Arch. Tierz., Dummerstorf 43 (2000) 3, 263-275

Chair of Animal Breeding[1] and Institute of Animal Sciences[2], Technical University of Munich, Weihenstephan, Germany

GEORG THALLER[1], LEO DEMPFLE[2], ANNA SCHLECHT[1], SABINE WIEDEMANN[1], HANS EICHINGER[1] and RUEDI FRIES[1]

Effects of the MHS locus on growth, carcass and meat quality traits in F_2 crosses between Mangalitza and Piétrain breeds

Dedicated to Professor Dr. D. Simon on the occasion of his 70th birthday

Summary

A total of 345 F_2 animals from a crossbred design Mangalitza (homozygous NN) x Piétrain (homozygous nn) were fed ad libitum at the institute's Thalhausen Research Station and slaughtered at a live weight of approximately 100 kg. MHS genotypes (67 nn, 192 Nn and 86 NN) were determined directly in a DNA test targeting the ryanodine receptor locus. Models for analysis of variance included sire, dam, pen, slaughter group, sex and MHS effects. Growth performance was generally lower and carcass composition minor compared to other breeds and crosses. No significant differences were found between MHS genotypes for growth traits but NN animals tended to be less efficient with respect to food conversion. However, nearly all measurements of the carcass showed significant differences between nn and NN which were especially pronounced for sidefat thickness (-7.1mm), fat over the *musculus longissimus dorsi* (-8.8 mm) and loin eye area (+8.7 cm^2) as well as fat area (-5.1 cm^2). We found Nn animals performing similar to NN animals due to incomplete dominance of the N allele. As expected, nn had a substantial negative influence on meat quality compared to NN and Nn (e.g. –0.61 and –0.15 for pH 45 min, respectively). Intramuscular fat content was at a high level and nn had significantly lower values with differences of -0.40 % and –0.25 % relative to NN and Nn, respectively. A whole genome scan is currently underway with emphasis on fat measurements which showed promising variation in this study.

Key Words: swine, Mangalitza x Piétrain, growth, carcass, meat quality, MHS

Zusammenfassung

Titel der Arbeit: **Einfluss des MHS-Gens auf die Merkmale Mastleistung, Schlachtleistung und Fleischbeschaffenheit von F_2 Kreuzungstieren der Rassen Mangalitza und Piétrain**

345 F_2 Kreuzungstiere der Rassen Mangalitza (homozygot NN) und Piétrain (homozygot nn) wurden in der dem Lehrstuhl zugehörigen Versuchsstation Thalhausen ad libitum gefüttert und mit einem Lebendgewicht von etwa 100 kg geschlachtet. Die MHS Genotypen (67 nn, 192 Nn, 86 NN) wurden gendiagnostisch am Ryanodinrezeptor bestimmt. Als Einflussfaktoren wurden im statistischen Modell der Eber, die Sau, die Mastgruppe, der Schlachttag/Schlachtort, das Geschlecht und der MHS Status berücksichtigt. Die Mast- und Schlachtleistungen waren im Vergleich zu anderen Rassen und Kreuzungen auf einem niedrigen Niveau. Hinsichtlich der Mastleistung wurden keine signifikanten Unterschiede zwischen den MHS Genotypen ermittelt, obwohl NN Tiere tendenziell schlechter abschnitten. Hingegen wurden bei fast allen Schlachtleistungsmerkmalen deutliche Unterschiede zwischen den MHS Genotypen nn und NN festgestellt, die bei der Seitenspeckdicke (-7,1mm) und dem Speckmaß B (-8,8 mm) sowie der Kotelett - (+8,7 cm^2) und der Fettfläche (-5,1 cm^2) besonders stark ausgeprägt waren. Nn-Tiere lagen eher im Bereich der NN Tiere und meist lässt sich zumindest auf partielle Dominanz des N-Allels schließen. Erwartungsgemäß verschlechterte der nn Genotyp die Fleischqualität, verglichen zu NN und Nn, erheblich (-0,61 bzw. –0,46 im pH 45 min). Der Anteil an intramuskulärem Fett war insgesamt sehr hoch und auch hier schnitten Tiere mit nn Genotyp deutlich schlechter als NN (-0,40 %) und Nn Tiere (-0,25 %) ab. Derzeit wird eine genomweite QTL-Analyse durchgeführt, bei der aufgrund der hohen Variabilität dieser Kreuzungskombination vor allem Merkmale des Fettansatzes vielversprechend erscheinen.

Schlüsselwörter: Schwein, Mangalitza x Piétrain, Wachstum, Schlachtmerkmale, Fleischqualität

1. Introduction

Over the past few years various laboratories worldwide have carried out genome mapping studies in pigs in order to detect quantitative trait loci (QTLs) responsible for economically important traits for the swine industry. Due to the lack of inbred lines, three generational cross breed designs mainly between subspecies or distant breeds (e.g. European wild boars x Large White (ANDERSSON et al., 1994) or Landrace x Chinese Meishan (JANSS et al., 1997)) were established. Segregation patterns within F_2 animals were used to find chromosome regions which to some extent are responsible for the observed phenotypic variation. These investigations showed that there are several QTLs for the various traits with large differences between the two homozygous genotypes. However, there is some doubt about the usefulness of such studies for practical swine breeding. It is not clear whether the presence of such huge effects can be expected within breeds under selection nor, how such QTLs act and interact in different genetic backgrounds. Therefore, it should be carefully investigated, whether putative QTLs are directly and causally responsible for all the effects on the phenotypes found or whether they might just be markers for linked QTLs. Consequently, an elimination of a confirmed negative variant for one trait, which could be achieved within only one generation, has to be thoroughly checked in advance with respect to consequences for correlated effects on other traits. The most prominent example in swine genetics where such properties could be studied is the MHS-locus, responsible for the halothane reaction which was assigned to a causal mutation at the ryanodine receptor locus by FUJII et al. (1991). This now allows to determine the genotype unambiguously in contrast to the use of former halothane and CK tests which could not separate susceptible (nn) from non susceptible (Nn, NN) genotypes with certainty and were not able to distinguish heterozygotes from homozygous negative animals. The test for the ryanodine receptor was implemented in nearly all populations in a straightforward manner and different selection strategies were applied to achieve economic benefits. Decisions were based on numerous investigation into the impact of MHS in different breeds and crosses. A clear picture emerged from all studies concerning the effects of positive halothane genotypes on meat quality traits, especially pH-values 45 min after slaughtering. However, effects reported on performance and carcass traits varied with respect to genotypes being superior as well as the size of effects. In the present study we want to report effects of MHS genotypes for growth, carcass and meat quality traits relative to a genetic background of F_2 crosses between Mangalitza and Piétrain breeds. Mangalitza and Piétrain represent contrasting extreme breeds with respect to lean meat content, Mangalitza being the fattest and Piétrain the leanest. Mangalitza is a domesticated European breed not selected against fatness due to special products produced. This set-up promised a large variation for traits connected with fat deposition in the F_2 generation and a genome wide scan is underway.

2. Materials and Methods

Animals

Mangalitza is a native Hungarian breed which is closely related to the wild boar, but domesticated. Its breeding history dates back to the 12^{th} and 13^{th} century, when two domesticated breeds with Mangalitza-like appearance existed. These were called the

'Szalont' and the 'Bakony' pig, and they were most probably descendents from the Hungarian wild boar. In the beginning of the 19th century these breeds were crossed with serbic 'Milos' pigs which gave rise to the Mangalitza breed. Although it was very popular in the 19th century due to its special properties (suited for extensive housing, selected for backfat thickness resulting in exorbitant meat- and fat quality) it is nowadays close to extinction (FLEGLER, 1999). Currently, about 1500 animals are registered worldwide, 500 of them in Hungary and 300 in Germany.

To establish the resource families, two Mangalitza boars with MHS genotypes NN

Table 1
Arithmetic means and standard deviations of growth, carcass and meat quality traits for females and castrates (Arithmetische Mittelwerte und Standardabweichungen für Merkmale der Mast- und Schlachtleistung sowie der Fleischbeschaffenheit getrennt nach weiblichen Tieren und Kastraten)

Trait[1]	Females		Castrates	
	N	Mean (Std Dev)	N	Mean (Std Dev)
Growth traits				
LWS [kg]	180	100.9 (6.7)	165	100.6 (7.0)
AS [d]	180	226 (28)	165	217 (30)
ADG [g/d]	179	533 (88)	165	565 (105)
ADG170 [g/d]	180	563 (78)	165	605 (83)
FI [kg]	179	258 (44)	165	250 (49)
FCR	179	4.05 (0.58)	165	4.01 (0.65)
Carcass traits				
CW [kg]	177	81.5 (5.6)	163	81.2 (5.6)
CL [cm]	180	91.2 (2.8)	165	90.5 (3.1)
KO [%]	177	80.8 (1.6)	163	80.7 (2.0)
ABF [mm]	180	33.9 (5.3)	165	36.1 (5.4)
SF [mm]	180	42.8 (9.3)	165	50.3 (8.1)
FMLD [mm]	180	24.4 (7.2)	165	27.2 (7.1)
LEA [cm²]	180	42.1 (6.4)	165	39.1 (6.3)
FA [cm²]	180	29.9 (5.4)	165	31.3 (5.0)
HAM [%]	177	30.9 (1.3)	158	30.4 (1.4)
LMC [%]	180	52.4 (3.5)	165	50.7 (3.2)
Meat quality traits				
PH_1M	180	6.14 (0.38)	165	6.06 (0.37)
$PH_{24}MV$	180	5.50 (0.13)	165	5.50 (0.11)
$PH_{24}MC$	180	5.47 (0.11)	165	5.49 (0.11)
$PH_{24}MD$	180	5.50 (0.11)	165	5.52 (0.13)
COLOR	180	72.8 (9.9)	165	70.3 (11.1)
IMF	178	2.20 (0.59)	165	2.62 (0.70)

[1] LWS = live weight at slaughter; AS = age at slaughter; ADG = average daily gain; ADG170 = average daily gain until day 170; FCR = food conversion ratio; FI = food intake; CW = carcass weight; KO = killing out percentage; CL = carcass length; ABF = average backfat thickness; SF = sidefat thickness; FMLD = fat thickness over musculus longissimus dorsi (MLD); LEA = loin eye area; FA = fat area; HAM = ham content; LMC = lean meat content; PH1M = ph 45 min MLD; PH24MV = ph 24 h MLD ventral; PH24MZ = ph 24 h MLD central; PH24MD= ph 24 h MLD dorsal; COLOR = meat color; IMF intramuscular fat

from a small population in Brandenburg (Northeast Germany) were mated to 22 purebred Piétrain sows with MHS status nn to produce F_1 animals. Out of these, 6 boars and 48 sows were selected as parents for the F_2 generation. They were mated randomly and some sows had two litters in the material collected so far. In total 345 slaughtered pigs (165 castrates and 180 gilts) from the F_2 were available for the analysis. The numbers for MHS genotypes of these animals were 67 nn, 192 Nn and 86 NN. Due to missing observations, not all animals could be evaluated for some of the traits (see Table 1).

Diet and housing

The pigs were born and kept at the Thalhausen Research Station. After the 5 week weaning period they were kept in flat decks with group sizes of about 30 animals up to a weight of 30 kg. For the fattening period, piglets were housed in pens with about 10 animals per pen and randomized with respect to sex and litter mates. The feeding regime was liquid feed ad libitum. The food contained 161 g/kg crude protein, 9.0 g/kg lysine and 13.6 MJ metabolizable energy (ME) per kg. The pigs were weighed every two weeks and sent to the abattoir with live weights between 88 and 119 kg. They were slaughtered at specially equipped slaughterhouse at the Bayerische Landesanstalt für Tierzucht in Grub or at the municipal slaughterhouse at the city of Munich.

Carcass traits

Carcass traits were recorded according to official guidelines for performance test stations (LITTMANN, 2000). Carcass weight (CW) is defined as the weight of the carcass immediately after slaughtering without interior fat, kidney, suet and midriff. Killing out percentages (KO) were calculated as the ratio of carcass weight over live weight at slaughter. Carcass length (CL) was measured between the bottom of the atlas vertebra and the anterior edge of the os pubis. Average backfat thickness (ABF) was calculated as the mean value of three measurements taken along the mid line of the back: at the first thoracic vertebra (thickest point), at the middle of the back (thinnest point) and between the third and the fourth lumbar vertebra. The cross section of the carcass between the 13^{th} and the 14^{th} thoracic vertebra was the subject of the following measurements: Sidefat thickness (SF) was measured at the ventral end of the *musculus latissimus dorsi*, fat over *musculus longissimus dorsi* (MLD) was measured at the thinnest point of the external fat, the loin eye area (LEA) is the planimetrically determined area of the MLD and the fat area (FA) is the area of the external fat over this muscle. The lean meat content (LMC) was estimated via equations based on multiple regressions using LEA, FA, ABF and SF as covariates (LITTMANN, 2000).

Meat quality

Meat quality was determined in the MLD 45 min after slaughtering (pH_1) and 24 hours post mortem at ventral, central and dorsal points of the MLD. Meat color was determined 24 hours post mortem as surface reflectance on a cross section of the MLD, using an Opto-Star apparatus (λ=640 nm). The extraction of intramuscular fat (IMF) was made by chloroform - methanol according to the modifications by HALLERMAYER (1976), determining the entire lipid content: 1.2 g of minced lean meat and 7 ml of chloroform p.a./methanol p.a. (1/1) were mixed for one minute in an Ultra Turrax ho-

mogenisator and afterwards centrifuged at 4000 U/min and 4 °C. The supernatant was filled in a separating funnel. This process was repeated once and the first and second supernatant were joined together. Then 14 ml of saline solution were added, the whole suspension was shaken vigorously for one minute and then was left for the separation of two phases for one hour. The lower chloroform phase containing all the lipids was drained off and dried in a rotation evaporator under nitrogen at 300 bar and 37 °C. The IMF content was calculated after weighing the dried lipids. All tubes and containers used were generally filled with nitrogen to avoid oxidation.

DNA-typing

Porcine genomic DNA was isolated from pig blood as described by SAMBROOK et al. (1989). For RFLP-analysis in the ryanodine receptor the protocol of FUJII et al. (1991) was modified. Sequences of PCR-primers were as follows: Forward primer, 5'-GTT CCC TGT GTG TGT GTG TGT GCA AT-3', and reverse primer, 5'-CTG GTG ACA TAG TTG ATG AGG TTT G-3'. PCR amplification (50 µl total volume) was performed using 100 ng genomic DNA, 5 pmol primers, 2.5 mM $MgCl_2$, 200 µM each dNTP, 67mM Tris HCl pH 8.8 16mM $(NH_4)_2SO_4$ 0.01 % Tween 20 and 1 unit Taq polymerase. The profile for thermal cycling was 94 °C for 3 min, then 30 cycles of 94 °C for 45 sec, 56 °C for 30 sec, 72 °C for 45 sec, followed by a final extension of 90 sec at 72 °C. The resulting 118 bp PCR product was digested with *Hha* I. This generates a 88 bp and a 33 bp fragment in N alleles, while lack of digestion indicates a n allele.

Statistical analysis

To account for common environmental and seasonal effects, animals were compared within the combined effect of pen and time period (date of housing) referred to as pen effect. As second litters were completely non overlapping with first litters with respect to time, the parity is confounded and therefore included in the pen effect. In the course of the experiment piglets of different dams were housed together in pens with a balanced sex distribution. Due to the mating scheme and facilities available there where four data sets completely disconnected with respect to dams and pens as well as slaughter group (same date and abattoir) but those effects were well cross-classified within such sets. Thus, the set was included as a main effect and dams, pens and slaughter group were nested within sets. Generally, sires were used across sets but unfortunately it turned out that one sire was used only three times within a given set and could not be included in the complete model in a proper statistical way. To extract as much information as possible we therefore applied two models. First, an analysis across sets accounting for the impact of the same sire in different sets but omitting information of one sire (model 1) and second, analyzing the data separately for each set, assuming sires being unrelated across sets but including all information (model 2).
The basic models for the statistical analysis using the procedure GLM of the program package SAS (1989) were:

Model 1:

$$y_{ijklmop} = \mu + sire_i + set_j + dam_k\,(set_j) + pen_l\,(set_j) + sgr_m\,(set_j) + sex_n + mhs_o + e_{ijklmop}$$

Model 2:

$y_{iklmop} = \mu + sire_i + dam_k\ (sire_i) + pen_l + sgr_m + sex_n + mhs_o + e_{iklmop}$

where

$y_{ijklmop}$	observation
μ_i	overall mean
$sire_i$	effect of sire (i = 1,..5)
set_j	fix effect of set (j = 1,..4)
dam_k	effect of dam k (k = 1,...48)
pen_l	fix effect of pen l (n = 1,....44)
sgr_m	fix effect of slaughter group o (o = 1,...54)
sex_n	fix effect of sex l (l = 1,2)
mhs_n	fix effect of MHS genotype m (m = 1 (NN), 2 (Nn), 3 (nn))
$e_{ijklmop}$	random residual

In both models the effect of age at slaughter was included as a covariate for growth traits instead of the slaughter group effect. Contrasts between nn and NN as well as Nn and NN genotypes for MHS and their standard errors were calculated using the ESTIMATE option of procedure GLM. For model 2, contrasts were estimated separately for each set and combined considering the appropriate variance-covariance structure of contrasts within sets:

$$\hat{contrast}_{comb.} = \left(X'V^{-1}X\right)^{-1} X'V^{-1}\,\hat{contrast}_{set}$$

with V being a block-diagonal matrix consisting of four 2x2 variance-covariance submatrices evaluated for the contrasts within sets.

3. Results and Discussion

The numbers of MHS genotypes in the slaughtered animals were significantly different from the expectation 1:2:1 in a F_2 cross (χ^2_{2df}=6.5; $p< 0.05$). The highest deviation from the expected number was found for the nn genotype and similar proportions were reported by HANSET et al. (1995). The contrasts between the homozygous MHS genotypes nn relative to NN and between the heterozygote genotype Nn relative to NN with their respective standard errors for growth, carcass and meat quality traits are shown in Tables 2 to 4. In addition to the estimates of the complete model (model 1) which accounts for all the effects simultaneously, results of model 2 are also presented. Standard errors of contrasts for model 2 are slightly smaller which is due to the fact that more information could be included in this analysis. As differences between both models are marginal, only the results from the complete model will be discussed in the following sections.

Growth traits

When analyzing performance measurements, significant effects were found for sires (FC), dams (LWS, ADG, ADG170, FC), different data sets (LWS, ADG, ADG170),

Arch. Tierz. 43 (2000) 3

Table 2
Estimates of contrasts between MHS genotypes for growth traits with standard errors and the corresponding significance level of MHS effect; results from model 2 in italics (Kontraste zwischen MHS Genotypen für Merkmale der Mastleistung sowie deren Standardfehler und das Signifikanzniveau für den MHS Effekt; Ergebnisse von Modell 2 kursiv)

Trait	Contrast ± standard error		Significance level[1]
	nn-NN	Nn-NN	
live weight [kg]	1.4 ± 1.1 n.s. *1.4 ±0.9 n.s.*	-0.8 ± 1.0 n.s. *0.3 ±0.7 n.s.*	t.
average daily gain [g]	11 ± 10 n.s. *11 ±9 n.s.*	-5 ± 8 n.s. *-6 ±7 n.s.*	n.s.
average daily gain [g] at day 170	20 ± 13 n.s. *25 ±13 t.*	-1 ± 10 n.s. *5 ±10 n.s.*	n.s.
food intake [kg]	3.7 ± 5.1 n.s. *1.2 ±3.7 n.s.*	-1.9 ± 4.0 n.s. *-4.5 ±3.2 n.s.*	n.s.
food conversion ratio [kg feed / kg gain]	-0.09 ± 0.08 n.s. *-0.05 ±0.05 n.s.*	-0.01 ± 0.07 n.s. *0.0 ±0.04 n.s.*	n.s.

[1]significance levels: ***: p<0.001; **: p<0.01; * :p<0.05; t.: p<0.10; n.s.: p>0.10

the pen effect (ADG, ADG170, FC,FCR) and the covariate age at slaughter (all traits). None of the growth traits was significantly affected by MHS genotypes (Table 2). There was, however, an slight MHS influence ($p<0.10$) on live weight at slaughter. A marginal superiority of nn relative to NN could be seen for all traits whereas the Nn genotypes performed worse compared to NN animals. Daily gain up to 170 days was additionally defined as it allows a comparison of growth for a time period where nearly no selection by early slaughtering occurred. It did, however, not show any differences with respect to MHS genotypes. In other studies (SCHOLZ and HARDGE, 1994; GÖDEKE et. al, 1998) no or only small differences between MHS were found not giving a clear picture in favor of any specific genotype. A superiority of Nn relative to nn of about 15 g to 30 g in daily gain was reported by ZHANG et al. (1992), HANSET et al. (1995) and LARZUL et al. (1997), whereas BIEDERMANN et al. (1997) found higher daily gains for nn compared to Nn in the range of 20 g. NN genotypes generally performed worse with a maximum of 40 g lower daily gains compared to nn (BIEDERMANN et al.,1997). No effects of MHS on food intake were apparent in this study and differences in food conversion ratio were not significant but in good agreement with LARZUL et al. (1997) and BIEDERMANN et al. (1997). However, in other studies MHS positive animals had a better food efficiency of up to –0.20 kg food per kg gain relative to homozygous negative animals and Nn animals performed either similar (WITTMANN et al., 1993 and 1994; SCHOLZ and HARDGE, 1994) or better as NN animals (LEACH et al., 1996).

Table 3
Estimates of contrasts between MHS genotypes for carcass traits with standard errors and the corresponding significance level of MHS effect; results from model 2 in italics (Kontraste zwischen MHS Genotypen für Merkmale der Schlachtleistung sowie deren Standardfehler und das Signifikanzniveau für den MHS Effekt; Ergebnisse von Modell 2 kursiv)

Trait	Contrast ± standard error		Significance level[1]
	nn-NN	Nn-NN	
carcass weight [kg]	1.6 ± 0.9 t. *2.1 ±0.7* **	0.1 ± 0.7 n.s. *0.5 ±0.6 n.s.*	n.s.
killing out percentage [%]	1.5 ± 0.3 *** *1.3 ±0.3* ***	0.5 ± 0.3 t. *0.4 ±0.2 t.*	***
carcass length [cm]	-1.8 ± 0.5 *** *-1.6 ±0.5* ***	-0.4 ± 0.4 n.s. *-0.6 ±0.4 n.s.*	**
average backfat [mm]	-2.8 ± 1.2 * *-2.0 ±1.1**	-0.6 ± 0.9 n.s. *-0.4 ±0.8 n.s.*	t.
sidefat [mm]	-7.1 ± 1.9 *** *-5.9 ±1.8* ***	-3.1 ± 1.5 * *-1.8 ±1.4 n.s.*	**
fat over MLD [mm]	-8.8 ± 1.5 *** *-7.2 ±1.4* ***	-3.3 ± 1.4 ** *-2.4 ±1.1 **	***
loin eye area [cm²]	8.7 ± 1.2 *** *7.8 ±1.2* ***	2.5 ± 1.0 ** *1.5 ±0.9 t.*	***
fat area [cm²]	-5.1 ± 1.0 *** *-4.0 ±1.0* ***	-1.7 ± 0.8 * *-1.2 ±0.8 n.s.*	***
ham percentage [%]	1.0 ± 0.3 *** *0.8 ±0.3* **	0.2 ± 0.2 n.s. *0.0 ±0.2 n.s.*	**
lean meat content [%]	4.2 ± 0.7 *** *3.7 ±0.6***	1.3 ± 0.5 * *0.9 ±0.5 t.*	***

[1]significance levels: ***: p<0.001; **: p<0.01; * :p<0.05; t.: p<0.10; n.s.: p>0.10

Carcass traits

The effect of the MHS locus was significant for all carcass traits with the exception of carcass weight and average backfat thickness, where only a tendency ($p<0.10$) of a possible MHS effect could be seen. Other significant effects in the analysis of variance were sires (CL), dams (KO, CL) and the effect of the slaughter group (CW, KO, CL) as well as sex (ABF, SF, FMLD, LEA, FA, HAM, LMC). Carcass weight was 1.6 kg higher for nn relative to NN animals, such a marginal difference was also reported by WITTMANN et al. (1993). The killing out percentage was in favor of nn animals with a differences of 1.5 % compared to NN which is close to effects of 1.1% and 1.2% found by HANSET et al. (1995) and LARZUL et al. (1997), respectively. Contrasts

of 0.5 % between Nn and NN animals were also obtained in studies of ZHANG et al. (1992), LARZUL et al. (1997) and GÖDEKE et al. (1998), whereas complete dominance of the N allele was reported by HANSET et al. (1995). On the other hand, homozygous positive animals produced shorter carcasses of -1.8 cm compared to homozygous negative animals the latter performing nearly equal to the heterozygotes. Corresponding differences between homozygotes in the literature were in the same range (e.g. HANSET et al., 1995) but also up to –5.0 cm (WITTMANN et al., 1994), with contrasts between Nn and NN varying from 0.1 cm (LUNDSTRÖM et al., 1995) to –2.0 cm (WITTMANN et al., 1994). According to the setup of the resource families high mean values and high variations for fat measures were found in our material (see Table 1). Whereas only a marginal effect of MHS on average backfat thickness was found with an superiority of nn or Nn relative to NN of -2.8 mm and -0.6 mm, respectively, corresponding differences observed for sidefat thickness were highly significant and amounted to -7.1 mm and -3.1 mm. Similar values for contrasts nn versus NN and Nn versus NN of –8.8 mm and –3.3 were found for the measurement 'fat over the MLD', respectively. The effect of MHS on average backfat varies across different studies from no influence (ZHANG et al., 1992; WITTMANN et al., 1993; GÖDEKE et al., 1998) to differences between the homozygotes (nn-NN) of -2.5mm (LARZUL et al., 1997) up to –4.3 mm (BIEDERMANN et al., 1997). Large differences for sidefat thickness between nn versus NN genotypes in the range of –0.35 mm to –6.0 mm were also reported by WITTMANN et al. (1993) and BIEDERMANN et al. (1997). Estimates for Nn animals did not show a clear pattern of dominance, with values close to NN animals (GÖDEKE et al., 1998) or between the homozygotes as in our study (e.g. WITTMANN et al., 1993; LUNDSTRÖM et al.,1995). Contrasts for fat thickness over MLD found in our material were –8.8 mm for nn versus NN, much higher than those reported in other studies, e.g. –3.3 mm (BIEDERMANN et al., 1997) or –5.0 mm (WITTMANN et al., 1993), and dominance patterns were unambiguous as seen before. The MHS locus also exhibits a strong influence on the carcass traits loin eye and fat area. Loin eye area was 8.7 cm^2 (2.5 cm^2) larger for nn (Nn) compared to NN and, conversely, the fat area was 5.1 cm^2 (1.7 cm^2) smaller for those comparisons, respectively. These values are high relative to differences between nn and NN found in other studies, which were in the range of about 5.1 cm^2 to 5.6 cm^2 (WITTMANN et al., 1993; SCHOLZ and HARDGE, 1994; BIEDERMANN et al., 1997). Values for Nn relative to NN in those investigations varied between 1.6 cm^2 and 2.9 cm^2 which were in good agreement with the estimates of WITTMANN et al. (1994) and GÖDEKE et al. (1998). In the literature, differences evaluated for fat area between homozygotes were from –2.5 cm^2 (WITTMANN et al., 1993) up to –5.3 cm^2 (BIEDERMANN et al., 1997), the latter being close to our finding. Consequently, there was a substantial difference in lean meat content between the three genotypes with nn animals having higher contents of 4.4 % and Nn animals being superior by 1.3 % compared to NN animals. Higher contrasts of 7.4 % between the homozygotes were reported by BIEDERMANN et al. (1997) and lower differences of about 3 % by SCHOLZ and HARDGE (1994). Ham percentage for nn was about 1% higher relative to Nn as well as NN genotypes which is consistent with studies of HANSET et al. (1995) and BIEDERMANN et al. (1997).

Table 4
Estimates of contrasts between MHS genotypes for meat quality traits with standard errors and the corresponding significance level of MHS effect; results from model 2 in italics (Kontraste zwischen MHS Genotypen für Merkmale der Fleischbeschaffenheit sowie deren Standardfehler und das Signifikanzniveau für den MHS Effekt; Ergebnisse von Modell 2 kursiv)

Trait	Contrast ± standard error		Significance level[1]
	nn-NN	Nn-NN	
pH 45 min	-0.61 ± 0.06 ***	-0.15 ± 0.05 **	***
	*-0.65 ± 0.05 ****	*-0.22 ± 0.04 ****	
pH 24 hours post mortem			
MLD ventral	-0.07 ± 0.02 **	-0.07 ± 0.02 ***	***
	*-0.04 ± 0.02 **	*-0.06 ± 0.01 ****	
MLD central	-0.07 ± 0.02 ***	-0.07 ± 0.02 ***	***
	*-0.05 ± 0.02***	*0.06 ± 0.01****	
MLD dorsal	-0.09 ± 0.02 ***	-0.08 ± 0.02 ***	***
	*-0.07 ± 0.02****	*-0.06 ± 0.01****	
meat color	-16.3 ± 1.7 ***	-3.5 ± 1.4 *	***
	*-16.0 ± 1.6****	*-3.4 ± 1.3 ***	
intramuscular fat [%]	-0.40 ± 0.12 **	-0.15 ± 0.10 n.s.	**
	*-0.35 ± 0.12 ***	*-0.13 ± 0.09 n.s.*	

[1]significance levels: ***: p<0.001; **: p<0.01; * :p<0.05; t.: p<0.10; n.s.: p>0.10

Meat quality

As expected, the impact of MHS genotype on all traits investigated was strongly significant, clearly confirming well known deteriorating effects of the stress susceptible nn genotype on meat quality. Additionally, significant effects of the slaughter group and the dam effects (with exception of pH 45 min) on pH measures and meat color were found in the analysis of variance, whereas only the sex effect, besides the MHS, was highly significant for the intramuscular fat content. A marked difference of -0.61 was found between nn and NN animals for pH values measured 45 min after slaughtering in the *musculus longissimus dorsi* (MLD) but was on the lower range compared to WITTMANN et al. (1993), SCHOLZ and HARDGE (1994), LARZUL et al. (1997) and BIEDERMANN et al. (1997). As stated by LARZUL et al. (1997), pH 45 min is undoubtedly lower in the Nn than in the NN genotype. The difference was –0.15 in our study, thus closer to NN than to nn which is similar to their finding. In contrast, BIEDERMANN et al. (1997) reported intermediate values for Nn and SCHOLZ and HARDGE (1994) evaluated Nn somewhat closer to nn. When defining meat quality as normal for pH 45 min greater than 5.8, then about 90 % of NN and Nn, but only 25 % of nn genotypes fulfilled this criterion which is in good agreement with WITTMANN et al. (1993). Corresponding contrasts for three measurements of pH 24 hours after slaughtering (ventral, central and dorsal) were much more subtle with values in the

range of -0.07 to -0.09 between nn and NN as well as between Nn and NN genotypes demonstrating complete dominance of the n over the N allele. SCHOLZ and HARDGE (1994) reported similar differences in favor of NN animals, whereas no significant effect was found in other studies. Only few animals (one nn, five Nn and four NN) were suspect to DFD condition which does not allow to conclude increasing problems due to the N allele. Meat color was also strongly influenced by the MHS locus and nn as well as Nn genotypes were 16.3 and 3.5 points worse compared to NN genotypes, respectively. In contrast to the pH-drop, Nn performed more like NN and a incomplete dominance of the N allele could be postulated considering similar estimates by WITTMANN et al. (1993), BIEDERMANN et al. (1997) and LARZUL et al. (1997). Extremely high contents for intramuscular fat were generally measured in the material and values for castrates were much higher than those for females (see Table 1). The decrease of –0.40 % for nn compared to NN was in agreement with SCHOLZ and HARDGE (1994). Their estimate for Nn animals differed significantly by –0.24 % from NN, which is not confirmed by our study which shows a non significant decrease of –0.15 % only.

4. Conclusions

Results for the influence of the MHS locus on growth, carcass and meat quality traits from an ongoing crossing experiment between Mangalitza and Piétrain designed for a whole genome scan were presented. F_2 animals, sharing the same polygenic background, were also analyzed by HANSET et al. (1995) and LARZUL et al. (1997) who used Piétrain x Large White crosses and by LUNDSTRÖM et al. (1995) based on European wild boar x Large White. However, in the latter study no homozygous nn animals were present. Other studies are based on individuals randomly taken from a given breed or cross with sometimes strongly unbalanced MHS genotypes (e.g. BIEDERMANN et al. (1997); 12 nn, 69 Nn and 156 NN). Furthermore, several investigations were conducted only permitting a comparison of either nn versus Nn (e.g. ZHANG et al., 1992) or Nn versus NN (e.g. GÖDEKE et al., 1998). Parents were also not as homogeneous as F_1 animals in those studies and MHS-effects could be biased if confounded with polygenic effects. Thus, the present study should provide a good impression concerning the impact of the MHS locus in a highly variable cross. First, no difference with respect to MHS for growth traits was observed. This is partly in agreement to other studies but in contrast to some authors who reported mostly higher food conversion efficiencies of nn genotypes. As our animals performed on a relatively low level it may be possible that MHS effects will not show up under such conditions. Alternatively, positive results in other studies might be caused by other QTLs on chromosome 6 with their superior allele preferably linked to the n allele. If so, it can be questioned why such loci do not segregate in our material. The MHS status influenced the various carcass traits to a different extent. Genotype nn performed better on carcass weight, although not significantly, carcass length and killing out percentage, but differences were relatively small compared to those found in the literature. On the other hand, huge effects for thickness of sidefat and fat over MLD were found which were much larger than differences reported in comparative studies. As raw

means were also large, there might be some scale effect involved, but there also might be Mangalitza specific alleles present which are linked to the MHS locus. Nevertheless, it is worthwhile to explore the substantial variation in these traits in more detail. The same is true for loin eye area and fat area, and, as a consequence, for the lean meat content, which was strongly influenced by the MHS locus. No clear pattern of dominance was observed for the carcass traits. Nn animals generally performed similar to NN animals, however significantly different just for those traits which were strongly influenced by the MHS locus. Effects of MHS genotypes on pH measurements did not differ from results found elsewhere, whereas their influence on meat color was comparatively high. Differences between homozygotes found for intramuscular fat were also large and in accordance to high differences obtained for sidefat and fat over MLD when assuming positive correlations between the these traits. Despite this general relationship there were several animals with low fat thickness and comparatively high IMF present in the material. According to JANSS et al. (1997) who postulated a second QTL for IMF, further efforts in molecular genetics might help to detect additional variation due to single loci and to describe possible interactions between loci responsible for fat deposition. Finally this would allow to directly select for the best combination of genes even for antagonistic traits.

Acknowledgment

The authors wish to thank Mr. Rudi Antes and Mr. Michael Paulini for genotyping the MHS locus as well as Dr. Gregor Durstewitz for critically reading the manuscript.

References

ANDERSSON, L.; ANDERSSON, K.:
Production, carcass and meat quality traits of F2-crosses between European Wild Pigs and domestic pigs including halothane gene carriers. Animal Science **61** (1995), 325-331

ANDERSSON, L.; HALEY, C.S.; ELLGREN, H.; KNOTT, S.A.; JOHANSSON, M.; ANDERSSON, K.; ANDERSSON-EKLUND, L.; EDFORS-LILJA, I.; FREDHOLM, M.; HANSSON, I.; HAKANSSON, J.; LUNDSTRÖM, K.:
Genetic mapping of quantitative trait loci for growth and fatness in pigs. Science **263** (1994), 1771-1774

BIEDERMANN, G.; PESCHKE, W.; WITTMANN, W.; BRANDT, C.:
The stage of reproductive, fattening and carcass performance traits of Piétrain pigs of different MHS-genotype produced in two breeding herds. Arch. Tierz., Dummerstorf **40** (1997) 6, 535-547

FALKENBERG, H.M.W.; SCHWERIN, M.:
MHS- und CK-Tests bei Schweinen, deren Beziehungen zueinander sowie zu weiteren Leistungsmerkmalen. Arch. Tierz., Dummerstorf **36** (1993) 2, 175-188

FLEGLER, J.:
Das Wollschwein. Gesellschaft zur Erhaltung alter und gefährdeter Haustierrassen (1999), 1-8

FUJII, J.; OTSU, K.; ZORZATO, F.; DE LEON, S.; KHANNA, V. K.; WEILER, J. E.; O'BRIEN, P. J.; MACLENNAN, D. H.:
Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia. Science **253** (1991), 448-451

GÖDEKE, K.; GLODEK, P.; MEYER, J.N.; BRANDT, H.:
Effect of the gene for the malignant hyperthermia syndrome on meat production and quality in progeny of Piétrain and Piétrain x Hampshire boars. Arch. Tierz., Dummerstorf **41** (1998) 5, 433-466

HALLERMAYER, R.:
Eine Standardmethode zur Bestimmung des Fettgehaltes in Lebensmitteln: I. Mitteilung: Die Bestimmung in Fleischwaren. Deutsche Lebensmittel-Rundschau **10** (1976), 356-359

HANSET, R.; DASNOIS, C.; SCALAIS, S.; MICHAUX, C.; GROBET, L.:
Génotypes au locus de sensibilité à l'halothane et caractères de croissance et de carcasse dans une F2 Piétrain x Large White. Genetics, Selection, Evolution **27** (1995), 63-73

JANSS, L.L.G.; VAN ARENDONK, J.A.M.; BRASCAMP, E.W.:
Bayesian statistical analysis for presence of single genes affecting meat quality traits in a crossed pig population. Genetics **145** (1997), 395-408

LARZUL, C.; LE ROY, P.; GUEBLEZ, R.; TALMANT, A.; GOGUE, J.; SELLIER, P.; MONIN, G.:
Effect of a halothane genotype (NN, Nn, nn) on growth, carcass and meat quality traits of pigs slaughtered at 95 kg or 125 kg live weight. Journal of Animal Breeding and Genetics **114** (1997), 309-320

LEACH, L., ELLIS, M., SUTTON, D. S., MCKEITH, F. K., WILSON, E. R.:
The growth performance, carcass characteristics, and meat quality of halothane carrier and negative pigs. J. Anim. Sci. **74** (1996), 934-943

LITTMANN, E.:
Schweinezucht und Schweineproduktion. Bayerische Landesanstalt für Tierzucht (2000)

LUNDSTRÖM, K.; KARLSSON, A.; HAKANSSON, J.; HANSSON, I.; JOHANSSON, M.; ANDERSSON, L.; ANDERSSON, K.:
Production, carcass and meat quality traits of F_2-crosses between European Wild Pigs and domestic pigs including halothane gene carriers. Animal Science **61** (1995), 325-331

SAMBROOK, I.; FRITSCH, E. F.; MANATIS, T.:
Molecular cloning - a laboratory manual, 2nd Ed. Cold Spring Harbour Laboratory Press (1989)

SAS/STAT:
User's guide, Version 6, Fourth Edition, Volume 2, Cary, NC: SAS INSTITUTE Inc, 1989

SCHOLZ, A.; HARDGE, T.:
Zum Einfluß von MHS-Genotyp und Genkonstruktion auf komplexe quantitative Merkmale der Mast- und Schlachtleistung sowie Fleischqualität beim Schwein. Arch. Tierz., Dummerstorf **37** (1994) 3, 245-256

WITTMANN, W.; PESCHKE, W.; LITTMANN, E.; BEHRINGER, J.; BIRKENMAIER, S.; DOVC, P.; FÖRSTER, M.:
Mast- und Schlachtleistungen von DL-Kastraten in Abhängigkeit vom MHS-Genotyp. Züchtungskunde, Stuttgart **65** (1993) 3, 197-205

WITTMANN, W.; LINNERT, B.; PFEIFFER, H.; PESCHKE, W.:
Der Einfluß von Genmarkern auf die Fruchtbarkeit und Fleischleistung beim Schwein, dargestellt an einer reinerbig-halothannegativen DL-Herde. Arch. Tierz., Dummerstorf **37** (1994) 3, 411-425

ZHANG, W.; KUHLERS, D. L.; and REMPEL, W. E.:
Halothane gene and swine performance. J. Anim. Sci. **70** (1992), 1307-1313

Received: 2000-03-15

Accepted: 2000-04-12

Authors' addresses
Dr. GEORG THALLER, ANNA SCHLECHT, SABINE WIEDEMANN,
Prof. Dr. HANS EICHINGER, Prof. Dr. RUEDI FRIES
Lehrstuhl für Tierzucht, TU München
Alte Akademie 12
D-85350 Freising-Weihenstephan
Germany

E-Mail: Georg.Thaller@flg.tum.de

Prof. Dr. LEO DEMPFLE
Institut für Tierwissenschaften, Professur für Biometrische Methoden in der Tierzucht,
TU München
Alte Akademie 12
D-85350 Freising-Weihenstephan
Germany

Arch. Tierz., Dummerstorf 43 (2000) 3, 276

Buchbesprechung

Praktische Schweinemast - Haltung, Fütterung, Gesundheit, Qualität, Markt, Ökonomik

EDGAR LITTMANN u.a.

160 Seiten, 40 Farbfotos, 80 s/w Fotos, 50 Zeichnungen, 78 Tabellen, BLV Verlagsgesellschaft mbH, München, Wien, Zürich, Verlagsunion Agrar, 2000, ISBN 3-405-14802-2, DM 49,90; öS 364,-; sFr 46,-

Gerade in Zeiten eines erhöhten Kostendruckes auf den Schweinehalter und -mäster sowie anderer sich negativ auf diesen Betriebszweig auswirkender Umstände, ist es das Verdienst der Autoren dieses Buch jetzt herausgebracht zu haben. Wohl wissend, daß um im Wettbewerb bestehen zu können, sowohl für die erfahrenen Schweinemäster als auch Landwirte, die diesen Zweig erweitern oder neu begründen wollen, die Anforderungen an fundiertes fachliches Wissen ständig steigen. Das Konzept, nämlich Antworten zu den ökonomischen Erfolgsaussichten und praktischen Lösungen unter den derzeitigen Preis- und Marktverhältnissen zu geben, liegt diesem Buch zugrunde.
Zunächst beantwortet das Buch die Frage „Warum Schweinemast?", wobei Beweggründe, Rahmenbedingungen und die Besonderheiten, die eine erfolgreiche Schweinemast zukünftig begleiten, diskutiert werden. Sieben Hauptabschnitte umfassen alle wichtigen die Mast tangierenden Themenkomplexe, wobei wissenschaftliche Gründlichkeit, hohe Sachkompetenz und die praktischen Erfahrungen der Autoren die Darstellung der Sachverhalte klar, verständlich und praxisrelevant erscheinen lassen. Anleitung zum Handeln bestimmt z.B. den 2. Hauptabschnitt „Stallbau und technische Anlagen" mit den Darlegungen der betrieblichen Situation, den Genehmigungsverfahren, den Planungsgrundlagen und Grundsätzen für verschiedene Haltungsverfahren, die baulichen Details, Stallklima und Fütterungstechnik. Sich auf das Wesentliche beschränkende Textdarstellungen, unterstützt durch zahlreiche Tabellen und Abbildungen, findet der Leser auch in den folgenden Hauptabschnitten zu den Themen Tiermaterial, Ferkelbezug und Stallbelegung, Fütterung, Gesunderhaltung, Vermarktung von Schlachtschweinen, Fleischqualität und Ökonomik. Wo notwendig, enthalten die einzelnen Abschnitte das gesamte Regelwerk und Richtlinien, die eine Haltung von Mastschweinen betreffen. Im Anhang finden sich die Verzeichnisse verwendeter und weiterführender Literatur sowie ein Adressenverzeichnis. Zu den letzten beiden wäre die Einbeziehung weiterer Quellen und Anschriften wünschenswert gewesen. Auch ohne das abschließende Stichwortverzeichnis verfügt das Buch über einen guten didaktischen Aufbau mit großer Übersichtlichkeit, so dass auf jede spezielle Frage zu allen Fachbereichen leicht die entsprechende Antwort gefunden werden kann.
Dieses Buch wendet sich an Landwirte, die ihr Wissen auf diesem Gebiet aktualisieren oder sich neu diesen Fragen zuwenden wollen um marktgerechte Schweine zu erzeugen und damit Produktionsreserven ihres Betriebes zu mobilisieren. Es ermöglicht Auszubildenden, aber auch in der Beratung Tätigen, zu allen Fachbereichen der Schweinemast aktuelle Informationen und kann daher eine wirksame Hilfe bei der Suche nach richtigen Entscheidungen sein.

ERNST RITTER, Dummerstorf