

# ASSOCIATION OF GROWTH HORMONE AND INSULIN-LIKE GROWTH FACTOR-1 GENOTYPES WITH GROWTH AND CARCASS TRAITS IN OFFSPRING OF PUREBRED SWINE

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## SUMMARY

Contribution of growth hormone (GH), insulin-like growth factor-1 (IGF-1), and linked loci to growth and carcass traits in offspring of purebred sires was examined through segregation analysis. Offspring (n=150, 195 and 148) from three sires were genotyped at the GH and IGF-1 loci and evaluated for preweaning and postweaning average daily gain, 10th rib backfat and loin-eye area. Paternal GH and IGF-1 marker inheritance was determined and their association with growth and carcass traits evaluated. Significant associations were observed between GH genotype and loin-eye area in one family and between IGF-1 genotype and postweaning average daily gain in two families. The results of this study suggest the possibility of an association between GH and IGF-1 and growth and carcass traits. Additional studies of a more comprehensive genomic scope are planned.

## INTRODUCTION

Effects of growth hormone (GH) on pig growth is well documented. Both studies with exogenous GH (Chung et al., 1985; Hacker et al., 1993) and with swine possessing GH transgenes (Pursel et al., 1990) have demonstrated the ability of GH to enhance growth and leanness. Effects of GH are in part mediated by insulin-like growth factor-1 (IGF-1) which itself has been shown to be directly associated with differences in growth. In mice, exogenous IGF-1 stimulates muscle protein synthesis (Pell and Bates, 1989), IGF-1 transgenes stimulate growth (Camacho et al., 1991), and selection for serum IGF-1 concentrations are associated with increased growth rate (Blair et al., 1989).

The objective of the present study was to examine the contribution of the GH and IGF-1 loci to variation in growth and body composition of swine. This study used offspring from purebred sires to address the contribution of these loci within improved lines. Tentative associations between GH genotype and loin-eye area and between IGF-1 genotype and growth were identified.

## MATERIALS AND METHODS

Large half-sib families were created by mating three purebred sires (two Yorkshire, one Landrace) each with 16-17 dams in separate mating periods. All matings were performed by artificial insemination with fresh semen (Swine Genetics International, Cambridge, IA, USA). A total of 150, 195 and 148 offspring were produced. Pigs were permanently identified by ear notching, and ear notches were retained for DNA extraction.

All individuals were genotyped with highly polymorphic markers systems at the GH and IGF-1 loci. GH markers consisted of double strand DNA conformation polymorphisms (Kirkpatrick et al., 1993) and restriction fragment length polymorphisms (Kirkpatrick, 1992a), and the IGF-1 marker was a microsatellite located in the 5' flank of the IGF-1 gene (Kirkpatrick, 1992b). Two of the GH polymorphisms are associated with base substitutions in the GH gene coding sequence which alter GH amino acid sequence. In addition, a third polymorphism is due to a base substitution in the GH promoter region. Sires were chosen on the basis of GH genotype to permit contrasts between different forms of GH and the GH regulatory region. In addition, sires were chosen for heterozygosity at the IGF-1 locus.

Offspring of the three sires were evaluated for growth and carcass traits. Weight was recorded at birth, weaning and periodically at 4 week intervals thereafter. Pigs were slaughtered at a weight of  $230 \pm 5$  lbs, and 10th rib backfat and loin-eye area were evaluated on the carcasses.

Data were analyzed separately for each sire group with a statistical model of the following form:

$$Y_{ij} = \mu + D_i + \beta_{cov} + \beta_{GH} + \beta_{IGF-1} + e_{ij}$$

where

$Y_{ij}$  = jth observation from the ith litter,

$\mu$  = population mean,

$D_i$  = effect of the ith dam,

$\beta_{cov}$  = covariate, birth weight for preweaning average daily gain, weaning weight for postweaning average daily gain, and carcass weight for carcass traits,

$\beta_{GH}$  = regression on probability of inheriting GH allele 1 from the sire,

$\beta_{IGF-1}$  = regression on probability of inheriting IGF-1 allele 1 from the sire,

$e_{ij}$  = random error.

Paternal marker inheritance was established by comparing offspring and parental genotypes. This determination was aided by the availability of four diallelic markers at the GH locus and a single multiallelic marker at the IGF-1 locus. For both GH and IGF-1 genotypes one sire allele was arbitrarily designated "1" and the alternative allele "2". Where paternal inheritance was unambiguous, probability of inheriting sire allele 1 was either 1 or 0. In cases where sire and dam had identical heterozygous genotypes, one half of the offspring would also have the same heterozygous genotype, and paternal inheritance could not be established. For these individuals the probability was 0.5 for inheritance of sire allele 1. Few individuals fell into this ambiguous class (from 6-15 % of observations for a given sire family).

## RESULTS

Significant associations between marker genotype and growth and carcass traits were observed in three cases. GH genotype was associated with loin-eye area in one family ( $p < 0.05$ , difference between alternative alleles of  $2.61 \pm 1.22 \text{ cm}^2$ ), and IGF-1 genotype was associated with postweaning average daily gain in two cases (difference between alternative alleles of  $24 \pm 11 \text{ g / day}$ ,  $p < 0.05$ , and  $32 \pm 10 \text{ g / day}$ ,  $p < 0.01$ ). No significant associations were observed between these candidate loci and preweaning average daily gain or backfat ( $p > 0.05$ ). Dam ( $p < 0.01$ ) and birth weight, weaning weight or carcass weight covariates ( $p < 0.05$ ) were significant sources of variance in all analyses.

Table 1. Means and differences associated with marker genotype

Trait	Sire	Mean $\pm$ SE	Effect of Genotype	
			GH	IGF-1
Preweaning average daily gain	A	.237 $\pm$ .002 kg	ns	ns
	B	.218 $\pm$ .004 kg	ns	ns
	C	.259 $\pm$ .001 kg	ns	ns
Preweaning average daily gain	A	.737 $\pm$ .001 kg	ns	.032 $\pm$ .010 kg **
	B	.710 $\pm$ .004 kg	ns	.024 $\pm$ .011 kg *
	C	.669 $\pm$ .004 kg	ns	ns
10th rib backfat	A	2.48 $\pm$ .22 cm	ns	ns
	B	2.31 $\pm$ .40 cm	ns	ns
	C	2.46 $\pm$ .36 cm	ns	ns
Loin-eye area	A	33.80 $\pm$ 6.86 cm <sup>2</sup>	ns	ns
	B	37.51 $\pm$ 13.71 cm <sup>2</sup>	2.61 $\pm$ 1.22 cm <sup>2</sup> *	ns
	C	36.19 $\pm$ 7.36 cm <sup>2</sup>	ns	ns

<sup>1</sup> Significance: ns =  $p > 0.05$ ; \* =  $p < 0.05$ ; \*\* =  $p < 0.01$ .

## DISCUSSION

Significant associations were observed between IGF-1 genotype and postweaning average daily gain and between GH genotype and loin-eye area in this study. However, the magnitude of the differences between alternative alleles was not dramatic. There was no support for hypotheses of an association between GH genotype and growth rate or fat thickness and no support for hypotheses of an association between IGF-1 genotype carcass composition in these families. Associations between GH genotype and loin-eye area or IGF-1 genotype and growth could potentially be verified by replicating the families used in this study. In the case of all three sires, frozen semen could be obtained to produce additional offspring.

Future studies with these families will be aimed at identifying quantitative trait loci (QTL) through a genomic search of broader scope. Recent development of representational difference analysis (Lisitsyn et al., 1994) provides one means to rapidly screen the entire genome for loci with major effect on a trait of interest. We intend to apply a modified form of this technique to these half-sib families to address the question of what is the likelihood of identifying QTL in improved (purebred) lines of swine.

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