

V i e w m e t a d a t a , c i t a t i o n C u e
p r o v i d e

1 **Post-mortem activity of the glycogen debranching enzyme and change in the**
2 **glycogen pools in porcine *M. longissimus dorsi* from carriers and non-**
3 **carriers of the RN^r gene**

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24 **Abstract**

25 Glycogen debranching enzyme (GDE) is together with glycogen phosphorylase responsible
26 for the degradation of glycogen. The present study compares the *post-mortem* activity of GDE
27 and breakdown of the glycogen pools in *M. longissimus dorsi* of RN⁻ carrier pigs and in wild
28 type animals. The activity of GDE (n=14) and pH (n=20) was measured 0.5, 3, 5, 24 and 48 h
29 *post-mortem*. The change in pro-glycogen and in macro-glycogen content (n=20) was
30 followed until 216 h *post-mortem* and the transcription level of GDE, glycogenin and
31 glycogen synthase m-RNA (n=19) were measured 0.5 h *post-mortem*. Both the activity of
32 GDE and the transcription level of GDE were found to be similar in RN⁻ carriers and wild
33 type animals shortly after slaughter. However, the activity declined faster in wild type animals
34 compared with RN⁻ carriers with increasing time *post-mortem*. The contents of both pro-
35 glycogen and macro-glycogen were higher in RN⁻ carriers compared with wild type animals,
36 and further, the proportion of macro-glycogen was higher in RN⁻ carriers compared with wild
37 type animals. During the *post-mortem* period, only degradation of pro-glycogen was observed
38 in both genotypes. The decrease in pH was faster and the ultimate pH lower in RN⁻ carriers
39 than in wild type animals. It was suggested that the higher GDE activity in the late phase of
40 the *post-mortem* period in muscles from RN⁻ carriers renders the extended pH decrease in
41 these muscles.

42

43 *Keywords:* Glycogen debranching enzyme; RN-genotype; Pig; Pro-glycogen; Macro-
44 glycogen

45

46 **1 Introduction**

47 The increased introduction of the Hampshire breed within pig breeding has caused a
48 widespread frequency of the RN⁻ gene in many countries, e.g. the frequency approach 70 % in
49 Swedish Hampshire crossbreeds (Enfält, Lundström, Karlsson, & Hansson, 1997b). The RN⁻
50 allele in the PRKAG3 gene on chromosome 15 is dominant and associated with an increased
51 glycogen content in porcine glycolytic muscles (Enfält et al., 1997b; Estrade, Vignon, Rock,
52 & Monin, 1993; Fernandez, Tornberg, Naveau, Talmant, & Monin, 1992). This has been
53 shown to result in a faster pH decrease (Josell, von Seth, & Tornberg, 2003a, b; Lindahl et al.,
54 2004) and lower ultimate pH in meat from RN⁻ carriers compared with the wild type (Enfält et
55 al., 1997b; Josell et al., 2003a; Le Roy et al., 2000; Lindahl et al., 2004).

56

57 Although the effects of the RN⁻ gene on the pH fall in *post-mortem* muscle and subsequent
58 influence on meat quality have been studied extensively (Enfält et al., 1997b; Josell et al.,
59 2003a; Lindahl et al., 2004), the understanding of the underlying mechanisms in the *post-*
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60 *mortem* glycogen metabolism between carriers and non-carriers of the RN⁻ gene is almost
61 absent. Considering that the differences in the *post-mortem* metabolism of glycogen between
62 genotypes are highly important for the quality of meat (Bendall & Swatland, 1988; Briskey,
63 1964; Monin & Ouali, 1991), a thorough understanding of the physiological mechanisms
64 giving rise to the fast rate of *post-mortem* pH decrease and low ultimate pH in meat of RN⁻
65 carriers may be crucial in the identification of biological markers of importance for future
66 breeding strategies aiming at production of high quality meat.

67

68 The biosynthesis of glycogen is initiated by a self-glucosylating protein, glycogenin
69 (Goldsmith, Sprang, & Fletterick, 1982; Gunja-Smith, Marshall, Mercier, Smith, & Whelan,
70 1970; Lomako, Lomako, & Whelan, 1988; Meléndez-Hevia, Waddell, & Shelton, 1993).
71 Subsequently, glycogen synthase and glycogen branching enzyme then complete the glycogen
72 molecules. Muscle glycogen exists in two forms: the acid-soluble, high molecular weight
73 (10⁷ Da) macro-glycogen rich in glucose molecules, and the acid-insoluble, low molecular
74 weight (400,000 Da) pro-glycogen, which is characterised by a higher protein to glucose ratio
75 (Lomako et al., 1991, 1993). These two glycogen pools seem to be metabolically distinct
76 (Graham, Adamo, Shearer, Marchand, & Saltin, 2001; Shearer, Marchand, Tarnopolsky,
77 Dyck, & Graham, 2001), although the physiological nature of the regulation of muscle
78 glycogen stores is poorly understood (Roach, 2002). It seems that macro-glycogen is
79 mobilised during aerobic exercise, while pro-glycogen is mobilised during anaerobic exercise
80 (Essén-Gustavsson, Jensen-Waern, Jonasson, & Andersson, 2005; Graham et al., 2001;
81 Shearer et al., 2001).

82

83 The degradation of glycogen progresses by cooperation of two enzymes: glycogen
84 phosphorylase (phosphorylase) and glycogen debranching enzyme (GDE) (Brown &
85 Illingworth-Brown, 1966). The phosphorylase breaks down linear glucose chains to the so-
86 called limit dextrin state whereupon GDE takes over and breaks down the branching point,
87 which enables the further action of phosphorylase (Brown & Illingworth-Brown, 1966;
88 Nelson, Kolb, & Larner, 1969). It has been suggested that GDE catalyses the rate-limiting
89 step in *post-mortem* glycogenolysis and thus glycolysis (Kylä-Puhju, Ruusunen, & Puolanne,
90 2005; Taylor, Cox, Kernohan, & Cohen, 1975; Ylä-Ajos, Ruusunen, & Puolanne, 2006).

91

92 The aim of this study was to further elucidate basic factors of importance for *post-mortem*
93 glycogen metabolism in relation to the pH fall by comparing the transcription levels of central
94 genes (GDE, glycogenin and glycogen synthase) involved in the glycogen metabolism, and
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95 measuring the activity of GDE and degradation of pro-glycogen and macro-glycogen in *M.*
96 *longissimus dorsi* from Hampshire crossbred animals with and without presence of the RN⁻
97 allele.

98

99 **2 Materials and Methods**

100 *2.1 Animals and sampling*

101 This study was part of a larger project studying the effect of the RN-gene on meat colour
102 stability and glycogen metabolism, described by Lindahl, Enfält, Andersen and Lundström (in
103 preparation). For the present study, twenty crossbred slaughter pigs, Hampshire x (Swedish
104 Landrace x Yorkshire) from four herds were stunned in CO₂ and slaughtered at a commercial
105 slaughterhouse in Sweden. Small muscle samples (*M. longissimus dorsi* and *M.*
106 *semimembranosus*) were obtained 0.5, 3, 5, 24 and 48 hours after bleeding. After 48 hours the
107 whole muscles were excised from the carcasses, vacuum-packed and stored at 5°C for another
108 2, 5 or 7 days before sampling. The collected samples were frozen in liquid nitrogen
109 immediately after sampling and stored at -80°C. The pH was measured (Knick portable pH-
110 meter equipped with a combination gel electrode, SE104, Knick Berlin, Germany) in *M.*
111 *longissimus dorsi* at the last thoracic vertebra and in the middle of *M. semimembranosus* at
112 0.5, 3, 5, 24 and 48 hours after bleeding. The pH electrode was calibrated in pH 4.01 and 7.00
113 buffers (Radiometer, Denmark) at ambient temperature when pH was measured 30 min *post-*
114 *mortem*, and at 4°C at the other time points.

115

116 *2.2 Genotyping*

117 The PRKAG3 alleles were identified with a DNA test using the polymerase chain reaction
118 (PCR) method described by Milan et al. (2000). Three alleles were designated as follows: RN⁻
119 (199V-200Q), rn⁺ (199V-200R) and rn^{*} (199I-200R). RN⁻ carriers had the combinations: RN⁻
120 /rn⁺, RN⁻/rn^{*}, and the wild type animals had: rn⁺/rn⁺, rn⁺/rn^{*}, rn^{*}/rn^{*}.

121

122 *2.3 The activity of GDE*

123 The *post-mortem* activity of GDE was determined from *M. longissimus dorsi* (n=14) and *M.*
124 *semimembranosus* (n=6) using the method of Nelson, Palmer & Larner (1970) with minor
125 modifications (Kylä-Puhju et al., 2005). The method is a colorimetric assay based on a shift in
126 the absorbance at 525 nm upon GDE-catalysed conversion of limit dextrin to glycogen. The
127 GDE activity measurements were made at 39°C in triplicate at three time points and the
128 activity was calculated from the slope of the linear phase of the absorbance curve. In addition,
129 the absorption spectra between 375 nm and 800 nm of the blank and the reaction mixtures

130 were obtained to ensure the conversion of limit dextrin to glycogen (results not shown). The
131 assay measures the combined activity of GDE, i.e. glycan transferase (EC 2.4.1.25) and
132 amylo-1,6-glucosidase (EC 3.2.1.33) activities.

133

134 The reproducibility of the assay was determined as follows: a large muscle sample was
135 ground in liquid nitrogen, aliquoted, stored at -80°C, and used as an internal standard. The
136 coefficient of variation (CV) for the internal standard was $\pm 18.3\%$ for the GDE activity.

137

138 2.4 Glycogen content

139 Pro-glycogen and macro-glycogen were separated as described by Adamo and Graham
140 (1998). In short, the pro-glycogen was precipitated by perchloric acid. After centrifugation
141 pro-glycogen in the pellet and macro-glycogen in the supernatant were hydrolysed for 2 h in
142 1M HCl. Glucose from the hydrolysed homogenates were analysed according to the
143 procedure of Passonneau & Lowry, 1990. The analysis method does not distinguish the origin
144 of the glucose molecules, thus glycogen, glucose and glucose-6-phosphate all contribute to
145 the total glucose amount in the two fractions. Since pro-glycogen is precipitated in the pellet,
146 the free glucose and glucose-6-phosphate will be included in the macro-glycogen fraction.
147 Thus, in the present study “macro-glycogen” = macro-glycogen + free glucose + glucose-
148 phosphates.

149

150 2.5 Gene expressions

151 The transcription levels of three genes (GDE, glycogen synthase and glycogenin) and two
152 housekeeping genes (the structural protein β -Actin and the glycolytic enzyme glyceraldehyd-
153 3-phosphate dehydrogenase i.e. GAPDH) were quantified in *M. longissimus dorsi* of RN⁻
154 carriers (n=9) and wild type animals (n=10). However, the housekeeping gene GAPDH was
155 excluded from the analyses because its transcription differed significantly between genotypes.
156 The samples for gene expression analyses were taken 0.5 h after slaughter and frozen in liquid
157 nitrogen. The RNA was purified from 30 mg of muscle sample using the method described by
158 Chomczynski and Mackey (1995). In short, muscle tissue was homogenised in TriReagent
159 (Molecular Research Center Inc. Cincinnati, Ohio), the phases were separated with 1-bromo-
160 3-chloropropane and finally the RNA was precipitated with isopropanol. The dry pellet,
161 containing RNA was solubilised in H₂O and stored at -80°C. Total RNA was determined by
162 measuring the absorbance at 260 nm. Equal amounts of RNA were reverse transcribed with
163 oligo-dT and Superscript II RNase H reverse transcriptase kit (Invitrogen, Taastrup,
164 Denmark) and ultrapure dNTPSet (Pharmacia Amersham) as described by Theil, Sørensen,
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165 Therkildsen and Oksbjerg (2006). Reverse transcribed material (1 µl) was amplified with
166 TaqMan Universal PCR Master Mix (Applied Biosystems, Stockholm, Sweden) using
167 primers specific for each gene. The signal was detected quantitatively by gene specific probes
168 labelled with FAMTM fluorophore in the 5' end. Primers and probes were designed by using
169 Primer Express (Applied Biosystem, Stockholm, Sweden) version 2.0 software, and either a
170 primer or a probe was designed to anneal to a splice site to avoid amplification of genomic
171 DNA. The primer pairs predicted 78, 74, 80, 113 and 76 bp fragments for GDE, glycogen
172 synthase, glycogenin, β-Actin and GAPDH, respectively. For real time RT-PCR, 40 cycles at
173 95°C for 15 s and 60°C for 60 s were applied to amplify the PCR products. The number of
174 PCR cycles required to reach the threshold for a gene of interest (Ct value) was used in the
175 statistical analysis. Serial dilutions for obtaining a standard curve were analysed in triplicate,
176 whereas unknown samples were analysed in duplicates using ABI 7900HT Sequence
177 Detection System (Applied Biosystems, Stockholm, Sweden).

178 The sequences of forward primers, MGB probes and reverse primers were as follows:

179 GDE: 5'-TGTTCTTTCTCGACATTATGTTTCATCT-3', 5'-

180 AGCGATCCCCTTGAAAGGACTTCCA-3', 5'-TGTCATTCTCGTTGGTCAGTT-3'

181 Glycogen synthase: 5'-CCGGCTTCGGCTGCTT-3', 5'-

182 CGCAGACCCCTCGGCTTACGGTATC-3', 5'-CCGCCGGTCCAGAATG-3'

183 Glycogenin: 5'-ATCAGCTGTTGCACCTTGCTT-3', 5'-

184 TGAGCAAGGTAGTTTTGATGGTGG-3', 5'-

185 GCTGCTAAAAAATGTGTTTCAGTAAACC-3'

186 β-Actin: 5'-ACCCAGATCATGTTCGAGACCTT-3', 5'-

187 CTGTATGCCTCTGGCCGCACCA-3', 5'-TCACCGGAGTCCATCACGAT-3'

188 GAPDH: 5'-GTCGGAGTGAACGGATTTGG-3', 5'-CGCCTGGTCACCAGGGCTGCT-3',

189 5'-CAATGTCCACTTTGCCAGAGTTAA-3'

190

191 2.6 Statistical analysis

192 The statistical analysis was carried out using the Statistical Analysis System version 8.02
193 (SAS Institute Inc., 1999). The MIXED procedure was applied when testing the differences in
194 the activity of GDE, pH and in the pro-glycogen and “macro-glycogen” content between the
195 genotypes. The model included the fixed effects of genotype, sex, time and interaction
196 between genotype and time and a random animal effect to account for repeated measurements
197 performed within the same animal. The correlation between pro-glycogen content and pH was
198 tested by using the GLM procedure with the factors sex, slaughter date and herd. Also the
199 differences in transcription levels between RN-genotypes were tested by using the GLM
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200 procedure. The model included the following factors: RN-genotype, sex, slaughter date and
201 interaction between RN-genotype and sex. The normalisation of transcriptional data was
202 obtained with the transcription of the housekeeping gene β -actin by calculating Δ Ct values
203 (Δ Ct = Ct of the target gene - Ct of the housekeeping gene). The calculations were made as
204 described by Theil et al. (2006). The difference between the genotypes was considered to be
205 significant when $P < 0.05$.

206

207 **3 Results**

208 The total muscle glucose content 0.5 h *post-mortem* was 77% higher in RN⁻ carriers compared
209 with wild type animals, 101.9 and 57.6 mmol/kg w.w., respectively (Table 1). Pro-glycogen
210 corresponded to 57% of the total muscle glucose content in RN⁻ carriers and to 66% in wild
211 type animals. Independent of genotype, only pro-glycogen was broken down *post-mortem*,
212 while no degradation of “macro-glycogen” was registered.

213

214 The degradation of muscle pro-glycogen continued until 96 h *post-mortem* in RN⁻ carriers,
215 while it was already abated 48 h *post-mortem* in muscles from wild type animals.

216 Interestingly, an increase in “macro-glycogen” content simultaneously with the decrease in
217 pro-glycogen content was observed in muscles from RN⁻ carriers in the period 48 h to 96 h
218 *post-mortem*. The “macro-glycogen” fraction, however, includes also glucose-6-phosphate
219 and free glucose and the observed increase in this fraction could be due to an increase in
220 content of these compounds.

221

222 In *M. longissimus dorsi*, the activity of GDE decreased slowly as a function of time *post-*
223 *mortem*, and the decrease was statistically significant in all animals until after 5 hours *post-*
224 *mortem*. The activity of GDE was similar in both RN-genotypes up to 5 hours after slaughter
225 (Figure 1). However, 24 h *post-mortem* the activity of GDE was significantly higher in RN⁻
226 carriers compared with wild type animals, and this difference was maintained up to 48 h *post-*
227 *mortem*.

228

229 In *M. semimembranosus*, no significant difference in the *post-mortem* activity of GDE
230 between the two genotypes was found (Figure 2). There was a tendency to a decrease in
231 activity of GDE with increasing time *post-mortem*, but it became significant only in the
232 muscles from wild type animals after 48 h.

233

234 The transcription levels of GDE and glycogen synthase were similar in both genotypes, while
235 a greater transcription of glycogenin was found in RN⁻ carriers. Thus, the glycogenin m-RNA
236 was more abundant in RN⁻ carriers compared with wild type animals (Table 2).

237

238 The pH 0.5 h *post-mortem* was not significantly different between the two genotypes
239 (Table 3). However, the rate of pH decrease was faster, and the ultimate pH was lower in the
240 *M. longissimus dorsi* from RN⁻ carriers compared with wild type animals. The correlation
241 between the degradation of pro-glycogen and pH decrease was high in RN⁻ carriers ($r=0.89$)
242 and in wild type animals ($r=0.93$). The pro-glycogen content 0.5 h *post-mortem* explained 44
243 and 48% of the variation in ultimate pH in RN⁻ carriers and in wild type animals, respectively.
244 No significant differences in pH in *M. semimembranosus* were found between the two
245 genotypes.

246

247 **4 Discussion**

248 The present study showed in accordance with a vast number of earlier studies that RN⁻
249 carriers possess a higher glycolytic potential, a faster initial pH decrease and a lower ultimate
250 pH than wild type animals. This results in a larger drip loss and cooking loss, a lower Napole
251 Yield, but improved tenderness in most cases (Enfält 1997a, b; Josell et al. 2003b; Lindahl et
252 al., 2004).

253

254 Glycogen exists in two forms in skeletal muscle: acid-soluble, high molecular weight macro-
255 glycogen and acid-insoluble, low molecular weight pro-glycogen (Lomako et al., 1991, 1993).
256 In the present study, the high glycolytic potential in RN⁻ carriers was found to result from
257 accumulation of both glycogen types, pro-glycogen and “macro-glycogen”, in the muscle. In
258 contrast, Essén-Gustavsson et al. (2005) reported that high glycogen content in RN⁻ carriers is
259 exclusively due to increased macro-glycogen content. The pigs were, however, younger and
260 lighter than in the present study. In RN⁻ carriers the proportion of “macro-glycogen” was
261 higher than in the wild type animals, which is consistent with several studies showing that the
262 macro-glycogen fraction increases with increasing muscle glycogen content (Adamo &
263 Graham, 1998; Adamo, Tarnopolsky, & Graham, 1998; Asp, Daugaard, Rohde, Adamo, &
264 Graham, 1999; Derave, Gao, & Richter, 2000; Shearer, Marchand, Sathasivam, Tarnopolsky,
265 & Graham, 2000). The pro-glycogen to “macro-glycogen” ratio in wild type animals was
266 similar as reported for pigs by Rosenvold, Essén-Gustavsson and Andersen (2003).

267

268 Only pro-glycogen was used for muscle energy production *post-mortem* (from 0.5 to 48 h),
269 which is consistent with the results of Rosenvold et al. (2003) who observed only pro-
270 glycogen degradation during the first 45 minutes *post-mortem*. Essén-Gustavsson et al. (2005)
271 showed recently that the breakdown of macro-glycogen takes place during aerobic, low
272 intensity exercise in both RN⁻ genotypes. In the present study, the analytical method for
273 measuring “macro-glycogen” fraction included also glucose-6-phosphate and free glucose.
274 Thus, it could be possible that also some of the macro-glycogen has broken down
275 *post-mortem* although the analytical method does not detect that. The “macro-glycogen”
276 content in *M. longissimus dorsi* in RN⁻ carriers increased in the period from 48 h to 96 h *post-*
277 *mortem*. The increase might be explained by accumulation of glucose-6-phosphate and free
278 glucose as a function of pro-glycogen degradation. This is supported by the results from
279 Monin and Sellier (1985), who found that the glucose-6-phosphate content, a day after
280 slaughter, was significantly higher in the Hampshire breed pigs (11 mmol/kg), which were
281 very likely RN⁻ carriers, compared with pigs from Large White (6 mmol/kg) and Pietrain
282 (6 mmol/kg) breeds. In pig muscle an hour after slaughter, the content of free glucose is
283 3-6 mmol/kg (Monin and Sellier, 1985). Furthermore, the action of GDE results in liberation
284 of free glucose (Brown & Illingworth-Brown, 1966). GDE, and probably also phosphorylase,
285 is still active 48 h *post-mortem* and hereby enables the accumulation of glucose-6-phosphate
286 and free glucose. Thus, this suggests that in RN⁻ carriers muscle glycolysis is ceased due to
287 inhibition of phosphofructokinase, which is generally considered a rate-limiting enzyme in
288 glycolysis (Stryer, 1988). The rate and quantity of muscle H⁺ production are consequences of
289 ATP hydrolysis coupled with glycolysis (Bendall, 1973; Hamm, 1977; Robergs, Ghiasvand &
290 Parker, 2004). Lactate production coincides with pH decrease, but against general belief this
291 is not a causal relationship, since lactate production retards, not causes, muscle acidosis
292 (Bendall, 1973; Robergs et al., 2004). The proposed hypothesis on inhibition of
293 phosphofructokinase in RN⁻ carriers agrees with studies reporting similar ultimate lactate
294 contents in RN⁻ carriers and in wild type animals despite differences in ultimate pH (Enfält,
295 Lundström, Hansson, Johansen & Nyström, 1997a; Lundström, Enfält, Tornberg & Agerhem,
296 1998). In wild type animals no change in the “macro-glycogen” fraction was observed.

297

298 The decrease in pH was faster, and the ultimate pH was lower in *M. longissimus dorsi* of RN⁻
299 carriers than in wild type animals, which agrees with earlier findings (Enfält et al., 1997b;
300 Josell et al., 2003a; Lindahl et al., 2004). The extended pH decrease in RN⁻ carriers is possibly
301 a result of longer maintenance of the high activity of GDE in these animals. The activity of
302 GDE was similar for RN⁻ carriers and wild type animals during the first five hours *post-*

303 *mortem*, which is in agreement with Estrade, Ayoub, Talmant & Monin (1994) who reported
304 an uniformity in the activity of GDE and of glycogen phosphorylase between the
305 RN-genotypes five minutes after slaughter. In both genotypes, the activity of GDE remained
306 at the level found shortly after slaughter for several hours, but was reduced significantly after
307 24 h *post-mortem*. However, the decrease was more pronounced in wild type animals. It is
308 possible that high muscle glycogen content protects the GDE from denaturation, since binding
309 on glycogen limit dextrin or to lesser extent on glycogen serves as protection from denaturing
310 agents (Gillard, White, Zingaro, & Nelson, 1980; Scraba, Bradley, Fitzgerald, & Madsen,
311 1988). Then again, the RN⁻ mutation is located in the gene coding for adenosine
312 monophosphate-activated protein kinase (AMPK), which is a key metabolic enzyme (Milan et
313 al., 2000). Activated AMPK inhibits the ATP-consuming pathways, stimulates ATP-
314 generating pathways (Hardie & Carling, 1997) and as reported recently by Shen and Du
315 (2005) is important for maintaining the activity of glycogen phosphorylase in *post-mortem*
316 muscle. Thus the mutation in the AMPK gene might explain why RN⁻ carriers exhibit a
317 prolonged high GDE activity, as found in the present study. The pH itself has only a minor
318 effect on the activity of GDE when the pH ranges between 5.5 and 7 (Kylä-Puhju et al.,
319 2005).

320

321 The differences between the studied muscles offer indirect support to the importance of the
322 activity of GDE in the development of ultimate pH between RN-genotypes. The change in the
323 activity of GDE was followed from 0.5 h to 48 h *post-mortem*. The activity was stable,
324 particularly in *M. semimembranosus* of RN⁻ carriers, where no significant decrease in the
325 activity of GDE with increasing time was found. Furthermore, in *M. semimembranosus* (n=6),
326 unlike in *M. longissimus dorsi*, the activity of GDE, the rate of pH decrease or ultimate pH
327 did not differ between the RN-genotypes. It seems that the activity of GDE might be related to
328 the formation of ultimate pH, and it remains to be investigated if a difference in the activity of
329 GDE late *post-mortem* between the RN-genotypes would lead to differences in ultimate pH
330 also in *M. semimembranosus*. Lindahl et al. (in preparation) found, with a larger number of
331 pigs from the same project, a faster pH decline and lower pH 3 and 5 h *post-mortem* in the *M.*
332 *semimembranosus* of the RN⁻ carriers compared with wild type animals, however, no
333 difference in ultimate pH. Although *M. longissimus dorsi* and *M. semimembranosus* are very
334 similar to each other in glycolytic potential, the activity of glycogenolytic enzymes (Fischer &
335 Dobrowolski, 2002; Ylä-Ajos et al., 2006) and fibre type composition (Ruusunen & Puolanne,
336 2004), the pH decrease is slower in *M. semimembranosus* (Henckel, Karlsson, Oksbjerg, &

337 Petersen, 2000). However, combining the data obtained from the present study concerning the
338 studied muscles, indicate that the activity of GDE affects the pH decline *post-mortem*.

339

340 It seems that immediately post slaughter, the glycogenolytic enzymes are not more active in
341 RN⁻ carriers than in wild type animals despite the higher glycogen content in RN⁻ carriers.
342 Besides the activity of GDE, also the transcription level of GDE was similar between the
343 genotypes. Thus, the differences in the activity of GDE between the genotypes do not explain
344 the faster pH decrease early *post-mortem* in RN⁻ carriers compared with wild type animals.
345 Hedegaard et al. (2004) found indications of an up-regulation of phosphofruktokinase enzyme
346 in RN⁻ carriers, which is the rate-limiting enzyme in glycolysis, and this would explain the
347 fast glycolysis during early *post-mortem* in RN⁻ carriers.

348

349 The mechanisms behind the high glycogen content in the glycolytic muscles of RN⁻ carriers
350 are not well described. Estrade et al. (1993) reported that the localization and ultrastructural
351 pattern of glycogen was similar in both genotypes, but the density of the glycogen particles
352 was higher in muscle fibres from RN⁻ carriers, which may indicate higher glycogenin activity.
353 The present study showed a slightly higher expression of glycogenin in RN⁻ carriers compared
354 with wild type animals. Glycogenin is an autocatalytic protein serving as substrate for
355 glycogen synthase, and theoretically, the number of glycogenin molecules available within
356 skeletal muscle would dictate the number of glycogen particles and hence the amount of
357 glycogen stored. Therefore the production of active glycogenin primer in the muscle fibre
358 could be the overall rate-limiting process in glycogen formation, capable of overriding the
359 role of the activity of glycogen synthase (Alonso, Lomako, Lomako, & Whelan, 1995).
360 Furthermore, Shearer et al. (2000) found a positive correlation in human muscle between
361 glycogenin activity and total glycogen content, pro-glycogen content as well as macro-
362 glycogen content.

363

364 Alternatively, the hyperaccumulation of glycogen in RN⁻ carriers could originate from the
365 higher expression of UDP-glucose pyrophosphorylase protein and high activity of the enzyme
366 reported by Hedegaard et al. (2004). Furthermore, Hedegaard et al. (2004) suggested that the
367 synthesis of glycogen in the muscles of RN⁻ carriers was increased due to increased influx of
368 glucose into the muscle fibres. Estrade et al. (1994) reported a tendency of higher glycogen
369 synthase activity in RN⁻ carriers compared with wild type animals. In the present study, no
370 difference in the transcription of the glycogen synthase between genotypes was found,
371 however, the transcription of a gene does not necessarily correspond to the activity of the
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372 enzyme for which it is coding. In the present study, the activities of glycogenin and glycogen
373 synthase were not analysed.

374

375 **5 Conclusions**

376 In *M. longissimus dorsi*, the decrease in the activity of GDE with increasing time *post-mortem*
377 is slower and less pronounced in RN⁻ carriers than in wild type animals. At the same time the
378 decrease in pH is faster and the ultimate pH lower in RN⁻ carriers than in wild type animals.
379 The long period of high GDE activity in RN⁻ carriers may enable the extended pH decrease.
380 The transcription of the glycogenin gene is slightly higher, and both pro-glycogen and macro-
381 glycogen are more abundant in RN⁻ carriers than in wild type animals, however, only the pro-
382 glycogen is degraded *post-mortem* irrespective of genotype.

383

384 **Acknowledgements**

385 The present study was supported by the Finnish Graduate School Program ‘Applied
386 Bioscience - Bioengineering, Food & Nutrition, Environment’ (ABS), the Nordic Network in
387 Meat Science (NNMS) and the Ministry of Food, Agriculture and Fisheries, Denmark. The
388 authors wish to thank Ronnie Samuelsson, Swedish Meats, Uppsala, for information about
389 herds and slaughter planning and Gertrud Andersson and Jens Askov Jensen for their
390 invaluable help during sampling and sample preparation. Acknowledgements are also given to
391 Head laboratory assistant Marianne Rasmussen, Laboratory technician Irja Korhonen, Senior
392 laboratory assistant Inge Lise Sørensen and Laboratory technician Anne-Grete Dyrvig
393 Petersen for their skilled technical assistance in the analyses.

394

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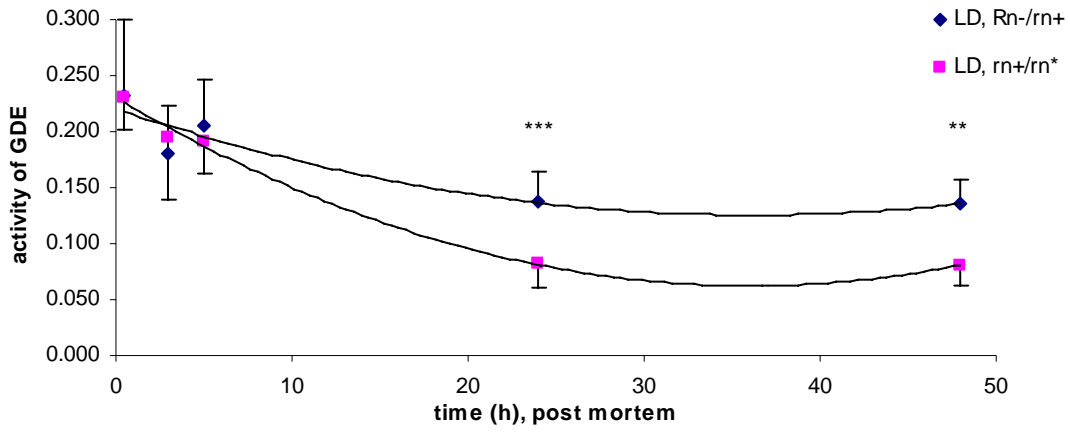
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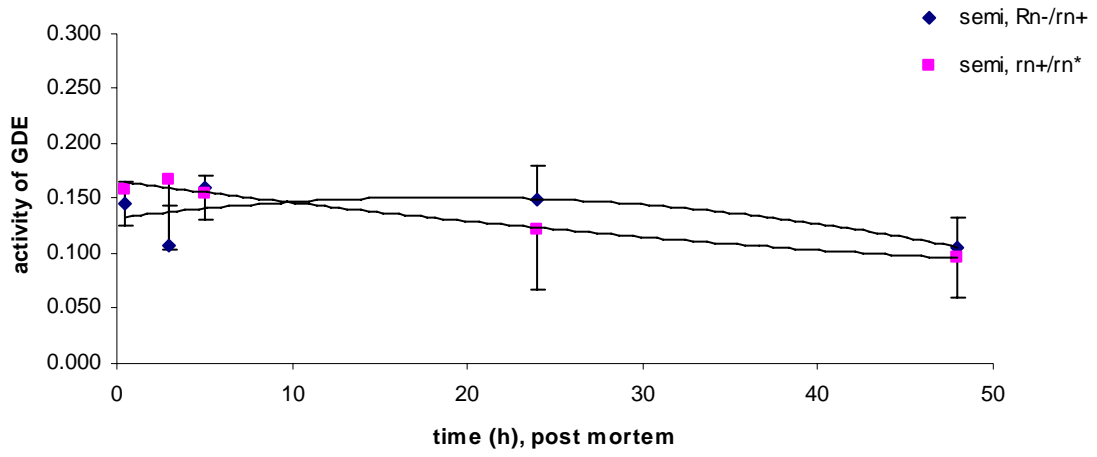
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540

541 Figure 1. Activity of GDE ($\Delta_{\text{abs}}/\Delta_{\text{min}}$, means and standard deviations) in *M. longissimus*
 542 *dorsi* of different RN-genotypes (◆ RN⁻ carriers, n=7, ■ wild type (rn⁺), n=7). Asterisks
 543 indicate significant difference between the two genotypes (***) P<0.001, ** P<0.01).
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549 Figure 2. Activity of GDE ($\Delta_{abs}/\Delta_{min}$, means and standard deviations) in *M.*
550 *semimembranosus* of different RN-genotypes (\blacklozenge RN⁻ carriers, n=3, \blacksquare wild type (rn⁺), n=3).
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557 Table 1. LSM means and SEM for pro-glycogen, “macro-glycogen” and total glucose contents
 558 in *M. longissimus dorsi* of RN⁻ carriers and wild type (rn⁺) animals during the *post-mortem*
 559 period

Time <i>post-mortem</i>	Pro-glycogen, mmol/kg		“Macro-glycogen”, mmol/kg		Total glucose content, mmol/kg	
	RN ⁻	rn ⁺	RN ⁻	rn ⁺	RN ⁻	rn ⁺
0.5 h	57.8±2.5a	38.2±2.7a	44.2±2.7a	19.3±2.9	101.9±3.9a	57.6±4.1a
5 h	46.8±3.8 b	30.0±3.7b	46.1±2.5ab	16.9±2.7	92.8±4.6b	47.0±4.9b
24 h	34.2±1.7c	9.4±1.8c	44.3±1.8a	15.7±1.9	78.4±2.4c	25.1±2.5c
48 h	22.9±1.1d	2.7±1.2d	49.0±1.8b	17.6±1.9	71.8±2.7d	20.4±2.8d
96 h	7.3±0.4e	1.6±0.4d	58.3±1.9c	15.4±2.0	65.5±2.0e	17.2±2.1d
168 h	6.8±0.5e	1.6±0.5d	60.6±2.4c	15.2±2.5	67.3±2.5de	17.0±2.7d
216 h	6.8±0.4e	1.5±0.4d	59.8±2.0c	14.5±2.1	66.5±2.3e	16.1±2.4d

560 When comparing the genotypes, both pro-glycogen content and “macro-glycogen” content as well as total
 561 glucose content differed significantly (p <0.001) between the genotypes at each stage.
 562 Different letter within a column indicates significant (P<0.05) difference between values.

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567 Table 2. Relative transcription of GDE, glycogen synthase and glycogenin genes in
 568 *M. longissimus dorsi* of RN⁻ carriers and wild type (rn⁺) animals.^a

Gene	RN ⁻	rn ⁺	p-value
GDE	0.75	1	0.142
glycogen synthase	1.14	1	0.330
glycogenin	1.62	1	0.0361

569 ^a Data are normalised according to the transcription level observed in wild type animals.
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574 Table 3. Decrease in pH (LSMeans±SE) in RN⁻ carriers and wild type (rn⁺) animals. For
 575 *M. longissimus dorsi* n=20 and for *M. semimembranosus* n=6.

Time <i>post-mortem</i>	<i>M. longissimus dorsi</i>			<i>M. semimembranosus</i>		
	RN ⁻	rn ⁺	p-value	RN ⁻	rn ⁺	p-value
0.5 h	6.53±0.06a	6.65±0.06a	0.223	6.59±0.09a	6.58±0.09a	0.979
3 h	6.14±0.08b	6.48±0.08a	0.007	6.11±0.09b	6.18±0.09b	0.595
5 h	5.96±0.07c	6.25±0.07b	0.004	6.21±0.09b	6.04±0.09b	0.169
24 h	5.38±0.03d	5.51±0.03c	0.017	5.36±0.09c	5.37±0.09c	0.894
48 h	5.21±0.03e	5.36±0.03d	0.002	5.29±0.09c	5.33±0.09c	0.709

576 Different letter within a column indicates significant (P<0.05) difference between values