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STRESS INDUCED MOBILISATION OF FREE FATTY ACIDS AND POST MORTEM CARCASS CHARACTERISTICS IN DIFFERENT GENOTYPES OF SWINE

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INTRODUCTION

Fat and carbohydrate are the major sources yielding energy for muscular exercise. During rest, they both contribute about equally to the energy supply (Astrand and Rodahl, 1986). During exercise, more and more fat is used as fuel, depending on the type of exercise (i.e., light or heavy, continuous or intermittent, brief or prolonged), the state of physical training, the diet, and also some pathological influences like diabetes (Ellestad, 1977). High work loads normally rely more on the use of carbohydrates, but prolonged workloads increase steadily the part of fat in various species including calves (Eichinger, 1980). Also the state of the physical training is a very important factor, which strongly increases the use of free fatty acids in the energy metabolism, thus, causing a glycogen saving effect. A fat rich diet can increase the proportion of fat used as energy fuel up to more than 90%, but also a carbohydrate based diet shows an increase of the fat combustion from 30% at the beginning, up to about 60% at the end of a prolonged exercise (Astrand and Rodahl, 1986). The utilization of fat as fuel for muscular exercise seems to be a great advantage, but little is known about genotypic differences when all other somatic and environmental parameters are kept constant and comparable. One other aspect is the direct dependence of the post-mortem glycogenolysis on the ante-mortem metabolism, whereas the connections between fatty acid metabolism and glycogen saving effects are still unknown. Therefore, it was the aim of this study, to investigate under different working conditions the concentrations of plasma free fatty acids from different MH-genotypes of pigs and to compare them with parameters of post- mortem glycolysis and meat quality.

MATERIAL AND METHODS

Nineteen male castrated German Landrace pigs with an average live weight of 84kg were selected to form three different Malignant Hyperthermia (MH) groups, i.e., five animals were homozygous MH positive, seven animals homozygous negative and seven animals were heterozygous for the MH locus. Animals were catheterized (v.cava cranialis) and blood samples were drawn before, during and after a treadmill test run. The stress testing protocol consisted of three work loads, i.e., six minutes at level, six minutes uphill at 4.5%, and further six minutes uphill at 9% at a speed of 0.8m/s. Plasma free fatty acids were analyzed by an enzymatic test colorimetrically (WAKO, Neuss, FRG): Approximately four weeks later, animals were slaughtered and pH, conductivity, reflectance value and the water binding capacity was measured 24 hours post-mortem in the *m.longissimus thoracis*. All analysis and measurements were done in duplicate. Results were calculated by ANOVA, using the SAS software package for personal computers.

RESULTS AND DISCUSSION

The course of the plasma free fatty acid concentrations in the compounded material indicates, that prolonged work with increasing workloads also increased the proportion of fat probably used as fuel for muscular energy metabolism. After cessation of the work, the values came back close to the initial range (Figure 1). But the mean values also show a

remarkable standard deviation, which increases with increasing work loads. The analysis of these variances shows clear separation of the plasma free fatty acid concentrations between the three genotypes under treadmill working conditions (Figure 2). With increasing workloads also the differences between the genotypes increase. The homozygous MH positive animals showed the highest increase and also the highest values throughout the experiment. The homozygous MH negative animals kept their free fatty acid concentration within rather closed limits during all work loads. And finally the MH heterozygous animals showed about the same pattern as the MH positive group, but did not reach at no time comparable high concentrations. Considering the rather short duration of the exercise, a strong increase of the plasma free fatty acid concentration under rather comparable exercise conditions (Blum and Eichinger, 1988). Furthermore, the use of a higher proportion of fat as substrate for aerobic ATP synthesis does not necessarily cause also an increase of the plasma free fatty acid concentration.

We conclude therefore, that the MH-gene affects the metabolic pathways of energy regeneration either by direct stimulation of the lipolytic system via catecholamine induced cAMP turnover and/or by indirect effects via the regulation of the glycolytic activities. It is well established, that MH positive animals are more stress susceptible and that these animals use much earlier anaerobic pathways under severe stress conditions. These facts are also supported by postmortem meat characteristics, which are initiated by an early anaerobic muscle metabolism and lead to pale, soft, and exudative pork. Our post-mortem measurements fit well this hypothesis, whereas the MH-gene carriers show throughout all criteria the lowest meat quality (Table 1).

CONCLUSION

We conclude, that the very early increase of plasma free fatty acid concentrations after short time exercise in MHpositive pigs is the result of a combination of glycogen saving mechanisms and increased sensibility of the lipolytic system, which in turn favours early post-mortem glycogenolysis and subsequently poor meat quality.

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Criteria: all 24h post-mortem	$\begin{array}{c cccc} MH\text{-genotype} \\ h+/h+ & H-/h+ & H-/H- \\ a & b & c \\ n=5 & n=6 & n=7 \end{array}$			Signif.
рН	5.50	5.49	5.57	NS
(U)	± 0.06	± 0.04	± 0.05	
conductivity (mS)	7.2 ± 1.3	4.9 ± 1.1	4.6 ± 1.1	NS
reflexion value	54.3	58.5	60.9	NS
(U)	± 3.7	± 3.0	± 3.1	
water binding	0.35	0.38	0.43	a:c**
capacity (M:T)	± 0.02	± 0.01	± 0.02	b:c*

Table 1. Meat quality criteria from three different MH-genotypes measured 24 hours post-morterm in the m.longissimus thoracis (German Landrace, n=18), (least square mean values \pm standard error).

h+/h+ = homozygous MH-positive

H-/h+ = heterozygous

H-/H- = homozygous MH-negative M:T = meat/total area