

Effect of IGF2 Gene on Sow Productivity Traits



MOHSEN JAFARIKIA¹, LAURENCE Maignel¹,
 STEFANIE WYSS¹, WIM VAN BERKEL², BRIAN SULLIVAN¹
¹CANADIAN CENTRE FOR SWINE IMPROVEMENT, OTTAWA, ONTARIO, CANADA
²WESTERN SWINE TESTING ASSOCIATION, LACOMBE, ALBERTA, CANADA
 contact: laurence@ccsi.ca

INTRODUCTION

The IGF2 gene is located on porcine chromosome 2 and a single nucleotide polymorphism (SNP) in intron 3 of this gene, which is paternally expressed, has been reported to have large effects on carcass quality traits and uniformity. It was reported in certain studies that this gene could also influence sow productivity and longevity. The aim of this study was to investigate the effect of the paternal allele of the IGF2 gene on several sow productivity traits such as litter size at birth and weaning, litter weight at weaning and farrowing interval in Canadian swine populations.

MATERIAL AND METHODS

Genotypes

- Sires were screened to identify heterozygous (AG) boars
- Daughters of heterozygous boars were genotyped
- Dams of these daughters were genotyped when available
- Table 1 shows numbers of daughters included in the analysis

Phenotypes

- Litter data from the Canadian Swine Improvement Program
- Landrace
 - 893 litter records in 16 herds from genotyped daughters of AG sires
 - 21,662 litter records on contemporaries also included in the analysis
- Yorkshire
 - 341 litter records in 11 herds from genotyped daughters of AG sires
 - 8,877 litter records on contemporaries also included in the analysis

Classification of daughters based on paternal allele

- AA daughters must have paternal A
- GG daughters must have paternal G
- For AG daughters
 - If dam is AA, must have paternal G
 - If dam is GG, must have paternal A
 - If dam is AG or unknown, daughter paternal allele based on probability
- Paternal allele probabilities were estimated according to Jafarikia et al., 2008

Statistical analysis

- Data analyzed using the GLM procedure from SAS
- Model included IGF2 paternal allele (A or G), contemporary group, sire, parity, service sire breed and inbreeding level of both the sow and the litter
- Least-square means for the traits analyzed are in Table 2

Table 2. Effect of IGF2 allele inherited from sire on sow productivity traits

Sow breed	Landrace		Yorkshire	
	A	G	A	G
Paternal allele inherited				
Number of sows	148	148	75	50
Number of litters	448	373	186	149
Average parity	3.10	2.61	2.39	2.85
Total piglets born/litter	11.92 ± 0.30	11.66 ± 0.31	12.95 ± 0.69**	11.61 ± 0.69**
Piglets born alive/litter	11.18 ± 0.30	10.84 ± 0.31	11.83 ± 0.65**	10.80 ± 0.66**
Stillborn piglets/litter	0.75 ± 0.12	0.83 ± 0.12	1.15 ± 0.28*	0.84 ± 0.29*
Piglets weaned/litter	9.79 ± 0.17*	9.96 ± 0.17*	9.34 ± 0.39	9.58 ± 0.38
Litter weight at weaning (kg)	64.1 ± 1.0*	66.6 ± 1.1*	58.4 ± 2.3	60.7 ± 2.7
Farrowing interval (days)	145.8 ± 0.7	146.1 ± 0.7	145.9 ± 1.1*	148.2 ± 1.2*

**Significantly different at 99% confidence level ($p < 0.01$)

*Significantly different at 90% confidence level ($p < 0.10$)

PROJECT DESIGN

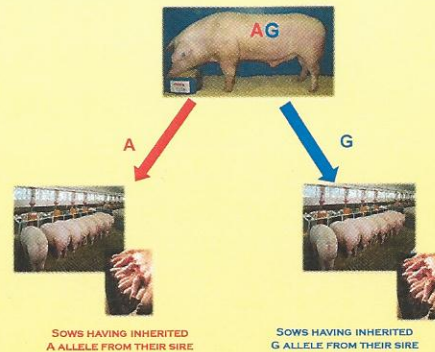


Figure 1. Main steps in IGF2 sow productivity project

Table 1. Numbers of daughters of AG boars having litter records in the CCSI database

Breed	AG boars	Originating herds of AG boars	Daughters by genotype (number of litters)			Total
			AA	AG	GG	
Landrace	23	10	144 (437)	156 (415)	13 (41)	313 (893)
Yorkshire	12	10	75 (186)	51 (151)	2 (4)	128 (341)

Imprinting allows for full benefit of both alleles since only the allele inherited from the sire is expressed

A allele
Higher carcass value and uniformity

G allele
Better sow productivity



100% of the A (lean) allele benefit using AA terminal line boars



100% of the G (fat) allele benefit using GG dam line boars

DISCUSSIONS AND CONCLUSIONS

- Higher total born and born alive in Yorkshire sows that inherited the paternal A allele in contrast to Buys et al. (2006)
- More stillbirths in litters born from Yorkshire sows that inherited the paternal A allele
- Tendency to higher numbers weaned and higher weaning weights for sows that inherited the paternal G allele, consistent with Buys et al. (2006)
- Genotyping of influential sires and to a lesser extent, dams has provided for accurate prediction of genotypes for many non-genotyped animals
- A lack of availability of DNA on some sires and dams of interest was a significant limitation

RECOMMENDATIONS

- Establish a system for routine storage of DNA for all nucleus parents
- Further study as more genotyping is done and more litter records accumulate to more accurately assess the impact on sow productivity
- Investigate other linked genes
- Evaluate the impact on productivity of crossbred sows (F1) through daughters of several GG vs. AA multiplier boars
- Genotype probabilities can be used to target further testing and mating to breed and select for specific genotypes

REFERENCES

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