Effect of *IGF2* on growth characteristics of F2 Meishan x White crossbreds.

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Introduction

A paternally expressed QTL affecting muscle percentage and back fat on the p-arm of SSC2 was found in F2 cross-breds using experimental lines (Nezer et al., 1999; Jeon et al, 1999; DeKoning et al., 2000). This QTL was fine mapped using a haplotype sharing approach (Nezer et al., 2003). Later it was shown that the causative mutation, a G/A nucleotide substitution, underlying this QTL occurs in intron 3 of *IGF2*, i.e. in a non-coding region. The mutation abrogates in vitro interaction with a nuclear factor, probably a repressor (Van Laere et al., 2003).
IGF2 plays an important role in myogenesis by affecting muscle cell proliferation and differentiation. An anabolic action of *IGF2* in muscle is associated with suppression of proteolysis. Also effects of *IGF2* on uptake of amino acids and glucose have been documented. For a review see Florini et al. (2005).

The objective of this s project was to study the effect of the paternally inherited *IGF2* allele on the growth characteristics of Meishan X White crossbred finishers.

Material and methods

Experimental population and phenotypes

For a detailed description of the population see Janss et al. (1997). Nineteen pure Meishan boars were crossed with 120 sows originating from five commercial Dutch sow lines including both Large White and Landrace breeds. Thirty nine F1 boars were mated with 264 F1 gilts and produced around 1500 F2-piglets.
Body weight was measured at birth, at weaning, at the start of the test period (for some animals), at the end of the test and at the slaughterhouse for the animals that were not selected. Sex was recorded at birth. Sexes were tested separately in groups of 8-10 animals per pen except for boars originating from 2 lines which were tested individually. The latter were fed ad libitum while the group tested animals were fed a restricted diet. At the end of test ultra-sonic back fat was measured using a Renco Lean Meter (Renco, Minneapolis, MN USA). The animals not selected for further breeding were slaughtered

and the Hennessy grading probe was used to determine the back fat thickness as well as the loin depth 6 cm from the spine between the 3rd and the 4th rib, counting from the rear.

Genotyping

The pure bred Meishan grandsires, the F1 boars and their dams were genotyped for *IGF2* using pyro-sequencing in the laboratory of Andersson as described by Van Laere et al. (2003). These *IGF2* genotypes were combined with marker data on SW2443, SWC9, SW256 and S0141 (map position 1, 2, 25 and 39 respectively) to reconstruct the paternal haplotype of all F2 progeny using Simwalk2 (Sobel and Lange, 1996).

Statistical analysis

Company, year*season, sex and the paternal *IGF2*-allele were included in the model as fixed effects while animal, litter and residual were included as random effects. Litter size at birth and age at the time of measurement of body weight were included as co-variable. For ultrasonic back fat and HGP-measurements end weight of test and slaughter weight respectively, were included as additional co-variables. Company by sex interaction replaced the main effect of company and sex in analysis of al phenotypes measurement beyond start of test because different test protocols were used for the sexes in some of the companies. For weaning weight days in lactation was included as co-variable because weaning occurred on a specific day during the week whereas farrowing occurred on different days.

Results and Discussion

Of the 38 F1 boars 15 originated from 2 Dutch Landrace lines while the others were from Large White origin. These 15 boars were homozygous for the wild type allele while 18 out 23 of the other F1 boars were heterozygous for *IGF2*.
The number of observations, the raw means, the significance and the substitution effect of the paternally inherited *IGF2*-allele are given in Table 1. The number of observations for start weight indicates that in some testing protocols start weight was not included. The number of animals slaughtered is lower than the number of animals tested because animals with the best test results were retained by the companies for their breeding program.

The paternal *IGF2*-allele had a (highly) significant effect on all phenotypes except for weaning weight. Cross fostering occurred but was not registered and could therefore not be taken into account in the statistical analysis. Cross fostering has a large effect on growth rate of piglet during lactation.
The substitution effect showed that F2-pigs that inherited the mutant *IGF2* allele, i.e. from Large White origin, were heavier at birth and continued to be heavier all through their life. They not only grew faster but also put on more protein and less lipids as is indicated by the ultra-sonic and HGP measurements.

Table 1. The significance and the effect of the paternal inherited *IGF2* allele

trait	units	# obs.	mean	F-statistic	p-value	$IGF2_{pat}$ effect	se
birth weight	gram	1191	1229	17.97	0.000	65	15
weaning weight	gram	1184	8140	1.58	0.209	125	99
start weight	gram	919	26450	6.40	0.012	760	289
end weight	gram	1126	86890	5.77	0.016	2040	830
slaughter weight	gram	767	69560	10.00	0.002	2840	897
early growth	gr/day	919	368	5.36	0.021	9.4	4.1
test growth	gr/day	919	663	6.87	0.009	24.0	9.2
life growth	gr/day	1126	525	5.98	0.015	12.1	5.0
ultrasonic back fat	mm	1126	15.61	43.03	0.000	-1.69	0.26
hgp back fat	mm	767	22.06	25.81	0.000	-2.55	0.50
hgp loin depth	mm	767	40.72	8.18	0.004	1.86	0.65
hgp meat %	%	767	48.61	33.50	0.000	2.16	0.37

The results above are in contrast with what was observed by Jeon et al (1999) and Nezer et al (1999). Both studies report a non significant effect of $IGF2_{pat}$ on birth weight as well as on growth rate. However, Nezer et al (1999) showed that imprinting also occurred in fetal muscle and Sibley et al (2004) showed that *IGF2* affects placenta efficiency. A difference in the effect of paternal *IGF2* alleles on birth weight is therefore not unexpected.

The effects of *IGF2* on body composition at the time of slaughter confirm the results shown by Nezer et al (1999) and Jeon et al (1999).Given the lower growth rate combined with the change in body composition towards less muscle and more fat for pigs receiving the wild type allele from their sire it can be deduced that these animals will also have a poorer feed efficiency. Since the breeding goal in specialized sire lines aim for more efficient and more lean animals it is not surprising that the frequency of the mutant allele is high in most terminal boar lines (Knol, personal communication).

Conclusion

Paternally expressed *IGF2* alleles have a significant effect on growth rate and components of growth and therefore on body composition at slaughter. The effect is al ready present at birth and increases with age/weight.

Acknowledgements

We thank Leif Andersson, Anne-Sophie Van Laere, Martien Groenen and Bart Jungerius for their assistance.

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