the nucleus (sibs of the candidates)
- slaughter quality traits
 - Fillet %
- But: ratio genotyping costs / value of fish ↑
 - i.e. 30,000 candidates to genotype

Breeding design



Within family GS & Low density genotyping

Within fam-GS for SIB and PROD trait

	ΔG	SIB%	ACC
CONV	1.67	37 %	0.56
6SNP/M	1.84	40 %	0.59
25SNP/M	1.91	38 %	0.61
100SNP/M	1.95	37 %	0.62

Lillehammer et al. 2013b

Inbreeding management in GS schemes



Introduction

- Past: pedigree relations used for ΔF control
 - Measures inbreeding at unlinked, neutral loci
 - Do these exist?
- Currently GBLUP: more accurate Gmatrix
- Optimum contribution selection
 - With genomic control of inbreeding ?

OC with ΔF constraint 0.005

	ΔG	ΔF -ped	ΔF -genom
ΔFA -TEBV	2.26	0.005	0.007
ΔFA -GEBV	3.08	0.005	0.021
ΔFG -GEBV	1.91	0.004	0.005

Sonesson et al., GSE, 2012

Conclusions ΔF manag.:

- Traditional selection acts on Mendelian sampling terms (MST)
- ΔF management: constrain $\text{Var}(\text{MST})$
 - OC acts on pedigree inbreeding
- Genomic selection acts on SNPs
- ΔF management should constrain $\text{Var}(\Delta q)$
i.e. variance of freq. change of SNPs
 - OC acts on G matrix based on SNPs
- If not OC finds 'holes':
 - ways to increase ΔF that are undetected by A

Conclusions dairy cattle breeding:

- Full GS scheme is best
 - Highest ΔG and ΔF
 - Can select more elite sires to reduce ΔF
 - Which also increases the reference population
 - BUT: perhaps risky
- Pre-selection scheme:
 - Close to current scheme
 - Can save some costs by reducing progeny test
 - Increase ΔG and reduce ΔF

Conclusions pig breeding

- GS for maternal trait in sow line:
 - $\Delta G < 45\%$ up; $\Delta F < 40\%$ down
 - genotyping females => more gain for fertility
 - GS on males to enter boar test
 - Increase ΔG by 5-11%
 - Did not alter the balance production/maternal traits
- other applications of GS were discussed

Conclusions fish breeding

- Large families facilitated within fam-GS
 - Low density marker panels
 - High selection accuracy (fam-size >16)
 - preselection on TEBV needed to further reduce genotyping costs
 - ΔG improvements of 15%; ΔF down by 15%
 - Better balance PROD vs. DISEASE ΔG

General Conclusions :

- GS => more sustainable breeding
 - Low h^2 traits improve relatively more
 - Improvement of fertility & disease resistance
 - Still need large scale recording
 - Re-estimate SNP effects