Juvenile IGF-I: an update

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Introduction

In past Pig Genetics Workshops, we have provided research results on the relationships between juvenile IGF-I and piglet or performance traits, and discussed how to use this information in your breeding programs. The purpose of this document is simply to update pig breeders on recent developments, including new parameters from a trial conducted in Germany by Mitteldeutscher Schweinezuchtverband e. V on German Landrace.

Developments

1. Default genetic parameters for IGF-I have been updated in PIGBLUP.

2. Pigmania, AGBU, and Primegro Limited have cooperated to develop an automated data entry system for IGF-I test results into the herd management software, and generate PIGBLUP data files with appropriate contemporary group coding for this trait. MIPS also have facilities to incorporate IGF-I test results into PIGBLUP data files.

3. Direct use of assay codes (provided by Primegro Limited in result files) in PIGBLUP for contemporary group formation is currently under development.

4. Herdsman (S & S programming, Indiana, United States) are incorporating IGF-I data into their integrated software for record keeping and genetic evaluation.

5. Licensee's of the technology have significantly increased. The total number of tests conducted for juvenile IGF-I in the past 12 months was approximately 25 000.

6. Analyses for new trial data obtained from Mitteldeutscher Schweinezuchtverband e. V. (German Landrace) has been completed.

7. Research into the use of IGF-I testing for cattle breeding is ongoing.

Trial results for Mitteldeutscher Schweinezuchtverband e. V. (MSZV)

1. Description of Trial

IGF-I data

Blood spot samples from 650 German Landrace (GL) animals were collected by Mitteldeutscher Schweinezuchtverband e. V. during the period of 5/12/2000 to 27/12/2001, inclusive, under a PrimeGRO IGF-1 trial license. Samples were collected on 48 separate occasions (test dates) with between 1-30 animals tested per occasion (average: 13.5 animals/test date). Nearly all GL animals entering the MSZV station for performance testing were bled. However, there were no individuals whose sire had also been tested for IGF-I as a juvenile.

At the completion of all performance testing (i.e. all sample cards were stored) Primegro assayed cards on three occasions, giving rise to nine assay groups in total (average: 72.2 animals/assay group, which incorporates assay date and assay plate). All blood spot samples collected were assayed regardless of whether pigs completed performance testing or not.

Performance data

Performance data were recorded for a large number of traits by MSZV. All German Landrace males that entered the test station during the IGF-I trial period were included in the performance data file, regardless of whether they commenced (at 30 kg) or completed (at 110 kg) performance testing. Thus, performance data was available for 786 animals; progeny of 49 sires and 306 dams, from 369 litters. Because of the extended trial period, several dams had progeny performance tested from more than one litter. Moreover, the use of AI sires provided links across the two farms from which progeny were sourced. The total number of animals in the pedigree was 1141.

Analyses focussed on traits for which EBVs are routinely produced (marked with *), along with some other traits that may be of interest. Traits for which parameter estimates were obtained include:

*FI_TOT:	total feed intake during performance test (kg)
ADG2:	daily gain during performance test (gm/day)
*ADG3:	lifetime average daily gain (gm/day)
FCR:	feed conversion ratio (kg feed/kg gain)
*US_BF:	ultrasound backfat thickness (mean of three measures: mm)
*M_AREA:	carcase muscle area (cm^2)
*BF_AREA:	carcase fat area (mm^2)
*PH1_K:	pH at 1 hour post slaughter
IMF:	intramuscular fat (%)
BELLY:	belly score (1-9 scale)

Traits used as linear covariates in models for analyses were:

US_WT:	weight when ultrasonic back fat measures were taken (kg)
END_WT:	weight at the end of performance test (kg)
HCC_WT:	hot carcase weight (kg)

The distribution of data for each trait (including covariates) was examined with PROC UNIVARIATE (SAS Institute) to identify outliers. For the majority of performance traits, no outliers were evident. However, values for END_WT were treated as missing if <98 kg or >127.8 kg; values for FCR were treated as missing if >3.4; and values for IMF > 2.0 were also deleted as outliers. Performance records for animals with missing design variables (eg. missing date of birth, slaughter date etc), or with covariates identified as outliers, were not included in analyses.

Models used for analyses

Examination of the IGF-I data showed that animals were not sampled for serum IGF-I levels at a consistent age throughout the entire trial. There were three distinct groups, with peak frequencies at 34-35 days, 41-42 days, and 48 days. Group codes were thus generated to distinguish, at least approximately, between animals measured at different ages and/or with different intervals from weaning to sampling. Groups were coded for the intervals 33-37 days, 38-45 days, and 46-49 days, based on the frequency distribution for age at sampling. Animals outside the age range of 33-49 days were excluded from the data. Outliers with IGF-I levels exceeding 450 *ng/ml* were also removed, leaving 576 animals after editing with records for IGF-I.

Estimates of genetic parameters for all animals present in the pedigree were obtained using ASREML for the edited IGF-I data. Fixed effects included test year and month, assay group, and group for age at testing. Age, fit as a linear covariate, was not significant when group was included in the model. Random terms included animal and litter effects, giving rise to estimates of heritability and common litter effects.

MSZV provided the models used in the estimation of breeding values for FI_TOT, M_AREA, BF_AREA, PH1_K, ADG3 and US_BF. However, these models are used for analyses that combine data from several test stations and abattoirs, along with data from on-farm performance recording. Thus, some of the model design variables are redundant for the analysis of this data (eg. test station, sex, abattoir). Systematic effects accounted for when estimating genetic parameters for each performance trait are shown in Table 1.

Table 1 Systematic effects for performance traits

Trait	Farm	PJM	FJQ	SJM	SOZ	US_WT	**END_WT**	**HCC_WT**
FI_TOT	✓	✓					✓	
ADG2		✓						
FCR		✓					✓	
ADG3			✓					
US_BF			✓			✓		
M_AREA	✓			✓				✓
BF_AREA	✓			✓				✓
PH1_K	✓				✓			
IMF	✓				✓			✓
BELLY	✓				✓			✓

farm: farm of origin (2 levels)
PJM: is year||month of test, based on performance end date (17 levels)
FJQ: is farm||year||quarter, based on performance end date (13 levels)
SJM: year||month of slaughter, based on slaughter date (17 levels)
SOZ: is slaughter date (66 levels)

For each trait, parameter estimates were obtained under an animal model (univariate analyses). Litter was fitted as additional random effect for ADG2, ADG3 and US_BF, and was also significant for PH1_K. However, MSZV do not include litter effects when estimating breeding values for PH1_K. Estimates of the correlations between IGF-I and the above performance traits were obtained from a series of bivariate analyses.

2. Results and Discussion

Raw data characteristics

Characteristics of the raw performance data, prior to editing, are presented in Table 2, along with characteristics of the IGF-1 data. Coefficients of variation (CV) tended to be relatively low for most traits, particularly PH_1K. The exceptions were US_BF and BF_AREA, with moderate coefficients of variation, and IMF and BELLY, which were highly variable relative to the mean value. The CV for juvenile IGF-1 was also large, reflecting the multiple age groups noted earlier.

Table 2 Characteristics of the raw data prior to editing (SD: standard deviation; Min: minimum value; Max: maximum value; CV: coefficient of variation)

Trait	N	Mean	SD	Min	Max	CV
IGF-I	576	127	63.8	24	432	50.2
FI_TOT	677	203	20.8	132	288	10.2
ADG2	678	853	99.5	495	1122	11.7
ADG3	684	634	52.3	439	801	8.25
FCR	677	2.50	0.23	1.66	3.69	9.20
US_BF	676	11.2	1.80	6.00	19.00	16.1
M_AREA	603	45.4	4.32	32.4	60.2	9.52
BF_AREA	603	19.8	3.46	11.4	32.4	17.5
PH1_K	604	6.33	0.21	5.42	6.80	3.32
IMF	603	0.96	0.39	0.21	8.00	40.6
BELLY	603	5.44	1.63	1.00	9.00	30.0

Estimates of genetic parameters

Parameter estimates from univariate analyses are presented in Table 3, along with the number of records used and trait means after editing (described above). Editing procedures had the greatest impact on mean values for ADG2, which was 8 g/day higher in the edited data set. However, this change is not significant.

Estimates of heritabilities ranged from 0.29±0.15 (IGF-I) to 0.89±0.12 (IMF). The magnitudes of heritability estimates are generally consistent with those reported for the same or similar traits elsewhere. MSZV use heritabilities of 0.45, 0.37, 0.66, 0.56 and 0.09 for FI_TOT, US_BF, M_AREA, BF_AREA and PH1_K when estimating breeding values. Although the heritability estimated from trial data is lower for FI_TOT, and higher for PH1_K, heritability estimates for the remaining traits are in very good agreement with the reported values. Estimates for IMF are very high, and the models

used for analysing this trait may require further development. For all traits standard errors are large due to the relatively small amount of data used.

Estimates of correlations between juvenile IGF-I and the performance traits are shown in Table 4. Genetic correlations between juvenile IGF-I and FI_TOT, FCR and US_BF were very high, positive, and significantly different from zero. This outcome is consistent with results from previous trials. Similarly, the genetic correlation between IGF-I and BF_AREA was high and positive. This would be expected given the very high (cv 0.74) genetic correlations between US_BF and BF_AREA.

Table 3 Estimates of heritabilities (h^2), common litter effects (c^2), along with additive (σ^2_a), common litter (σ^2_c) and phenotypic variances (σ^2_p), from univariate analyses

Trait	N	Mean	h^2	c^2	σ^2_a	σ^2_c	σ^2_p
IGF-I	576	127	0.29±0.15	0.25±0.08	802	709	2810
FI_TOT	653	204	0.30±0.10	-	96.6	-	317
ADG2	653	861	0.44±0.14	0.13±0.07	3316	997	7506
ADG3	678	635	0.34±0.13	0.14±0.07	877	368	2546
FCR	651	2.49	0.32±0.09	-	0.014	-	0.044
US_BF	669	11.2	0.39±0.14	0.09±0.07	1.10	0.25	2.82
M_AREA	603	45.4	0.68±0.12	-	10.2	-	14.9
BF_AREA	603	19.8	0.58±0.11	-	6.78	-	11.7
PH1_K	603	6.33	0.32±0.12	-	0.012	-	0.038
IMF	601	0.95	0.89±0.12	-	0.060	-	0.068
BELLY	603	5.44	0.54±0.12	-	1.46	-	2.72

Table 4 Phenotypic variances for IGF-I (σ^2_{p1}) and the performance trait (σ^2_{p2}), along with genetic (ra), common litter (rc), residual (re) and phenotypic correlations (rp) between IGF-I and performance traits, from bivariate analyses

Trait	σ^2_{p1}	σ^2_{p2}	ra	rc	re	rp
FI_TOT	2803	316	0.78±0.26	-	-0.12±0.12	0.15±0.05
ADG2	2809	7483	-0.18±0.34	0.11±0.29	0.12±0.15	0.01±0.05
ADG3	2815	2544	-0.03±0.36	0.33±0.26	0.09±0.13	0.10±0.05
FCR	2791	0.044	0.81±0.26	-	-0.13±0.12	0.15±0.05
US_BF	2831	2.81	0.66±0.26	0.20±0.32	0.05±0.14	0.28±0.05
M_AREA	2823	14.9	-0.47±0.22	-	0.07±0.19	-0.17±0.05
BF_AREA	2810	11.7	0.69±0.20	-	-0.06±0.16	0.26±0.05
PH1_K	2813	0.038	0.001±0.29	-	-0.02±0.13	-0.01±0.05
IMF	2808	0.067	0.20±0.25	-	-0.35±0.34	0.01±0.06
BELLY	2814	2.71	-0.58±0.24	-	-0.13±0.15	-0.28±0.05

Genetic correlations between IGF-I and BELLY or M_AREA are high and negative. Genetic correlations between IGF-I and the remaining traits are very low (PH1_K and ADG3) to moderate (ADG2 and IMF). The relatively low genetic correlations between IGF-I and growth are consistent with the average of estimates from previous trials. As with some other trials where performance testing was to a high average end weight genetic correlations between growth while on test and juvenile IGF-I were in a favourable direction.

Residual correlations between IGF-I and the performance traits tended to be low, and not significantly different from zero. This result is consistent with traits measured at very different times (~ 5 months apart) during an animal's life. Overall, phenotypic correlations were positive, and significantly different from zero, between IGF-I and FI_TOT, FCR, US_BF and BF_AREA, while they were negative for M_AREA and BELLY.

3. Conclusions

Genetic and phenotypic correlations indicate that animals with lower juvenile IGF-I should have lower feed intake, feed conversion ratio, backfat and back fat area, and higher muscle area and belly score.

Results from this trial are overall consistent with those from previous trials, supporting a downward selection strategy for juvenile IGF-I. However, relatively few records available for analyses contributed to the large standard errors for all parameter estimates. Subsequently, it is recommended for implementation to use estimates pooled across trials, where possible.

Acknowledgments

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Further Reading

Bunter, K., Hermesch, S., Luxford, B.G., Lahti, K. and Sutcliffe, E. (2002). IGF-1 concentration measured in juvenile pigs provides information for breeding programs: a mini review. *Proceedings of the 7th World Congress on Genetics Applied to Livestock Production*, Session 03: Pig breeding, Communication No. 03-09.