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APPENDICES

Appendix 1: Description of cooking procedure for slash boned hams and string boned middles (K. Rhonefeld,1994; pers. comm.).

Cooking of hams:

- 90 minutes drying with oven temperature set to 80°C; internal probe temperature of ham set to 70°C.
- 30 minutes smoking, oven temperature set to 70°C
- 30 minutes of smoking in humidity; oven temperature set to 70°C; steam spray on for two seconds per minute.
- 240 minutes cooking or until internal probe temperature of ham has reached 70°C; oven temperature set to 85°C; steam spray on for four seconds per minute.
- after cooking, showering for 20 minutes
- storing at 4°C and weighing the next day

Cooking of middles:

- 90 minutes drying with oven temperature set to 75°C; internal probe temperature of middle set to 58°C.
- 30 minutes smoking with oven temperature set to 60°C
- 30 minutes of smoking with oven temperature set to 60°C; steam spray on for two seconds per minute.
- 180 minutes cooking or until internal probe temperature of middle has reached 58°C, oven temperature set to 80°C; steam spray on for four seconds per minute.
- after cooking, showering for 20 minutes
- storing at 4°C and weighing the next day

Appendix 2: Information recorded on all sheets

Information on boar test station data sheet:

General:

- starting date of test period
- finishing date of test period

For each individual pig:

- animal identification
- ear mark of animal
- animal weight at 18 weeks
- animal weight at 23 weeks
- feed intake during test period
- backfat measurements with real time ultrasound
- muscle depth measurement with real time ultrasound

Information on abattoir data sheet:

- animal identification
- hot carcase weight
- backfat depths measured with Hennesy chong machine
- muscle depth measured with Hennesy chong machine
- pH measurement at 45 minutes after slaughter

Information on boning room data sheet (I):

- animal identification
- colour of *m. longissimus dorsi* (L-value)
- colour of *m. multifidus dorsi* (L-value)
- pH measurement at 24 hours after slaughter
- weight of meat sample before drying
- weight of meat sample after drying

Information on boning room data sheet (II):

- animal identification
- weight of whole back leg
- weight of ham

Information on intra muscular fat content data sheet:

- animal identification
- first measurement of intra muscular fat content
- second measurement of intra muscular fat content limited to 0.1 to 7%
- information on method used for analysis (Soxhlet or NIR)

Information on processing data sheets (hams and middles):

General:

- date of slaughter
- date of pickling
- date of cooking
- temperature of pickle
- salt content of pickle

For each animal:

- animal identification
- weight of ham/middle before processing
- weight of ham/middle after pickling
- weight of ham/middle after tumbling
- weight of ham/middle after cooking

Appendix 3: Structure of data set containing reproductive performance of sows

General:

- tag of sow
- birthdate of sow
- litter size the sow was born in
- litter size the sow was weaned in
- module born
- line of sow
- strain of sow
- weight of sow at test
- weighting date
- backfat of sow
- reason for culling

information for each parity

- parity
- module mated
- mating date
- information about kind of mating: AI or natural mating
- information about number of matings: first mating or return mating
- service sire
- line of service sire
- strain of service sire
- module farrowed
- date of farrowing
- number born alive
- litter birth weight
- recording date of litter birth weight
- still births
- mummies
- number after transfer
- 21 day litter weight
- recording date of 21 day litter weight
- total deaths to weaning
- number weaned
- date of weaning

Appendix 4: Univariate analysis of lifetime average daily gain for different sizes of data set

		Data recording until:				
		6/93	**12/93**	**6/94**	**12/94**	**5/95**
LW model 1	N	446	893	1194	1598	1722
	σ^2_a	failed	1533	1152	1015	1135
	σ^2_e		2625	2842	2781	2672
	σ^2_p		4159	3995	3797	3807
	h^2 with s.e.		0.37 (0.18)	0.29 (0.11)	0.27 (0.09)	0.30 (0.09)
LW model 2	N	446	893	1194	1598	1722
	σ^2_a	0	109	245	285	275
	σ^2_c	546	1055	803	736	784
	σ^2_e	3095	2790	2844	2669	2661
	σ^2_p	3641	3955	3893	3692	3721
	h^2 with s.e.	0.00 (0.11)	0.03 (0.04)	0.06 (0.05)	0.08 (0.05)	0.07 (0.05)
	c^2 with s.e.	0.15 (0.02)	0.27 (0.05)	0.21 (0.05)	0.20 (0.04)	0.21 (0.04)
	sampl. corr.[1]	failed	-0.38	-0.43	-0.43	-0.43
LR model 1	N	410	746	988	1380	1469
	σ^2_a	2875	2624	2438	2444	2514
	σ^2_e	1990	1946	2039	1993	1951
	σ^2_p	4865	4571	4477	4437	4465
	h^2 with s.e.	0.59 (0.16)	0.57 (0.12)	0.54 (0.10)	0.55 (0.09)	0.56 (0.08)
LR model 2	N	410	746	988	1380	1469
	σ^2_a	2629	246	2062	2129	2120
	σ^2_c	82	86	192	191	212
	σ^2_e	1935	1944	2012	2023	1978
	σ^2_p	4647	4437	0.4267	4345	4310
	h^2 with s.e.	0.57 (0.18)	0.54 (0.13)	0.48 (0.11)	0.49 (0.09)	0.49 (0.10)
	c^2 with s.e.	0.02 (0.09)	0.02 (0.06)	0.05 (0.05)	0.04 (0.04)	0.05 (0.04)
	sampl. corr.[1]	-0.62	-0.56	-0.57	-0.58	-0.58

[1] sampling correlation between heritability and litter effects

Abbreviations:

LW: Large White
LR: Landrace

Appendix 5: Genetic correlations (first row), with standard errors (in brackets), ennvironmental correlations (second row) and phenotypic correlations for Large White

	pH24		CLD		CMD		DLP		IMF	
pH45	-0.11	(0.47)	-0.13	*	0.12	(0.37)	0.20	(0.39)	0.45	(0.41)
	0.15		-0.17		-0.12		-0.24		0.07	
	0.12		-0.17		-0.08		-0.17		0.13	
pH24			-0.82	(0.42)	0.10	*	-0.30	(0.40)	-0.03	(0.42)
			-0.49		-0.27		-0.34		-0.13	
			-0.53		-0.21		-0.33		-0.11	
CLD					0.47	(0.32)	0.12	(0.34)	*	
					0.34		0.57			
					0.36		0.49			
CMD							-0.36	(0.30)	0.27	(0.30)
							0.22		0.09	
							0.09		0.14	
DLP									-0.32	(0.39)
									-0.05	
									-0.01	

* analysis failed to converge

Abbreviations

pH45: pH recorded 45 minutes after slaughter

pH24: pH recorded 24 hours after slaughter

CLD: colour of the *m. longissimus dorsi*

CMD: colour of the *m. multifidus dorsi*

DLP: drip loss percentage

IMF: intra muscular fat content

Appendix 6: Genetic correlations (first row), with standard errors (in brackets), ennvironmental correlations (second row) and phenotypic correlations for Landrace

	pH24		CLD		CMD		DLP		IMF	
pH45	-0.03	(0.39)	-0.28	(0.34)	0.19	(0.34)	-0.54	(0.31)	0.59	(0.34)
	0.05		-0.10		-0.08		0.06		-0.12	
	0.04		-0.17		-0.02		-0.20		0.08	
pH24			-0.76	(0.36)	-0.03	(0.31)	-0.65	(0.28)	-0.26	(0.33)
			-0.47		-0.21		-0.22		-0.04	
			-0.53		-0.16		-0.35		-0.10	
CLD					0.49	(0.26)	0.81	(0.34)	0.30	(0.29)
					0.32		0.31		0.09	
					0.38		0.53		0.17	
CMD							0.15	(0.25)	0.19	(0.27)
							-0.01		0.06	
							0.05		0.11	
DLP									0.08	(0.28)
									0.06	
									0.03	

Abbreviations

pH45: pH recorded 45 minutes after slaughter
pH24: pH recorded 24 hours after slaughter
CLD: colour of the *m. longissimus dorsi*
CMD: colour of the *m. multifidus dorsi*
DLP: drip loss percentage
IMF: intra muscular fat content

Appendix 7: Heritabilities with standard errors (s.e.) and variance components for reproduction traits for Large White and Landrace sows.

Trait	Breed	N	h^2	s.e. of h^2	Va	Ve	Vp
NBA_1	LW	3747	0.06	0.02	0.35	5.31	5.66
	LR	2239	0.11	0.03	0.67	5.61	6.28
NBA_2	LW	2722	0.09	0.03	0.51	5.34	5.85
	LR	1391	0.11	0.05	0.64	5.44	6.08
NBA_3	LW	2058	0.08	0.03	0.48	5.33	5.81
	LR	907	0.08	0.06	0.53	6.11	6.64
LBW_1	LW	2930	0.11	0.03	0.66	5.42	6.08
	LR	1541	0.13	0.04	1.04	7.27	8.31
LBW_2	LW	1773	0.11	0.04	0.83	6.68	7.51
	LR	748	0.29	0.10	2.76	6.60	9.36
LBW_3	LW	1131	0.19	0.07	1.87	7.86	9.73
	LR	293	0.22	0.19	2.65	9.64	12.29
ABW_1	LW	2895	0.13	0.03	14911	100289	1152000
	LR	1501	0.19	0.05	25784	112578	138363
ABW_2	LW	1763	0.12	0.04	12342	88871	101214
	LR	733	0.12	0.07	16381	121381	137773
ABW_3	LW	1127	0.08	0.04	5968	72391	78359
	LR	290	0.31	0.19	26915	59012	85928

Abbreviations:

$NBA_{1,2,3}$: Number born alive for the first to third parity
$LBW_{1,2,3}$: Litter birth weight for the first to third parity
$ABW_{1,2,3}$: Average piglet weight at birth for the first to third parity

Appendix 8: Genetic parameters and variance components for average daily gain, feed intake, lean meat percentage and ham weight obtained from three trait analysis

	variance components	ADG3	LEANL	LMW
ADG3	σ^2_a : 1241	0.29	0.38	0.67
	σ^2_e : 2565	0.10	0.29	0.74
	σ^2_p : 4231		0.30	0.72
	σ^2_c : 425			
LEANL	σ^2_a : 3.22		0.63	0.69
	σ^2_e : 1.90			0.55
	σ^2_p : 5.12			
LMW	σ^2_a : 0.19			0.42
	σ^2_e : 0.23			
	σ^2_p : 0.46			
	σ^2_c : 0.04			

ADG3: Lifetime average daily gain

LEANL: Lean meat percentage based on real time ultrasound measurements

LMW: Lean meat weight of back leg

[1] on diagonal: heritabilities and c^2 effects

[2] above diagonal: genetic correlation (first row), environmental correlation (second row) and phenotypic correlation (third row)