

# Single-step Marker Assisted Selection in breeding value estimation:

## *Do markers add value?*

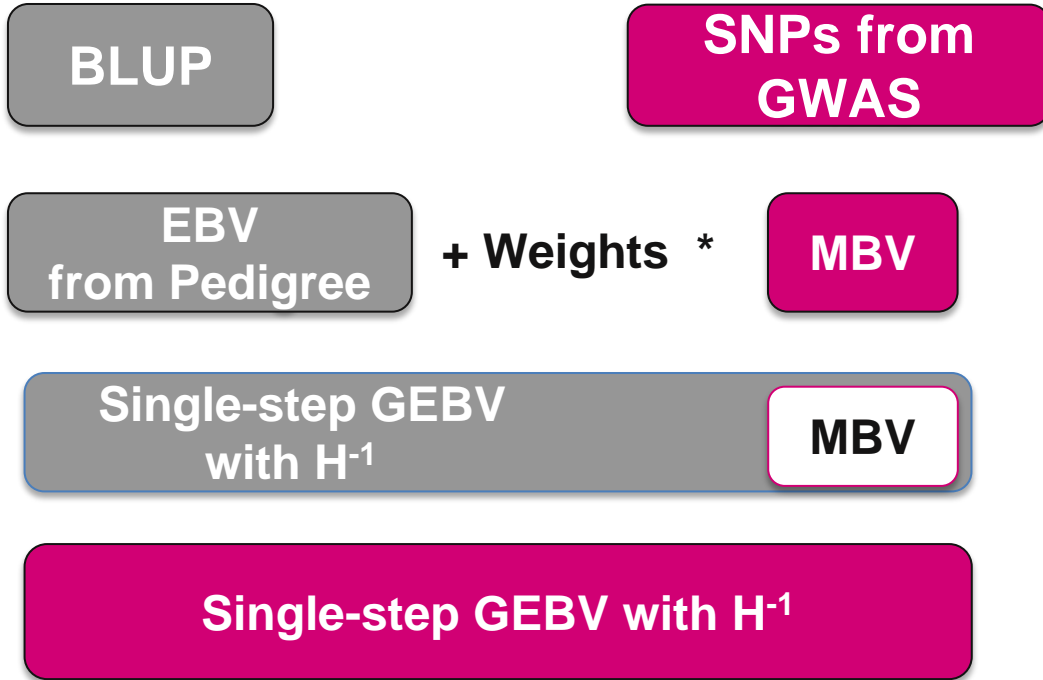
Birgit Zumbach, Marcos Lopes,  
Susan Wijga, Rob Bergsma, Egbert Knol



**Topigs Norsvin**

PROGRESS IN PIGS

# Use of genotype information in breeding value estimation



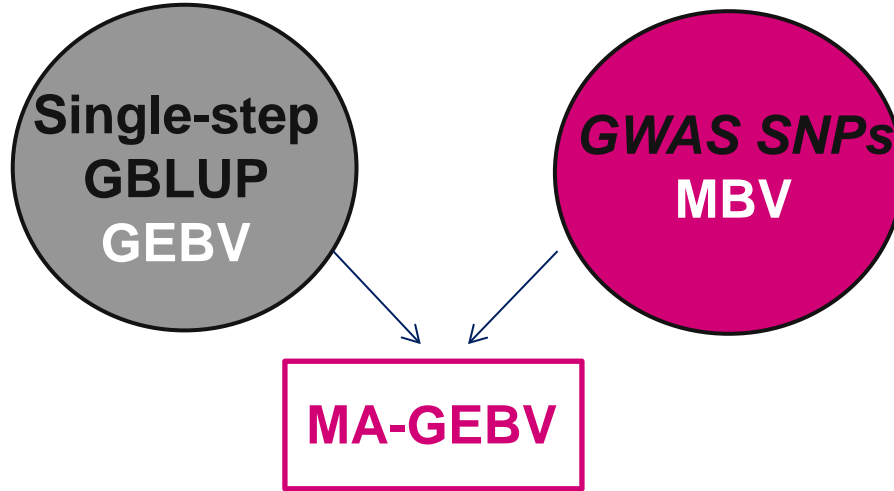
# MA-ssGBLUP

012101112200.....00112012221022211110000  
 211122200012.....00120011122211112221100

All available SNP  
genotypes' H

1 1 2 1 0 1 0  
 1 0 0 1 2 2 1

Selected SNPs  
with large effects



MiXBLUP-  
1step  
procedure

- **GEBV**=single step GBLUP Breeding Value
- **MBV**= Breeding value due to the effect of special markers with a large effect in GWAS analyses ( $MBV = \sum_{i=1}^n p_i * m_i$ ) *m*= marker effect, *p*=number of copies of an allele/genotype probability, *n*=number of markers
- **MA-GEBV**=Single step Marker assisted breeding value ( $MA-GEBV = GEBV + MBV$ )

# GWAS for Number of teats

Duijvesteijn *et al.* *BMC Genomics* 2014, **15**:542  
<http://www.biomedcentral.com/1471-2164/15/542>



**RESEARCH ARTICLE**

**Open Access**

## High-resolution association mapping of number of teats in pigs reveals regions controlling vertebral development

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# GWAS for Number of teats

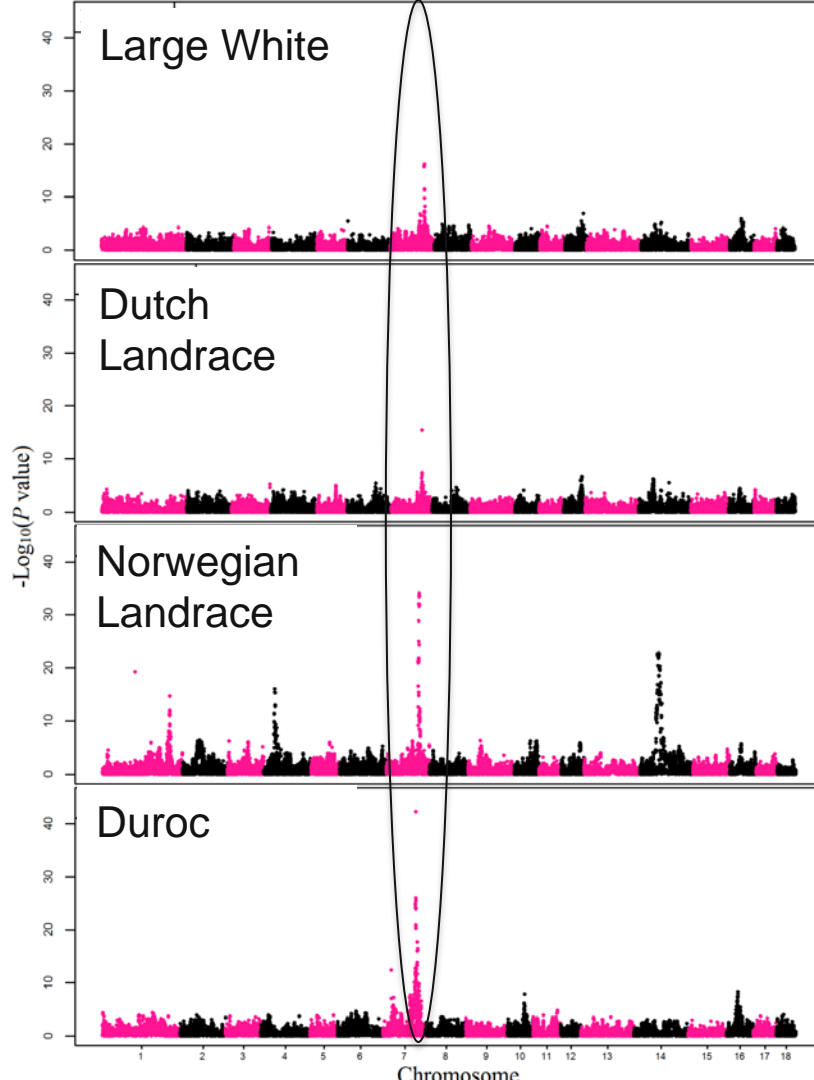
## Using markers with large effect in genetic predictions

Marcos S Lopes<sup>1,2</sup>, Henk Bovenhuis<sup>2</sup>, Maren van Son<sup>3</sup>, Øyvind Nordbø<sup>3</sup>,  
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Norsvin, 2317, Hamar, Norway





**QTL at SSC7, pos ~103 MB**  
Comparable to DGAT in Holstein

**GWAS on number of teats**  
in four pig populations

## Number of teats GWAS SNPs – Large White

SNP	Chrom.	Position (MB)	SNP effect (GWAS)
1	7	103.5	0.33

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## Number of teats GWAS SNPs – Large White

SNP	Chrom.	Position (MB)	SNP effect (GWAS)
1	7	103.5	0.33
2	10	52.6	0.12
3	12	40.0	0.11
4	16	30.7	0.11



# Genotype probabilities

## Genotyped animals

N~14,000

Real genotypes

Id	M1	M2	M3	M4
1	0	1	2	2
2	2	1	0	0
3	2	1	1	0

## Genotyped and non-genotyped animals

N~740,000

Genotype probabilities

Id	M1	M2	M3	M4
1	0.125	0.963	1.753	1.641
2	1.832	1.106	0.403	0.102
3	1.792	1.112	0.875	0.305

Genotype probability:  $y = \mu + a + e$   
 $Va=0.99; Ve=0.01$

→ Scale to range [0;2]

→ Genotype probability also for non-genotyped animals

# Genotype probabilities

Range of genotype probabilities:  $< 0$  to  $> 2$

→ Transformation to a range  $[0,2]$

$$f(x) = \frac{(b-a)(x-min)}{max-min} + a$$

$x$ = genotype probability

$min$ =minimum genotype probability

$max$ =maximum genotype probability

$a$ =minimum of new range=0

$b$ =maximum of new range=2



# Reproduction data Large White

## Phenotypes:

- January 1995 to November 2015
- 13 traits

## Number of teats - simple statistics

N	Mean	SD	Min	Max
735,971	15.1	1.2	8	20

~14,000 genotypes



# Statistical Model

MiXBLUP single trait / 13-trait evaluation

Number of teats = fixed effects + **a** + e

→ **ssGEBV**



# Statistical Model

## MiXBLUP single trait / 13-trait evaluation

Number of teats = fixed effects + **marker effects** + **a** + e

$$\underbrace{b_1 * m_1 + b_2 * m_2 + b_3 * m_3 + \dots b_n * m_n}$$

*b* = regression coefficient  
(fixed);  
*m* = marker;

→ **GEBV**, **MBV**, **MA-GEBV**

$$\text{MA-GEBV} = \text{GEBV} + \text{MBV}$$

$$\underbrace{\sum_{i=1}^n p_i * b_i}$$

*p* = number of copies of  
allele /  
genotype probability;  
*n* = number of markers;

$$\text{ssGEBV} \neq \text{GEBV}$$

# Validation

	<b>N</b>	<b>Mean</b>	<b>SD</b>	<b># typed</b>
Training	539,106	14.9	1.1	8,767
Validation	196,865	15.5	1.1	4,961

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Validation = 27% youngest animals; 36% genotypes



## Results: SNP effects

SNP	Single Trait (4 SNPs)	13-Trait (4+10 SNPs)	<i>GWAS</i>
1	0.39	0.39	0.33

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## Results: SNP effects

SNP	Single Trait (4 SNPs)	13-Trait (4+10 SNPs)	<i>GWAS</i>
1	<b>0.39</b>	<b>0.39</b>	0.33
2	0.14	0.18	0.12
3	0.14	0.14	0.11
4	0.10	0.16	0.11

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# Results: Predictive Ability

Correlation between adjusted phenotype and predicted breeding value

- 13-trait model, genotyped animals -

Breeding value	NTE SNP 1 + 10
MBV	0.130
GEBV	0.449
MA-GEBV	0.465
<i>ssGEBV</i>	<i>0.462</i>

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# Results: Predictive Ability

Correlation between adjusted phenotype and predicted breeding value  
- 13-trait model, genotyped animals -

Breeding value	NTE SNP 1 + 10	NTE SNPs 1-4 + 10
MBV	0.130	0.208
GEBV	0.449	0.428
MA-GEBV	0.465	0.469
<i>ssGEBV</i>	<i>0.462</i>	<i>0.462</i>

# Discussion



## Using markers with large effect in genetic predictions

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## Size of reference population

Population	# genotypes Training	predictive ability	
		ssGBLUP	MA-ssGBLUP
Large White	2,620	0.361	0.370
Norwegian Landrace - all	6,090	0.474	0.477

---



## Size of reference population

Population	# genotypes Training	predictive ability	
		ssGBLUP	MA-ssGBLUP
Large White	2,620	0.361	0.370
Norwegian Landrace - all	6,090	0.474	0.477
-reduced	2,400	0.423	0.446

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## Size of reference population

Population	# genotypes Training	predictive ability	
		ssGBLUP	MA-ssGBLUP
Large White	2,620	0.361	0.370
Norwegian Landrace - all	6,090	0.474	0.477
-reduced	2,400	0.423	0.446
<i>Large White - 1 SNP</i>	<i>8,767</i>	<i>0.462</i>	<i>0.465</i>

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# Summary

- Trait with obvious QTL
- SNP effects MA-ssGBLUP are similar to GWAS SNP effects
- MA-GBLUP run:  
Increase in accuracy of MBV → Reduction in accuracy of GEBV  
→ Part of animal variance is shifted toward the SNP effects
- Marginally increased accuracy of MA-ssGBLUP vs ssGBLUP
- GWAS and calculation of genotype probabilities for MA-ssGBLUP





# Conclusion

- Large enough genotyped animals in reference population

negligible increase in accuracy

=> No added value of MA-ssGBLUP



# Thank you !

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