



GenSAP

Status on GenSAP for assessment and optimisation

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What GenSAP can do for us

- Time for development of tools
- Time for uncovering and understanding mechanism underlying consequences of selection
- Both of these support the industry projects





Diminishing marginal returns from genomic selection as more selection candidates are phenotyped

T. O. Okeno, M. Henryon and A. C. Sørensen





> Hypotheses

- There is diminishing marginal return from genomic selection as more candidates are phenotyped
- Phenotyping candidates based on *a priori* information is beneficial
- ✓ There is a best distribution of phenotypes on the sexes with respect to genetic gain and inbreeding rate







ΔG , genotypic standard deviation









ΔG , genotypic standard deviation



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ΔG , phenotypic standard deviation







Diminishing return as more candidates are phenotyped

Use of *a priori* information to select animals to phenotype is beneficial

- Mainly phenotyping sex with high selection intensity is beneficial at low phenotyping proportions
- Less intensively selected sex should also be considered at high phenotyping proportions



Specific challenges adressed in GenSAP SFA3

Extended tool box

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- Non-additive genetic variation (<u>Hadi</u>)
- Selection across multiple environments
- Use of genomic information for handling inbreeding (<u>Huiming</u>)
- Proof-of-concept (<u>Kristian</u>)





Maximizing crossbred performance through purebred genomic selection

Hadi Esfandyari Christian Sørensen Piter Bijma





Aims

• To investigate the benefits of GS of purebreds for CP based on purebred information

• To compare separate pure line reference populations with a joint reference population



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Predicting crossbred performance

- Predicting additive and dominance effects of each marker
- Purebred breeding value of an animal depends on allele frequency in its own breed
- Crossbred breeding value of an animal depends on allele frequency in the other breed





Performance of crossbreds







Conclusions

- Selecting the pure lines for crossbred performance increases phenotypic performance of crossbreds
- Selecting for crossbred performance increases the expression of heterosis
- If the breeds are closely related a joint reference population is beneficial





Maintenance of genetic diversity in genomic selection

Huiming Liu

Supervisors:

- Elise Norberg
- Peer Berg
- Christian Sørensen
- Theo Meuwissen





How to maintain the genetic diversity?

Putting more weight on the rare favourable alleles (WGEBV)

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 Optimum contribution selection (OCS)

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Selection design







Genetic gain







Conclusion

The strategy that combines WAF and OCS is very promising ⁽ⁱ⁾





Genomic selection in mink (*Neovison vison*): A simulation study



Kristian Meier Anders Christian Sørensen Janne P. Thirstrup Mogens Sandø Lund



Breeding plan without genomic information







Simulation design

• Do we need to make DNA analysis on all selection candidates?

Number of DNA analysis				
Selection candidates	Number			
All	6000			
Best 10% males	300			

- How high accuracy do we get with genomic selection in mink?
 - We don't know?
 - We simulate scenarios with low, medium and high accuracy





Monetary genetic gain

Genomic selection		Total economic gain Dkr pr. female pr. year	
Accuracy	DNA analysis	V	
High	All	97	
	10 % best males	71	
Low	All	60	
	10 % best males	57 4	
Breeding plan without genomic information		54 🖌	





Genetic gain in traits

Geno	mic selection	Contribution (%) from five traits to the total economic gain				
		Litter size	Weight	Barren females	Pelt quality	Feed efficiency
Accuracy	DNA analysis					
High	All	42	19	19	0	20
	10 % best males					
		26	37	12	-5	30
Low	All	12	51	7	-8	39
	10 % best males	10	54	4	-9	41
Breeding pl ir	an without genomic nformation	4	59	2	-10	45





Conclusion

- Genomic selection increases total economic gain
- Increased genetic gain for litter size, barren females and pelt quality
- Even at low accuracy and few DNA analyses genetic gain is increased





Future work

- Evaluate different economic weights
- Cost (DNA) benefit (economic gain) analysis
- Future infrastructure supporting genomic selection







Wrap-up

- So far, we have just scratched the surface
- Recruitment allows us to speed up from January
 - PhD at NMBU started September 1st 2014
 - Post Doc jointly with SFA1 starting January 1st
 2015
 - Post Doc assisting with ADAM programming starting January 1st 2015



Specific challenges adressed in GenSAP SFA3

- Extended tool box (Huiming, Jørn, Mark, Beatriz)
- Non-additive genetic variation (<u>Hadi</u>)
- Selection across multiple environments
- Use of genomic information for handling inbreeding (<u>Huiming</u>, Gebreyohans, Tobias)
- Proof-of-concept (<u>Kristian</u>)

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