

Halothane genotype and pork production. 1 Growth, carcass and meat quality characteristics

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The effect of the halothane gene on certain growth and meat quality characteristics were investigated by comparing the three known halothane genotypes (NN, Nn, nn). Fifty nine Landrace × Large White pigs (gilts = 25, castrates = 34; NN = 31, Nn = 17, nn = 11) were reared from 27 to 86 kg liveweight, whereafter the pigs were slaughtered and meat and carcass quality characteristics measured. Average daily gain (ADG), days to slaughter and carcass length showed significant genotype × sex interaction. The nn pigs showed the highest ADG and least days to slaughter, followed by the NN and then the Nn pigs. The castrates grew significantly faster with a higher ADG ($p < 0.05$) and fewer days to slaughter ($p < 0.001$). Carcass length did not differ for different genotypes or sexes. NN pigs had the highest meat depth, predicted lean meat percentage (LMP) and lowest fat thickness, followed by the Nn and nn pigs. The castrates had a higher fat thickness ($p < 0.05$) with a resultant lower LMP ($p < 0.05$) compared to gilts. None of the genotypes or sexes showed differences in chilling loss, but drip loss differed between genotypes ($p < 0.05$) and sexes ($p < 0.001$), with nn pigs having the lowest drip loss. The pH₁ values differed ($p < 0.05$) between genotypes, with NN the highest and nn the lowest. No differences in pH₂₄ were observed between genotypes. The pH₁ and pH₂₄ values did not differ between sexes. Although the presence of the halothane gene positively affected growth rate, this increase in growth rate was largely due to undesirable fat deposition. Furthermore, the gene did not positively affect meat quality (pH₁) or carcass quality (LMP). Therefore, the intentional use of the halothane gene is discouraged.

Die invloed van die halotaangeen op sekere groei- en vleiskwaliteiteienskappe is ondersoek deur die drie bekende halotaangenotipes (NN, Nn en nn) te vergelyk. Nege-en-vyftig Landras × Grootwit varke (soggies = 25, burgies = 34; NN = 31, Nn = 17, nn = 11) is groot gemaak vanaf 27 tot 86 kg lewendemassa, waarna die varke geslag is en vleis- en karkaskwaliteiteienskappe bepaal is. Gemiddelde daaglikse toename (GDT), dae tot slagting en karkaslengte het betekenisvolle interaksie getoon. Die nn-varke het die hoogste GDT en minste dae tot slagting gehad, gevolg deur die NN- en dan die Nn-varke. Die burgies het 'n betekenisvolle hoër GDT ($p < 0.05$) en minder dae tot slagting ($p < 0.001$) as die soggies getoon. Karkaslengte het nie betekenisvol verskil tussen genotipes of geslag nie. Die NN-varke het die grootste oogspierdeursnit, hoogste persentasie voorspelde maervleis en laagste vetdikte gehad, gevolg deur die Nn- en nn-varke. Die burgies, in vergelyking met die soggies, het 'n groter vetdikte ($p < 0.05$) en gevolglik 'n laer persentasie voorspelde maervleis ($p < 0.05$) gehad. Geen verskille tussen genotipes of geslag is vir koelverlies waargeneem nie, maar drupverlies tussen genotipes ($p < 0.05$) en geslagte ($p < 0.001$) is waargeneem, met nn-varke wat die laagste drupverlies getoon het. Die pH₁-waardes het verskil tussen genotipes ($p < 0.05$), met NN- die hoogste en nn-varke die laagste. Geen verskille tussen genotipes is vir pH₂₄ waargeneem. Geen verskille tussen geslagte is vir pH₁ en pH₂₄ waargeneem nie. Alhoewel die teenwoordigheid van die halotaangeen die groeitempo positief beïnvloed, kan hierdie toename hoofsaaklik toegeskryf word aan ongewenste vetneerlegging. Voorts het die geen ook nie vleiskwaliteit (pH₁) of karkaskwaliteit (persentasie voorspelde maervleis) positief beïnvloed nie. Die doelbewuste gebruik van die geen word dus afgeraai.

Keywords: halothane gene, carcass quality, meat quality, pigs

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Introduction

The effect of the halothane gene on certain growth and meat quality characteristics have been well documented (Sather *et al.*, 1991; Jones *et al.*, 1988; Pommier *et al.*, 1992). Stressful conditions, such as transportation, mating or pre-slaughter handling, or halothane anaesthesia, can trigger malignant hyperthermia (MH) in homozygous halothane positive (nn) pigs, ultimately leading to stress-induced deaths, or to the development of pale, soft and exudative (PSE) meat when such animals are slaughtered (Barton-Gade *et al.*, 1988). It is believed that the halothane gene in heterozygous halothane negative (Nn) pigs has certain beneficial effects on carcass composition, but little or no effect on the incidence of PSE meat (Webb *et al.*, 1982). It is a well known fact that especially energy level of the ration can affect fat thickness in growing pigs (Whittemore, 1985). However, since the present

study was conducted to evaluate the effect of the halothane genotypes, a typical commercial ration was fed to all pigs in this trial. This eliminates clustering of nutritional and genotype effects.

Research indicated that the 'meat quality' of the Nn genotype is intermediate between that of the homozygous halothane negative (NN) and nn genotypes (Jensen & Andersen, 1980; Barton-Gade, 1984a), although some reports have suggested that this is not the case (Eikelenboom *et al.*, 1980; Jensen, 1981). The development of PSE is not only exclusive to pigs that possess the halothane gene. Any genotype may produce PSE meat, depending on pre-slaughter energy levels and handling practice (Barton-Gade, 1984b).

The purpose of this study was to evaluate the three halothane genotypes [identified by means of the polymerase chain reaction (PCR) technique] (Fujii *et al.*, 1991) under commer-

cial production conditions and to determine if the inclusion of the halothane gene under South African commercial conditions holds any advantages for producers and/or meat traders/processors.

Materials and methods

Fifty-nine Landrace × Large White pigs (gilts = 25, castrates = 34) of the three halothane genotypes (gilts: NN = 11, Nn = 7, nn = 6; castrates: NN = 19, Nn = 10, nn = 5) were sourced from a stud in the Western Cape. The pigs originated from a population of known halothane genotype which were tested using the protocol adapted from the method described by Fujii *et al.* (1991).

The pigs were reared at the commercial piggery of the University of Stellenbosch during the growth phase (defined below) of the trial. Upon reaching *ca* 27 kg live weight the pigs were individually weighed and entered the growth phase, which was from *ca* 27 to *ca* 86 kg live weight. Average daily gain (ADG) was calculated during the growth phase. Days to slaughter was expressed as the number of days each pig spent in the growth phase. Groups of pigs were housed in 10 m² partially slatted pens. Each pen contained no more than 10 pigs at any time, all of similar genotype. Under group feeding conditions, which simulate production conditions, the individual feed conversion ratios (FCR) cannot be calculated. Sexes were not housed separately, as split sex feeding is not commercially practised in the Western Cape. Feeding was *ad lib.* on a maize based ration containing 16% crude protein and 13.2 MJ ME/kg, balanced for amino acid availability. Upon reaching an individual live weight of *ca* 86 kg the pigs were weighed and weight recorded. Feed was withdrawn for *ca* 12 h prior to slaughter. This was done to ensure an empty gut at slaughter and minimise any possible risk of meat contamination during slaughter.

Transportation to the abattoir was by road (\pm 25 km), with no overcrowding or mixing of unfamiliar pigs. A 2 h resting period was maintained prior to stunning (90 V AC, ear to ear, 3–5 s) and slaughtering, by sticking within 30 s of stunning, after which the carcasses were suspended by the hind legs, shower scalded for 10 min at 60°C, followed by mechanical removal of hair and dressing.

The initial measurements (warm carcass mass, pH₁, carcass length) were taken 60 min after stunning. These included fat thickness, muscle thickness and percentage lean in the carcass, utilising a Hennessey Grading Probe and pH meter. The individual measurements were taken on a position between the second and third last rib, 45 mm from the midline, as prescribed by the South African classification system (Government Notice No. R. 1748, 26 June 1992). Carcasses were split into left and right hand sides by cutting through the vertebrae on the dorsal midline. The heads remained intact on the right hand side. Carcass length was also determined at the classification point, measured as the distance (in cm) from the cranial side of the 1st thoracic vertebra to the nearest visible point of the pelvic bone. After chilling for 24 h at 2°C additional measurements (pH₂₄, cold carcass mass) were recorded. Chilling loss was expressed as weight lost from the carcass during the first 24 h of chilling after slaughter. After removal of the head, front and back trotters (elbow and ankle joint respectively) the carcasses were cut into four commercial

joints, namely the shoulder (by cutting between the fifth and sixth thoracic vertebra at a 90° angle to the dorsal midline), the leg (by cutting between the last lumbar and first sacral vertebra at a 90° angle to the dorsal midline) and the belly and back (by cutting through the ribs on a line 18 cm from the dorsal midline). All the left-hand side carcass joints were then removed from the production line. The subcutaneous fat, skin and bone were removed from the backs, leaving a subcutaneous fat layer of *ca* 1 cm. The hams were deboned and all visible skin and subcutaneous fat removed. The topside and silverside of each ham was then removed according to factory specifications. Both the backs and ham cuts were individually wrapped, tagged, fast frozen and kept at –40°C for further processing. Drip loss determination was done by removing a 25 mm thick slice from the cranial end of each back at the position of the sixth thoracic vertebra and then measuring the amount of exudate over a 48 h period at 2°C (Murray *et al.*, 1989). The samples used for determining drip loss were removed before the backs were deboned and defatted, thus avoiding undue drip loss.

Statistical procedures

Analyses of variance were performed on all the variables measured using the General Linear Models (GLM) procedure of SAS (Statistical Analysis System Institute, Inc., 1988). A full model was fitted for main effects (sex, genotype) and sex within genotype, as well as interactions. This model was

$$Y_{ij} = \mu + G_i + S_j + GS_{ij} + e_{ij}$$

where Y_{ij} is the dependent variable, μ = the overall mean, G_i = the genotype effect, S_j = the sex effect, GS_{ij} = the interaction between genotype and sex and e_{ij} = the residual. The differences between genotypes and sexes were, where appropriate, tested separately by means of the null hypothesis (H_0), with $H_0: \mu = \mu_0$ and the alternate hypothesis (H_a) being $H_a: \mu \neq \mu_0$. This was done by means of contrast analyses and estimated least square means (\pm std error) as reported in Table 1. Differences between the variables were accepted as being significant if the probability of rejection of H_0 was less than 5% ($p < 0.05$) for genotypes and sex. The actual probabilities are, where applicable, reported in the text, but are only indicated by superscripts in Table 1 if less than 0.05. The actual probabilities for genotype by sex interaction are, however, reported in Table 1.

Where applicable, significant ($p < 0.05$) correlation values between variables are given, expressed as the correlation coefficient (r), measuring the degree of closeness of the linear relationship between two variables. The correlation coefficient is calculated as:

$$r_{xy} = \frac{\sum(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{[\sum(x_i - \bar{x})^2 \sum(y_i - \bar{y})^2]}}$$

where \bar{x} and \bar{y} are the sample means of X and Y .

Results and discussion

Interaction

ADG, days to slaughter and carcass length showed significant genotype × sex interaction ($p = 0.0209$, $p = 0.0319$ and $p = 0.0351$ respectively, Table 1). For these variables sex interac-

Table 1 The effect of genotype and sex on growth, carcass and meat quality characteristics (mean \pm std error)

	Genotype			Sex		Genotype \times Sex interaction
	NN	Nn	nn	C	G	P > t
Growth characteristics						
Days to slaughter	81.2 (\pm 1.62)	84.6 (\pm 2.19)	74.1* (\pm 2.72)(\pm 1.49)	77.3*** (\pm 1.74)	85.7*** (\pm 0.014)	0.0319
ADG	0.729 (\pm 0.012)	0.710 (\pm 0.018)	0.765 (\pm 0.022)	0.757* (\pm 0.012)	0.694* (\pm 0.014)	0.0209
Carcass characteristics						
Warm carcass mass	71.7 (\pm 3.35)	72.0 (\pm 2.78)	70.6 (\pm 2.25)	71.4 (\pm 3.27)	71.8 (\pm 2.66)	0.2542
Cold carcass mass	68.5 (\pm 3.32)	68.6 (\pm 3.18)	66.9 (\pm 1.79)	68.3 (\pm 3.32)	68.3 (\pm 2.76)	0.2431
Carcass length	76.5 (\pm 0.361)	76.7 (\pm 0.488)	75.2 (\pm 0.606)	76.6 (\pm 0.410)	76.1 (\pm 0.352)	0.0351
Fat thickness	20.0 (\pm 0.665)	18.8 (\pm 0.899)	26.1*** (\pm 1.12)	22.4* (\pm 0.709)	18.7* (\pm 0.826)	0.1047
Meat depth	50.9 (\pm 0.807)	52.4 (\pm 1.09)	46.8* (\pm 1.35)	49.8 (\pm 0.818)	51.7 (\pm 0.954)	0.1056
LMP	66.1 (\pm 0.329)	66.7 (\pm 0.445)	63.0*** (\pm 0.554)	64.9* (\pm 0.354)	66.7* (\pm 0.412)	0.0773
Meat quality characteristics						
Chilling loss	4.4 (\pm 0.245)	4.7 (\pm 0.466)	5.2 (\pm 0.580)	4.4 (\pm 0.327)	4.9 (\pm 0.381)	0.2852
Drip loss	1.69* (\pm 0.148)	2.39* (\pm 0.199)	1.06* (\pm 0.248)	1.43*** (\pm 0.146)	2.23*** (\pm 0.169)	0.1577
pH ₁	6.05* (\pm 0.051)	5.65* (\pm 0.069)	5.82* (\pm 0.085)	5.94 (\pm 0.056)	5.83 (\pm 0.063)	0.5989
pH ₂₄	5.87	5.81	5.80	5.87	5.80	0.9095

* Values in the same row with the same caption (genotype or sex) differ ($p < 0.05$), according to contrast analyses (see text).

*** Values in the same row with the same caption (genotype or sex) differ ($p < 0.001$), according to contrast analyses (see text).

tion may be expected. No other interactions were observed. No significant differences for sex within genotype were observed. As the sex of the animal is unalterable and the main effect of the halothane gene is considered important in pork production, this interaction was ignored, although statistically not justifiable. This was done mainly to compare the results with existing literature. The values for genotypes and sex are reported in Table 1.

Growth characteristics

The results show that the nn pigs had the highest ADG (0.765 kg.day⁻¹), followed by the NN (0.729 kg.day⁻¹) and Nn pigs (0.710 kg.day⁻¹). These differences were, however, not statistically significant and no trend is evident. The values for ADG in Table 1 indicated that nn pigs had the highest ADG compared to the other two genotypes, although none of the differences were significant in the present study. This is also in accordance with previous studies (Pommier *et al.*, 1992; Sather *et al.*, 1991), that did not indicate any differences in ADG between NN and Nn pigs. However, the nn pigs had a significant ($p < 0.05$) advantage (74.1) in days to slaughter when compared to both NN (81.2) and Nn pigs (84.6). There

were no significant differences between NN and Nn pigs, similar to the results of Sather *et al.* (1991) and Pommier *et al.* (1992). Castrates finished the growth phase significantly quicker ($p = 0.0005$) than gilts (77.3 vs. 85.7 days respectively), which is in agreement with Pommier *et al.* (1992). A similar pattern was observed for ADG with castrates showing a significant ($p = 0.0012$) advantage over gilts (0.756 vs. 0.694 kg.day⁻¹, respectively).

Carcass and meat quality characteristics

Warm and cold carcass mass showed no significant differences for genotypes or sexes. Carcass length showed genotype \times sex interaction, with no significant difference between genotypes. Consistent with the results from this study, Pommier *et al.* (1992) also reported no length differences between sexes. The nn pigs had a significantly higher ($p < 0.001$) fat thickness (26.1 mm) over the loin area compared to the NN (20.0 mm) and Nn pigs (18.8 mm), which in turn did not differ from each other. Fat thickness showed significant ($p < 0.05$) correlation with both ADG and days to slaughter ($r = 0.41$ and $r = -0.48$), indicating that faster growth was accompanied by an increase in fat thickness and not carcass lean,

thus leading to a lower carcass classification. The fat thickness values from this study are not consistent with reported values (Eikelenboom *et al.*, 1980; De Smet *et al.*, 1992; Fisher *et al.*, 1994), that indicated that the carcasses of nn pigs had the lowest fat thickness values, with Nn intermediate and NN the highest. The results from this study, however, support Jones *et al.* (1988) who reported that nn pigs had significantly higher fat thickness values measured over the loin area when compared to NN pigs. However, it must be emphasised that various reports (Jones *et al.*, 1988; Pommier *et al.*, 1992; Sather *et al.*, 1991) indicated that a single fat thickness measurement may not necessarily identify the greater lean content of carcasses from pigs with the halothane gene in either heterozygous (Nn) or homozygous (nn) form. Comparison of gender shows values (gilts = 18.7 mm, castrates = 22.4 mm) consistent with other studies (Jones *et al.*, 1988; Sather *et al.*, 1991; Pommier *et al.*, 1992) which report that gilts have significantly lower fat thickness values than castrates. These apparent contradictions may be explained by the non-significant interaction ($p = 0.1047$, Table 1), which leads one to disregard interaction and examine genotype and sex main effects separately. It is possible, however, that the presence of the halothane gene may manifest itself differently in different sexes with regard to fat and lean growth.

The nn pigs had a significantly lower ($p < 0.05$) meat depth (46.9 mm) over the loin area compared to both the NN (50.9 mm) and Nn pigs (52.4 mm). The gilts had a higher meat depth (51.7 mm) than the castrates (49.8 mm), though not statistically significant. Similar arguments as above for interaction ($p = 0.1056$) may hold for this variable. Since LMP is calculated using both fat thickness and muscle depth a similar, but inverse, trend to fat thickness can be expected and was observed. The nn pigs had a significantly lower ($p < 0.001$) predicted lean meat percentage (LMP) (46.8 %) than both NN (66.1 %) and Nn pigs (66.7 %), that did not differ. Gender comparison showed that the gilts had a significantly higher ($p < 0.05$) LMP (66.7 %) than the castrates (64.9 %).

Various reports indicate that the LMP from Nn pigs is expected to be approximately equal to the mid-value of the NN and nn pigs, with nn the highest and NN the lowest (Andresen *et al.*, 1981; Sather & Murray, 1989; Fisher *et al.*, 1994). However, the results from this study indicate that faster growth was not reflected as an increase in lean content of the carcasses. Both meat depth and LMP had a low positive correlation with days to slaughter ($r = 0.30$ and $r = 0.48$, respectively), and LMP had a low negative correlation with ADG ($r = -0.40$). This suggests that any advantages that the halothane gene may have regarding superior growth characteristics are also accompanied by inferior carcass characteristics.

The inclusion of the halothane gene seemed to cause an increase in the percentage chilling loss (Table 1), although none of the differences between the genotypes were significant, similar to the results from Fisher *et al.* (1994), with no significant differences between sexes either. Drip loss, however, showed considerable differences ($p < 0.05$) between genotypes with Nn the highest (2.39 %), nn the lowest (1.06 %) and NN intermediate (1.69 %). A significant difference ($p < 0.001$) between sexes was observed with the gilts (2.23%) having a higher percentage drip loss than the castrates (1.43

%). These results are contrary to most studies (Murray *et al.*, 1989; De Smet *et al.*, 1992; Sather *et al.*, 1991; Lündstrom *et al.*, 1989) that indicated that the presence of the halothane gene caused an increase in drip loss. As an explanation it follows that the higher the LMP of a carcass, the higher the amount of lean in a drip sample, thus the higher the potential loss of moisture from such a sample under conditions which promote exudate, since the lean portion contains more moisture. Slower chilling rates, caused by higher isolation from subcutaneous fat, may lead to increased exudate. Since such samples will have less lean, the potential to lose a higher quantity of moisture than samples from fast chilled (lean carcasses) are limited, leading to confusing results when exudate is expressed as a percentage of the total (fat, lean and bone) sample mass. In this study the LMP was lower for nn pigs, with more subcutaneous fat. A further explanation for the lower drip loss values observed in the nn carcasses would be that PSE muscles release their 'drip' within the first day post mortem (hence the higher percentage chilling loss), levelling off afterwards, whereas normal meat releases 'drip' with a lag phase after the second day post mortem (Honikel *et al.*, 1986). However, Murray *et al.* (1989) reported no significant differences in drip loss between Nn and nn pigs, and Barton-Gade (1985) reported that WHC values for Nn and NN pigs were not significantly different. In a breed comparison Moss (1985) reported that some carcasses classified as non-PSE (pH > 5.9) had a drip loss as high as PSE (pH < 5.9) carcasses.

Genotypic comparison showed that the NN pigs had a significantly higher ($p < 0.05$) pH₁ value (6.05) compared to Nn and nn pigs (5.65 and 5.82, respectively), with no significant differences between Nn and nn pigs (Table 1), and no significant differences between sexes. Results from other studies (Fisher *et al.*, 1994; Murray *et al.*, 1989; Oliver *et al.*, 1993) indicate that NN pigs had the highest pH₁ values, with nn the lowest and Nn intermediate. However, Cheah *et al.* (1995) and Sellier (1987) reported that crossbred Nn pigs (Landrace × Large White) showed a large variation in meat quality, as defined by pH₁, ranging from 43% normal to 57% PSE. The results reported in Table 2 confirm these findings. The large proportion of PSE carcasses, especially among the NN pigs, do suggest that poor pre- and/or post-slaughter management cannot be excluded in producing these results, as proposed by Barton-Gade *et al.* (1988).

The average pH₂₄ values for the three genotypes (Table 1) indicate no significant differences, ranging from 5.80 (nn) to the highest value of 5.87 (NN), with Nn intermediate (5.81). Similarly, no significant differences were observed for sexes. The post mortem decline in pH was relatively small, com-

Table 2 Classification of meat quality within genotypes

Meat quality	Genotype		
	NN	Nn	nn
Normal	(64.5%)	(23.5%)	(36.4%)
(pH ₁ > 5.9, pH ₂₄ < 6.2)			
DFD	(6.5%)	(5.9%)	(0)
(pH ₂₄ > 6.2)			
PSE	(29.0%)	(70.6%)	(63.6%)
(pH ₁ < 5.9)			

pared to results from other studies (Fisher *et al.*, 1994; Murray *et al.*, 1989; Schmitten *et al.*, 1987). As the average pH₂₄ did not reach 5.5, which is the iso-electric point of the principal muscle proteins (Lawrie, 1984), the subsequent denaturation of these proteins were not as acute, thus lessening the characteristic features of PSE meat (such as a high drip loss). The pH₂₄ is determined by muscle glycolytic potential (GP) prior to slaughtering (Monin *et al.*, 1981), whereas the rate of pH decline post mortem is determined by, among others, the halothane genotype (Monin & Sellier, 1985). It is thus probable that a low GP at slaughter could, to a certain degree, mask the rapid decline in pH (a characteristic of nn pigs), since the small amount of substrate would only allow limited glycolysis. This could then lead to a diminished difference in meat quality between genotypes as defined by pH₁, pH₂₄, colour, chilling loss and drip loss.

The potential advantages in growth (days to slaughter, ADG) associated with the halothane gene were not favourably reflected in most of the carcass and meat quality characteristics. It therefore seems of less value to incorporate this gene in pig production as practised in the Western Cape. It is suggested that objective meat colour determination be included in future studies since pH₁ alone is only a moderate predictor of ultimate meat quality. Further trials with varying energy and protein levels with different genotypes can be recommended before final recommendations regarding the use of the halothane gene can be made. The manifestation of the halothane gene in different sexes also warrants further investigation.

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