AARHUS
UNIVERSITY

CENTER FOR QUANTITATIVE
GENETICS AND GENOMICS

Model comparison based on genomic predictions of litter size and piglet mortality

X. Guo, O. F. Christensen, T. Ostersen, D. A. Sorensen,
Y. Wang, M. S. Lund, G. Su

AARHUS
UNIVERSITY

CENTER FOR QUANTITATIVE
GENETICS AND GENOMICS

Profile

➢ Xiangyu (Carol)

- > Ph.D student
- > Center for Quantitative Genetics and Genomics
- > Department of Molecular Biology and Genetics
- > Aarhus University, Denmark

Outline

- Introduction
- Materials & Methods
- Results & Discussion
- Conclusions

Outline

- **Introduction**
- **Materials & Methods**
- **Results & Discussion**
- **Conclusions**

Litter size & mortality

- Litter size & mortality
  - reproductive traits of major economic importance
- Total number born
  - litter size at weaning ↑ mortality ↑
- Litter size at d 5
  - litter size at weaning ↑ mortality ↓

Genomic selection

- Genomic selection
  - widely used in livestock breeding
- Advantage of genomic selection
  - higher accuracy of prediction in pigs
- Single-step
  - using both genotyped and non-genotyped animals

Objective

- Compare the accuracy of traditional BLUP, genomic BLUP, and single-step methods, for genetic evaluation of litter size and piglet mortality in Danish Landrace and Yorkshire populations

Outline

- Introduction
- **Materials & Methods**
- Results & Discussion
- Conclusions

Data

- Phenotypes
  - TNB: total number of piglets born
  - LS5: litter size at five days after birth
  - Mort: mortality rate before day 5
- Genotypes
  - Illumina PorcineSNP60 BeadChip
- Pedigree
  - traced back to 1994

Size of data

	Landrace	Yorkshire
Birth	1998 to 2012	
Litter	778,095	472,001
Sow	309,362	190,760
Pedigree	332,795	207,255
Genotyped individual	3,445	3,372
Boar	1,366	1,241
Sow	2,079	2,131
Marker	38,435	38,631

Size of data

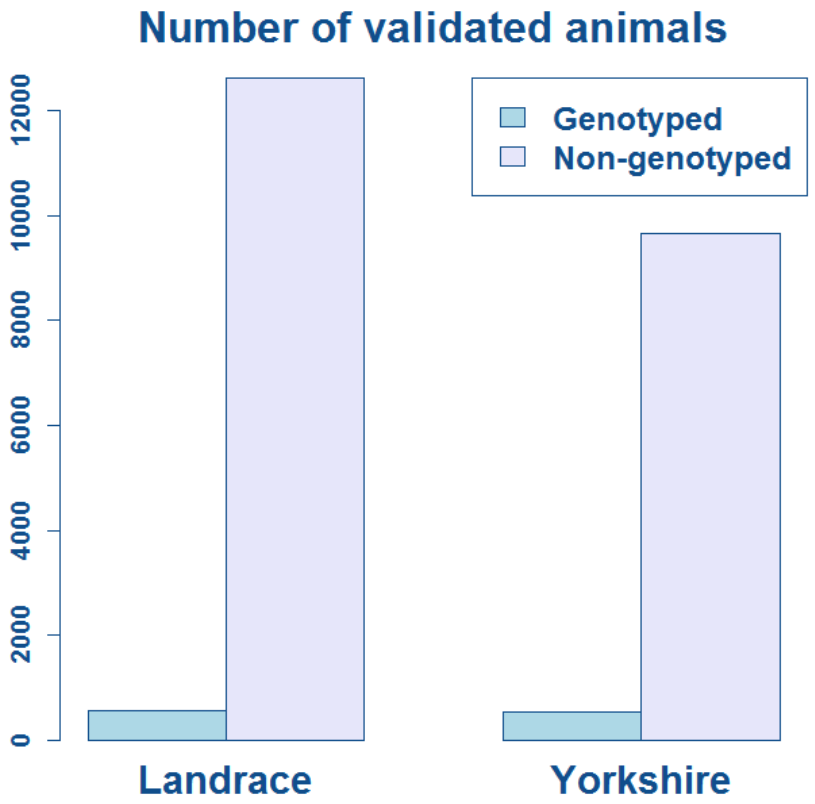
	Landrace	Yorkshire
Birth	1998 to 2012	
Litter	778,095	472,001
Sow	309,362	190,760
Pedigree	332,795	207,255
Genotyped individual	3,445	3,372
Boar	1,366	1,241
Sow	2,079	2,131
Marker	38,435	38,631

Statistical models

- BLUP
  - pedigree-based relationship matrix
  - all records
- GBLUP
  - marker-based relationship matrix
  - pseudo records of genotyped animals
- Single-step
  - combined relationship matrix constructed from marker and pedigree
  - all records

Validation

- Cut-off birth date: 1st April, 2012
- $r^2 = \frac{cor^2(EBV, y_c)}{h^2_{y_c}}$
- $y_c = \hat{a} + \frac{\sum \hat{e_i}}{n_p}$



Outline

- Introduction
- Materials & Methods
- **Results & Discussion**
- Conclusions

Descriptive statistics and h^2

Breed	Trait	Average	h^2
Landrace	TNB	15.04	0.11
	LS5	12.25	0.09
	Mort	0.18	0.09
Yorkshire	TNB	15.54	0.09
	LS5	12.54	0.08
	Mort	0.18	0.09

Descriptive statistics and h^2

Breed	Trait	Average	h^2
Landrace	TNB	15.04	0.11
	LS5	12.25	0.09
	Mort	0.18	0.09
Yorkshire	TNB	15.54	0.09
	LS5	12.54	0.08
	Mort	0.18	0.09

- Average TNB, LS5 and Mort were around 15, 12 and 0.18

Descriptive statistics and h^2

Breed	Trait	Average	h^2
Landrace	TNB	15.04	0.11
	LS5	12.25	0.09
	Mort	0.18	0.09
Yorkshire	TNB	15.54	0.09
	LS5	12.54	0.08
	Mort	0.18	0.09

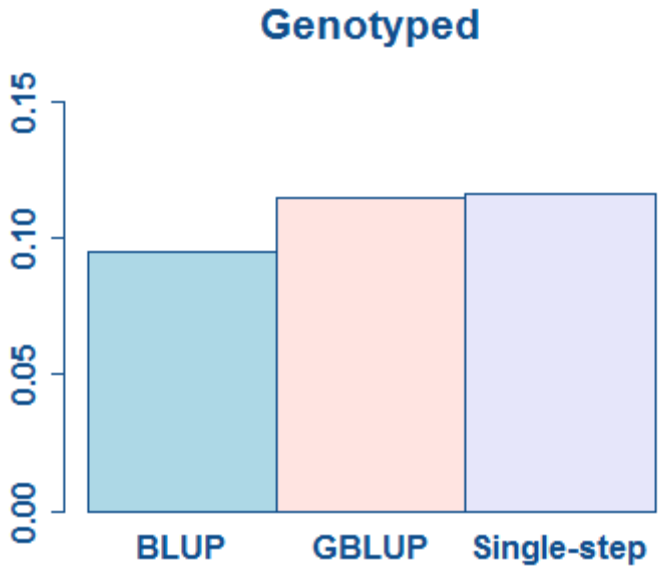
- Average TNB, LS5 and Mort were around 15, 12 and 0.18
- The estimates of heritability were low

Reliability of EBV

Breed	Trait	All		Genotyped			Non-genotyped	
		BLUP	Single-step	BLUP	GBLUP	Single-step	BLUP	Single-step

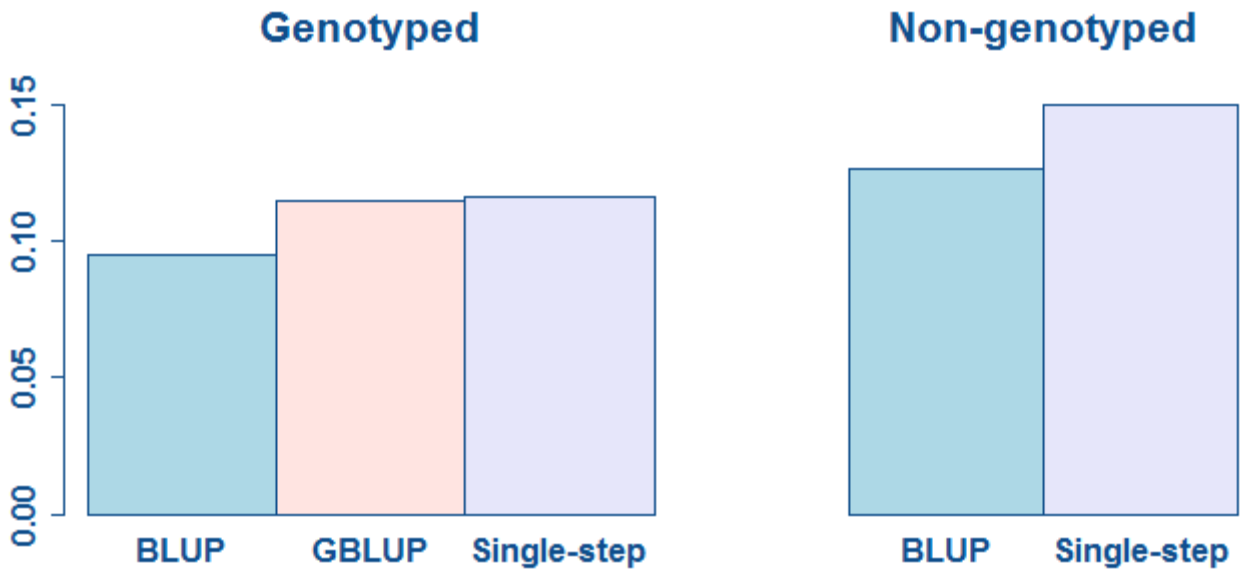
Reliability of EBV

Breed	Trait	All		Genotyped			Non-genotyped	
		BLUP	Single-step	BLUP	GBLUP	Single-step	BLUP	Single-step
Landrace	TNB	0.128	0.155*	0.095	0.115	0.116	0.126	0.150*



Reliability of EBV

Breed	Trait	All		Genotyped			Non-genotyped	
		BLUP	Single-step	BLUP	GBLUP	Single-step	BLUP	Single-step
Landrace	TNB	0.128	0.155*	0.095	0.115	0.116	0.126	0.150*



Reliability of EBV

Breed	Trait	All		Genotyped			Non-genotyped	
		BLUP	Single-step	BLUP	GBLUP	Single-step	BLUP	Single-step
Landrace	TNB	0.128	0.155*	0.095	0.115	0.116	0.126	0.150*
	LS5	0.071	0.081	0.004	0.080	0.018	0.072	0.079
	Mort	0.066	0.086*	0.030	0.229*	0.205*	0.068	0.081*
Yorkshire	TNB	0.148	0.178*	0.251	0.241	0.451	0.143	0.163*
	LS5	0.061	0.083*	0.120	0.245	0.334	0.059	0.074*
	Mort	0.074	0.085	0.044	0.115	0.128	0.076	0.084
Mean		0.091	0.111	0.091	0.171	0.209	0.091	0.105

- Methods with marker information provided more accurate predictions

Reliability of EBV

Breed	Trait	All		Genotyped			Non-genotyped	
		BLUP	Single-step	BLUP	GBLUP	Single-step	BLUP	Single-step
Landrace	TNB	0.128	0.155*	0.095	0.115	0.116	0.126	0.150*
	LS5	0.071	0.081	0.004	0.080	0.018	0.072	0.079
	Mort	0.066	0.086*	0.030	0.229*	0.205*	0.068	0.081*
Yorkshire	TNB	0.148	0.178*	0.251	0.241	0.451	0.143	0.163*
	LS5	0.061	0.083*	0.120	0.245	0.334	0.059	0.074*
	Mort	0.074	0.085	0.044	0.115	0.128	0.076	0.084
Mean		0.091	0.111	0.091	0.171	0.209	0.091	0.105

- Methods with marker information provided more accurate predictions
- Single-step method provided most accurate predictions

Outline

- Introduction
- Materials & Methods
- Results & Discussion
- **Conclusions**

Conclusions

- Genomics can increase reliabilities of EBV for litter size and piglet mortality
- Increased reliabilities were observed for genotyped as well as for non-genotyped animals
- Single-step is a useful method for practical genomic prediction

Thanks for your attention

Ole F. Christensen

Tage Ostersen

Daniel A. Sorensen

Yachun Wang

Mogens S. Lund

Guosheng Su

PIG RESEARCH
CENTRE

Take-home messages

- Genomics can increase reliabilities of EBV for litter size traits and piglet mortality
- Increased reliabilities were observed for genotyped as well as for non-genotyped animals
- Single-step is a useful method for practical genomic prediction