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### EFFECT OF GENOTYPE ON PRODUCTION POTENTIAL IN PIGS REALIZED IN THE SPHERE OF PRODUCTION HERDS IN CZECH REPUBLIC.

### ŠPRYSL,M., STUPKA,R., CÍTEK,J.

*Czech University of Agriculture, Department of Pig and Poultry Science, Prague, Kamycka, 165 21, Czech Republic* 

### INTRODUCTION

The presently pig populations bred and sold in the Czech Republic achieve high performance rate but at the expense of increasing costs.

If we omit the area of reproduction where the requirement is 21 and more reared of piglets per swine and a year regardless the genotype (CEROVSKÝ, 1997), then selection of genotype is the most decisive factor in the production area (RUSSO,1988, HOVORKA, 1989).

Selection of genotype may be carried out upon results of the pig population tests that are being carried out in the Czech Republic in the

- Stations for pig heredity and fattening capacity testing, where pure-bred progeny of boars and sows is tested,
- Station of Central Control and Testing Institute for Agriculture, where the crossbred combinations from abroads corporation is tested,
- Field tests of crossbred pigs in fattening operations where crossbred combinations are tested in large-scale operations using a great sample of pigs (ŠPRYSL, et al., 1988),
- Overstanard pig-test station of Czech Univerzity of Agriculture Prague.

### MATERIAL AND METHODS

Verification of genotype impact on production performance rate indicators of the final pig hybrids bred in the commercial breed in the Czech Republic is the objective of the trial.

The trial / test was carried out on 576 heads of final pig hybrids at an average age from 60 to 84 days from their birth and of a total average live weight from 21.8 to 27.9 kg. 8 recommended cross-breeding combinations were tested in the period between 1993 and 2003 where basic fattening capacity parameters and carcass values were evaluated. In particular the combinations were  $(LW_m xL)x LW_s$ , D, PN,  $(LW_s xBL)$ , (PNxD), (PNxH), Seghers and PIC.

72 heads, in particular 36 young boars and 36 young swine were taken into the testing station from each genotype for the purposes of monitoring their fattening capacity, growth abilities and carcass values. Their housing was in compliance with the testing methodology of pure-bred and hybrid pig-housing so that the principle of housing the animals by couples in a pen was observed and the pigs were regularly weighted in 7 days intervals.

Standardization of the station environment was ensured by a monitoring system by AGE C.Mezirící assuring forced air circulation according to temperature and humidity (MARTÍNEK,2003).

Pig nutrition was in compliance with the nutrition need standards (ŠIMECEK, et al., 2000) in ad-libidum way in three phases with a continuous transition. The complete feeding mixtures (CFM) used in the tests composed of three components using wheat, barley, soy meal and

feeding additive while these components were mixed individually for each pen in accordance to the following feeding plan.

	Feeding phase						
Nutritions	< 35 kg	35-65 kg	>65 kg				
Protein (g/kg)	196,70	184,00	156,30				
MEp (MJ/kg)	13,30	13,20	12,90				
Fibre (g/kg)	39,84	38,76	40,75				
LYZ (g/kg)	11,40	10,20	8,30				
THRE (g/kg)	7,20	6,50	5,40				
MET (g/kg)	3,20	2,90	2,40				
Ca (g/kg)	7,20	6,80	6,10				
P(g/kg)	5,50	5,40	4,60				

For evaluation of fattening and growing performance all pigs were weighted regularly weekly where following traits were monitored:

- average live weight (ALW) in kg,
- feeding conversion ratio (FCR) in kg,
- daily feed intake (DFI) in kg,
- average daily weight gain (ADG) in g.

For lean meat share determination in the carcass all pigs were periodically measured by the sonography instrument ALOCA SSD 500 – MIKRUS cca from 65 kg live-weight. The lean meat share of pigs were evaluated by the help of FOM-formula.

For the purposes of processing an objective analysis of the fattening capacity indicators and the carcass values the set is divided into

- Fattening capacity analysis with a view to the genotype and with a conversion to a uniform age,
- Meat share analysis in a carcass body with a view to the genotype and with a conversion to a uniform age.

The test results were evaluated by using a statistic program SAS® Propriety Software Release 6.04, processed in tables and graphs schemes while differences between the individual monitored signs were tested by means of single /multiple analyses of variance.

#### **RESULTS AND DISCUSSION**

The table and graph 1 show evaluation of the pigs' live weight course. Due to the fact that problems in keeping of weaners in many commercial breeds, practically all taken in pigs did not achieve the recommended growth of the starting optimum, which fluctuates according to GUYOKRMA (1994) in the interval between 29 and 38 live weight for pigs 75 days old. The lowest starting weight in the test of 12.9, respectively 18.7 kg showed genotypes of (LW<sub>m</sub> xL)xD, (LW<sub>m</sub> xL)x LW<sub>s</sub>, and contradictorily higher, 27.0 kg, (LW<sub>m</sub>xL)x(PNxD). The monitored genotypes however overcome this handicap soon (in particular in approximately 4 weeks), while in the end of the test (173 days) they corresponded or even exceeded the recommended weight standard [PIC, (LW<sub>m</sub>xL)x(LW<sub>s</sub>xBL), (LW<sub>m</sub>xL)x(PNxH)].

Culmination of growth intensity of the individual genotypes can be seen out of the reached daily gain values (table and graph 2). It is obvious that a maximum growth (approximately 1000 g/day) in genotypes  $(LW_mxL)xD$ ,  $(LW_mxL)xLW_s$ ,  $(LW_mxL)x(PNxH)$ , Seghers and PIC is reached at the age of 130 - 140 days, i.e. by twenty days sooner than the standard presents, while there is a steep decline of recommended values in further period especially of genotypes  $(LW_mxL)xLW_s$ ,  $(LW_mxL)x(PNxH)$  and Seghers. The other ones demonstrate their maximum growth potential sooner (100-115 days), while the genotype

 $(LW_m xL)x(PNxD)$  shows the highest growth intensity only at the beginning of the test. As it is obvious out of the table and graph 2 a significant drop of growth intensity can be seen in monitored genotypes from approximately 130 days, while many genotypes [ $(LW_m xL)x(PNxD)$ , PIC,  $(LW_m xL)x(LW_s xBL)$  ( $LW_m xL)xPN$ ] show high gains from 75 days of age already (750–940 g).

If we evaluate appetite (see the table and graph 3), it fluctuates about the level of 2.7 kg in most evaluated genotypes. Genotype PIC is an exception reaching 120% of piggery of the others and  $(LW_mxL) \times LW_s$  and Seghers with the lowest piggery level of 91% (2.5 kg).

As regards the course of feed conversion (see the table and graph 4), then genotype  $(LW_m xL)xD$  (2.75 kg) shows to be the best, then  $(LW_m xL)xLW_s$  (2.88; respectively 2.91 kg). Genotypes using PN breed boars in C-position are the opposites.

With a view to the fact that the tables and graphs evaluate courses of the individual signs according to converted values, an evaluation of genotypes according to average phenotype values for a period identical for all tests (13 weeks) was carried out by conclusion and it is shown in the Table 5.

It may be stated that significant differences exist among all genotypes within the evaluated feature ( $P \le 0,001$ ). Knowledge of this fact may serve as a lead for selection and implementation of particular genotypes in practice. It is obvious that genotype ( $LW_mxL$ )xD seems to be best from growth intensity, appetite and feed conversion which is in compliance with the conclusions of SIGVARDSSON, ANDERSSON (1985). The three-breed combination using PN breed in a C-position seems to be the least convenient one (HOVORKA, et al., 1978, 1981, HOVORKA, 1989, PAVLÍK, 1987).

While evaluating the body meat formation it may be stated out of the received values (table and graph 6) that there is gradual almost linear decline of meat rate in all genotypes. In an average live weight of 65 kg an interval between 59.5 and 61.2 % of meat was found out with a drop to the level between 53.5 and 56.2 % corresponding to live weight of 110 kg. As it is obvious from the table significant differences were proved between the evaluated genotypes (P $\leq$ 0.001; 0.05) from the lean meat share in the carcass viewpoints.

It was also proved that genotypes may be divided into combinations with a high meat rate at the beginning and in the end of the test reaching the lean meat share of approximately 61%, respectively 56% [(LW<sub>m</sub>xL)xD, (LW<sub>m</sub>xL)xLW<sub>s</sub>, (LW<sub>m</sub>xL)x(LW<sub>s</sub>xBL), Seghers] and combinations that show a lower one reaching at the beginning 60% and 54 – 55% in the end of the test [(LW<sub>m</sub>xL)xPN, (LW<sub>m</sub>xL)x(PNxH), (LW<sub>m</sub>xL)x(PNxD), PIC].

It may be stated that if the first group reaches in 110 kg a meat share of approximately 56% in carcass body, in the second group a weight lower by 5 to 10 kg corresponds to this rate. In feeding of these genotypes to higher weights the breeder shall count with a higher fat generation at the expense of a steeper drop of the meatiness rate and thereby worse realization in slaughterhouses. It is also obvious that PIC genotype does not reflect its high growth intensity in meat generation (HOVORKA, 1989, JAKUBEC et al., 2002).

Therefore, genotypes  $(LW_mxL)xD$ , Seghers,  $(LW_mxL)x(LW_sxBL)$  that show a high rate of meatiness in higher slaughter weights (over 110 kg) may be recommended for the commercial area. As regards the other genotypes a lower slaughter weight of about 105 kg with view to their realization shall be recommended then.

### CONCLUSION

It may be stated out of the achieved results that in respect of:

- Fattening capacity
  - The monitored and evaluated genotypes show highly provable differences in growth intensity,

## Tab. 1. Fattening capacity with respect to genotype - ALW (kg)

ALW-values are fitted by polynominal curves

	ALW										
Age	[kg]										
(days)	(LWmxL)xLWs	(LWmxL)xD	(LWmxL)xPN	(LWmxL)x(LWsxBL)	(LWmxL)x(PNxD)	(LWmxL)x(PNxH)	Seghers	PIC			
	KLBb	HIJAa	GJQa	NOD	PEHKNc	QFILMOP	ABCDEFG	MCbc			
	x	x	— X	x	x	x	x	x			
75	18.7	12.9	22.4	25.5	27.0	21.3	24.6	25.8			
82	25.1	19.4	29.2	32.6	34.1	26.6	30.1	33.6			
89	31.6	25.9	35.8	39.5	41.0	32.1	35.7	41.3			
96	37.9	32.6	42.4	46.3	47.7	37.7	41.4	49.0			
103	44.3	39.3	48.8	52.9	54.2	43.5	47.1	56.5			
110	50.6	46.1	55.2	59.4	60.6	49.4	52.8	64.0			
117	56.9	52.9	61.4	65.8	66.7	55.6	58.6	71.4			
124	63.1	59.8	67.6	72.1	72.7	61.9	64.5	78.7			
131	69.4	66.7	73.6	78.2	78.5	68.3	70.4	85.9			
138	75.5	73.7	79.5	84.2	84.2	74.9	76.4	93.0			
145	81.7	80.8	85.4	90.1	89.6	81.7	82.5	100.1			
152	87.8	87.9	91.1	95.8	94.9	88.7	88.5	107.0			
159	93.8	95.1	96.7	101.5	100.0	95.8	94.7	113.9			
166	99.8	102.4	102.3	106.9	104.9	103.0	100.9	120.7			
173	105.8	109.7	107.7	112.3	109.6	110.5	107.2	127.4			

Diferences between averages with the same type are statistically significant. P<0,001 A,B,C,D,..., P<0,05 a,b,c,d...

# Tab. 2. Fattening capacity with respect to genotype - ADG (g)

ADG [g/day] Age (LWmxL)x(LWsxBL) (LWmxL)x(PNxD) (days) (LWmxL)xLWs (LWmxL)xD (LWmxL)xPN (LWmxL)x(PNxH) Seghers PIC ABCDEFG MBH HIJKLA GLQ RDIN EJOR FKP NOPQCM x x x x x x  $\overline{\mathbf{x}}$ x 

ADG-values are fitted by polynominal curves

Diferences between averages with the same type are statistically significant. P<0,001 A,B,C,D,..., P<0,05 a,b,c,d...

### Tab. 3. Fattening capacity with respect to genotype - DFI (kg)

DFI-values are fitted by polynominal curves

	DFI										
Age	[kg CFM/day]										
(days)	(LWmxL)xLWs	(LWmxL)xD	(LWmxL)xPN	Seghers	PIC						
	ABCDEFG	HIJKLAa	MNOBH	PQRSCIM	TUDJNP	VEKQT	WFLRU	GOSVW a			
	x	x	X	x	x	x	x	x			
75	0.9	0.5	1.4	1.3	1.6	0.7	1.0	1.5			
82	1.2	0.8	1.7	1.6	1.8	1.1	1.3	1.9			
89	1.4	1.2	1.9	1.9	2.0	1.4	1.5	2.2			
96	1.7	1.5	2.1	2.1	2.2	1.8	1.8	2.6			
103	1.9	1.8	2.3	2.3	2.3	2.0	2.0	2.8			
110	2.1	2.1	2.5	2.5	2.5	2.3	2.2	3.1			
117	2.3	2.3	2.6	2.7	2.6	2.5	2.3	3.3			
124	2.5	2.5	2.7	2.8	2.7	2.7	2.5	3.4			
131	2.6	2.7	2.8	2.9	2.8	2.9	2.6	3.5			
138	2.7	2.9	2.9	2.9	2.9	3.0	2.7	3.6			
145	2.8	3.0	3.0	3.0	2.9	3.1	2.8	3.6			
152	2.9	3.2	3.0	3.0	2.9	3.2	2.8	3.6			
159	2.9	3.2	3.0	2.9	3.0	3.2	2.9	3.5			
166	2.9	3.3	2.9	2.8	3.0	3.2	2.9	3.4			
173	2.9	3.4	2.9	2.7	2.9	3.2	2.9	3.3			

Diferences between averages with the same type are statistically significant. P<0,001 A,B,C,D,..., P<0,05 a,b,c,d...

Genotype	ADG [g/day]					DFI [kg CFM/day]				FCR [kg CFM/kg gain]					
	$\frac{1}{x}$		±	s <sub>x</sub>	s	$\frac{1}{x}$		±	s <sub>x</sub>	S	$\frac{1}{x}$		±	s <sub>x</sub>	s
(LWmxL)xLWs	868.62	IC	±	100.88	12.14	2.49	IJKLMG	±	0.36	0.04	2.88	LMNOPF	±	0.31	0.04
(LWmxL)xD	983.54	CDEFGHA	±	88.40	10.49	2.70	GHA	±	0.29	0.03	2.75	FGHIJKA	±	0.21	0.02
(LWmxL)xPN	836.09	HMOQ	±	61.39	10.69	2.72	FMQ	±	0.16	0.03	3.26	EKPR	±	0.23	0.04
(LWmxL)x(LWsxBL)	891.07	NOEJa	±	97.04	11.52	2.69	CJN	±	0.23	0.03	3.04	QRHM	±	0.26	0.03
(LWmxL)x(PNxD)	849.67	PFKN	±	73.49	9.05	2.70	DKO	±	0.18	0.02	3.20	CINQ	±	0.30	0.04
(LWmxL)x(PNxH)	900.74	QGLPb	±	107.02	18.09	2.77	ELP	±	0.29	0.05	3.10	DJO	±	0.35	0.06
Seghers	854.44	ABab	±	84.94	14.16	2.47	ABCDEF	±	0.17	0.03	2.91	ABCDE	±	0.30	0.05
PIC	1049.21	JKLMBDI	±	101.10	16.85	3.25	NOPQBHI	±	0.27	0.05	3.11	BGL	±	0.29	0.05

### All-inclusive view of fattening capacity with respect to common test-duration (13 weeks)

Diferences between averages with the same type are statistically significant.

P<0,001 A,B,C,D,..., P<0,05 a,b,c,d...

Tab. 5.

## Tab. 6. Meat formation in the carcass with respect to genotype after conversion to uniform live weight

	Lean meat share								
Weight	.t [%]								
[kg]	(LWmxL)xLWs	(LWmxL)xD	(LWmxL)xPN	(LWmxL)x(LWsxBL)					
	HIcdea	GAb	FMe	CJc					
65	61.0	61.2	60.5	59.4					
70	60.6	60.6	60.0	59.2					
75	60.1	60.1	59.4	58.9					
80	59.6	59.6	58.8	58.7					
85	59.1	59.1	58.2	58.4					
90	58.5	58.5	57.5	58.0					
95	58.0	58.0	56.8	57.7					
100	57.4	57.4	56.1	57.2					
105	56.8	56.7	55.4	56.8					
110	56.2	56.0	54.7	56.2					
		Lean me	eat share						
Weight		[%	6]						
[kg]	(LWmxL)x(PNxD)	(LWmxL)x(PNxH)	Seghers	PIC					
	DIKb	ELd	ABCDEFa	JKLMBGH					
65	59.8	59.9	60.9	59.5					
70	59.6	59.4	60.9	59.0					
75	59.2	58.8	60.7	58.4					
80	58.7	58.2	60.2	57.7					
85	58.1	57.6	59.6	57.0					
90	57.4	57.0	58.8	56.4					
95	56.6	56.2	58.0	55.8					
100	55.8	55.4	57.2	55.2					
105	54.9	54.5	56.5	54.8					
110	54.0	53.5	55.9	54.4					

- Demonstrate their highest growth potential in a weight / age of approximately 60kg/130 days,
- Do not prove/ show the feed intake and feed conversion according to the recommended standards,
- Progress of meat formation
  - Show significant statistic differences among each other with a higher or a lower linear drop of meat rate / meat percentage,
  - Genotypes may be divided into those which show high degree of meatiness in higher slaughter weights exceeding 110 kg [(LW<sub>m</sub>xL)x LW<sub>s</sub>, D, (LW<sub>s</sub>xBL), Seghers], and genotypes that reach only the required meat percentage only up to 105 kg [(LW<sub>m</sub>xL)xPN, (PNxD), (PNxH), PIC].

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### **CONTACT ADDRESS**

Ing. Michal Šprysl, CSc, Czech University of Agriculture, Department of Pig and Poultry Science, Prague, Kamycka, 165 21, Czech Republic Tel. +420 220 922 251, +420 224 383 062; e-mail: sprysl@af.czu.cz, Research was sponsored by the CMEPt No.412 100 003