

1 **Replacing soybean meal with rapeseed meal and faba beans in pig diet: effect on growth**
2 **performance, meat quality and metabolite changes**

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32 **Abstract**

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34 Rapeseed meal and faba beans (RSM/FB) can serve as an alternative to imported soybean meal
35 (SBM). In this study, forty Norwegian crossbred ([Landrace x Yorkshire] x Duroc) growing-
36 finishing pigs (108.7±4.2 kg final BW) were fed a diet with either SBM or RSM/FB as protein
37 sources. RSM/FB increased feed conversion ratio (P=0.04) in the finishing period, reduced
38 lightness (P=0.04) and yellowness (P=0.004) of meat, changed amounts of individual fatty acids,
39 but not of total SFA, MUFA and PUFA. Importantly, RSM/FB reduced the glucose level (P <
40 0.05) in meat. Lower pyroglutamic acid (P = 0.06) in RSM/FB indicate lower oxidative stress in
41 pre-rigor muscle cell. Increased abundance of free amino acids, sweet tasting metabolites, reduced
42 warmed-over flavor and flavor attributes indicated desirable properties of RSM/FB meat. To
43 conclude, RSM/FB in pig diet supported a high growth performance and carcass quality
44 comparable to SBM and had a positive effect on meat quality.

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46 **Keywords**

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48 Local diet, carcass traits, pork meat, chilled storage, metabolites, sensory quality

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63 1. Introduction

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65 Modern pig production in Europe heavily relies on imported soybean meal (SBM) as the main
66 protein supplement in animal diet (Jezierny, Mosenthin, & Bauer, 2010). Considering the often
67 large price fluctuations for SBM, an overall economic pressure on pork production (Florou-Paneri
68 et al., 2014), and also the high reliance of imported protein rich feedstuffs in Norway and Europe,
69 an alternative is to increase the use of rapeseed meal (RSM) and faba beans (FB) as locally
70 produced high-protein ingredients in Europe (Jezierny et al., 2010; Sobotka, Pomianowski, &
71 Wójcik, 2012). In addition, the possibility of replacing SBM with protein ingredients from
72 European agricultural systems can contribute to more sustainable pork production (Hanczakowska
73 & Świątkiewicz, 2014; van Zanten, Bikker, Mollenhorst, Meerburg, & De Boer, 2015). Some
74 studies showed no adverse effects of replacing SBM with alternative protein sources on the growth
75 performance of growing-finishing pigs (Partanen et al., 2003; Skoufos et al., 2016). A meta-
76 analysis showed that the use of up to 30% rapeseed meal in growing-finishing pig diets did not
77 compromise growth performance compared to a SBM based diet when added to a nutritionally
78 balanced diet (Hansen et al., 2020). However, limited information exists on the metabolic
79 adaptation of pigs and metabolite changes in pork meat resulting from replacing SBM with RSM
80 and FB.

81 Metabolite analysis are more often used in human interventions identifying metabolites associated
82 with the intake of nutrients and different dietary patterns (Esko et al., 2017; Lécuyer et al., 2020),
83 while it has not been commonly used to study the impact of metabolites on animal performance
84 and meat quality in farm animals. Chen et al. (2018) reported that RSM in diets (200 g/kg of feed)
85 for young pigs induced changes in metabolite profile of liver and plasma by increasing the level
86 of oxidized metabolites (*e.g.* oxidized glutathione) and compromised redox balance. Metabolite
87 analysis of meat, may show similar changes. However, Skugor et al. (2019) showed that feeding
88 rapeseed based diets contains natural antioxidants that led to an increased expression of genes that
89 gives protection against oxidative stress and removes free radicals in the muscle. Different energy
90 sources, such as low starch, high fiber and fat content diets, can modulate physiological and
91 nutritional condition of muscle, *i.e.* glycogen storage (Li et al., 2015), having indirect effect on
92 early *post mortem* mechanisms that leads to conversion of muscle into meat (Li et al., 2017).
93 However, diet-induced metabolite changes in early *post mortem* pork muscle tissue and during

94 storage have not been studied so far. Overall, both variations in nutritional and antinutritional
95 composition of growing-finishing pig diets can cause the changes at metabolic level that can affect
96 the sensory traits. Hanczakowska & Świątkiewicz (2014), however, reported that pigs fed a RSM
97 and field beans based diet, replacing SBM resulted in a less tasty, but more tender pork compared
98 with pigs fed a SBM based diet.

99 The aim of the current research was to address the effect of replacing SBM (142.6 g/kg) with
100 RSM/FB (120 g/kg of RSM and 161.12 g/kg of FB) on growth performance, carcass quality,
101 metabolite status and meat quality in Norwegian crossbred growing-finishing pigs. In addition,
102 sensory attributes were evaluated to understand the effect of diet on flavor and texture development
103 of pork meat.

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105 **2. Materials and methods**

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107 *2.1. Experimental animals and housing*

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109 The study was conducted at the Center for Animal Research, Norwegian University of Life
110 Sciences, Ås, Norway and the experimental protocol for the study was approved by the Norwegian
111 Food Safety Authority (ID:8217). All animals were cared for according to laws and regulations
112 controlling experiments with live animals in Norway (the Animal Protection Act of December
113 20th, 1974, and the Animal Protection Ordinance concerning experiments with animals of January
114 15th, 1996).

115 Forty Norwegian crossbred pigs ([Landrace x Yorkshire] x Duroc) from 5 litters with equal
116 distribution of gender were included in the study. The mother line was Norwegian Landrace x
117 Duroc (LY), and the sire line was Duroc (DD). The initial average body weight (BW) was $27.7 \pm$
118 2.9 kg and final average BW was 108.7 ± 4.2 kg. The pigs were split in groups of 4 pigs per pen
119 assigned to 2 dietary treatments. Pigs were housed in an environmentally controlled barn with
120 partially slotted concrete floor.

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122 *2.2. Feed composition and use*

123

124 Animals were randomized and allocated to one of two dietary treatments: 1) a control diet based
125 on barley, oat and soybean meal (SBM), and 2) a local diet based on barley, oat, 18% inclusion of
126 commercial expeller pressed rapeseed (Mestilla, UAB, Klaipeda, Lithuania) and 16% inclusion of
127 faba beans (RSM/FB). Level of Standardized ileal digestible (SID) lysine was adjusted to 8.4 g
128 FUp⁻¹ by using crystalline amino acids. The diets were formulated to be isonitrogenous,
129 isoenergetic, and to contain equal levels of methionine + cysteine, and threonine. The diets were
130 produced and pelleted to 3-mm diameter at a commercial feed factory (Felleskjøpet Kambo, Moss,
131 Norway). Diets were formulated to meet or exceed the nutritional requirements (NRC, 2012). A
132 cumulative feed sample from each dietary treatment was taken for chemical analysis. Chemical
133 composition of diets was determined as previously described by Skugor et al. (2019) and presented
134 in Table 1. The analyzed fatty acid composition of the two diets is shown in Table 2. All pigs were
135 individually fed twice per day according to a restricted Norwegian feeding scale (Øverland et al.,
136 2000). The pigs within the same dietary treatment received the same diet during the growing and
137 finishing period.

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139 2.3. Slaughter procedure and tissue sampling

140

141 All animals were transferred to a commercial slaughterhouse (Nortura Tønsberg, Norway). The
142 last feeding was 2.5 – 3 hours before slaughter. Pigs were anesthetized using CO₂ followed by
143 exsanguination. Five minutes after bleeding, 15 g samples of *longissimus thoracis* from the left
144 side of carcass were excised, trimmed from adipose tissue and placed on dry-ice for subsequent
145 fatty acid and metabolite analysis in *pre rigor* phase. The samples were taken from SBM (N = 20)
146 and RSM/FB (N = 19) carcasses. One carcass was missed on the slaughtering line. The samples
147 were transported on ice to the research laboratory at Norwegian University of Life Sciences,
148 vacuum packed and stored at -80 °C.

149 Hot carcass weight was recorded for dressing percentage determination (hot carcass weight/live
150 weight × 100). Carcass lean percentage was determined using a GP7Q pistol (Hennessy System
151 Ltd., Auckland, New Zealand) to measure the depth of *longissimus thoracis* and the back fat
152 thickness at two sites (behind the last rib, 6 cm from the midline). The prediction of carcass lean
153 percentage was done according to Gangsei et al. (2016). Carcasses were then chilled according to
154 standard commercial routines at 1-3°C for 20 h until the core temperature in the ham was 7 °C.

155 Further, carcass and meat quality assessment was performed 24 hours *post mortem* on thirty-one
156 carcasses (N = 15 from SBM and N = 16 from RSM/FB dietary treatment) that were selected based
157 on dietary treatment, litter and hot carcass weight (65.9 – 74.9 kg) at the Norwegian Meat and
158 Poultry Research Centre. The carcasses were subjected to commercial cutting procedure to
159 determine primal cut yields of backpart, midpart and frontpart (Råvarebok,
160 <https://www.totalmarked.nortura.no>) to measure percent carcass lean and fat as described by
161 Øverland et al. (2000). Back fat thickness was measured behind the last rib, 6 cm from the midline
162 using a ruler. In addition, *longissimus thoracis* muscle was removed from 31 carcasses for meat
163 quality analysis. Based on similar carcass weight, carcass lean % (GP7) and fat % of the muscle,
164 24 *longissimus thoracis* muscles (N = 12/dietary treatment) were subjected to metabolite and
165 warmed-over flavor analysis. Samples were stored for 7 days at 4 °C, vacuum packed and kept at
166 -20 °C until analysis. Furthermore, to evaluate the effect of dietary treatment on sensory attributes
167 (flavor and texture) of pork meat, napping test was performed on smaller subset of samples (N =
168 4/dietary treatment).

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170 2.4. Meat quality measurements

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172 The pH_u at 24 h *post mortem* was measured in *longissimus thoracis* muscle with a portable pH
173 meter equipped with electrode (WTW 82362, pH 330i, Welheim, Germany) suitable for meat
174 penetration.

175

176 The color of *longissimus thoracis* muscle prior to packaging (approximately 24 h *post mortem*,
177 after 1 h blooming time at 4 °C) was measured using a Minolta CR400 (Minolta Co. Ltd., Osaka,
178 Japan). CIELAB (L*, a*, b*) measurements were done in triplicate.

179

180 Drip loss was measured using gravimetric EZ-driploss method (Christensen, 2003) on the cutting
181 day using a slice of 10 g *longissimus thoracis* (20 mm thickness). From the middle of slice along
182 the fibre direction, two pieces were cut using a 25 mm diameter circular knife and placed in vertical
183 fibre direction in the containers. After 24 h at 4 °C, the containers were reweighed to calculate drip
184 loss.

185 Collagen, fat, protein and water content of meat were analysed using a FOSS FoodScan TM
186 (Anderson, 2007).

187
188 Measurement of thiobarbituric reactive substances (TBARS) was used to determinate the
189 development of warmed-over flavor (WOF). TBARS was performed on defrosted and
190 homogenized (IKA 11 basic Analytical mill, Germany) pork meat preheated to 71 °C and chill
191 stored 24 h to accelerate oxidation. Then, 2 g of meat was mixed with 10 mL TBA stock solution
192 (0.38% TBA and 15% TCA in 0.25 N HCl). The mixture was incubated for 10 min in boiling water
193 bath. The tubes were quickly cooled on ice to reach room temperature. Solution (1.5 mL) was
194 transferred to Eppendorf tube and centrifuged for 25 min at 21500 × g at 4 °C. The absorbance
195 was measured at 532 nm using Synergy H4 Hybrid Microplate Reader BioTek (ThermoFisher,
196 Göteborg, Sweden). The calculation of malondialdehyde (MDA) concentration in meat sample
197 was based on extinction coefficient of 1.56×10^5 /M/cm. The results were expressed as mg
198 MDA/kg of meat. Each sample was analyzed in duplicate.

199 200 2.5. Fatty acid analysis

201
202 Muscle samples (N = 31) obtained in *pre rigor* phase were used for fatty acid analysis. These
203 samples were removed from carcasses that were later selected for primal cut and meat quality
204 assessment. Prior to analysis, frozen meat samples were homogenized using laboratory
205 homogenizer (IKA 11 basic Analytical mill, Germany). Samples of 0.25 g was extracted as
206 described by Yi, Haug, Nyquist, & Egelanddal (2013). Briefly, 1 mL of tridecanoic acid was
207 added to meat samples as an internal standard dissolved in methanol (0.5 mg C13:0/mL MeOH).
208 The samples were dissolved and hydrolysed using 0.56 mL of 10 N KOH in water and 4.2 mL of
209 methanol. The tubes were incubated in water bath at 55 °C for 1.5 h with hand shaking for 5 s
210 every 20 min. After cooling, 0.46 mL of 24 N sulphuric acid in water was added, tubes were
211 incubated and cooled. The fatty acid methyl esters (FAME) were separated with 3 mL of hexane
212 by mixing for 5 min and centrifuging at 653 × g for 10 min. The hexane layer with FAME was
213 transferred to GC vials and kept at -20 °C until analysis. FAME analysis were carried out on Carlo
214 Erba GC 8000 GC instrument equipped with a Carlo Erba EL 980 Automatic Sampler, flame
215 ionization detector (Carlo Erba AS V570 FID, Carlo Erba Instruments, Milano, Italy) and CP 88

216 capillary column (length: 50 m, i.d.: 0.25 mm, film thickness: 0.20- μ m; Varian, Agilent
217 Technologies, Matriks, Norway) as reported by Inglingstad et al. (2017). The FA present in
218 samples were identified and quantified using four standard solutions prepared from a FAME Mix
219 (Supelco 37 component FAME Mix). Finally, the FA concentration was expressed as mg FA/100
220 g of meat.

221

222 2.6. Extraction, derivatization, and GC/MS analysis of meat metabolites

223

224 Metabolites were extracted from *pre rigor* muscle (N = 39) and chilled meat samples (N = 24).
225 The extraction was done using 1g of homogenized lean meat with water: methanol: chloroform (1:
226 2.5: 1) and as internal standard ribitol (66 μ g/mL) was added. The mixture was vortexed, incubated
227 at 60 °C for 60 min in sonication bath and centrifuged for 10 min at 1469 \times g. Finally, 1 mL of
228 supernatant was transferred into a 1.5 mL Eppendorf tube, dried in a SpeedVac (SPD111V-230,
229 Thermo Scientific, Gothenburg, Sweden) at room temperature. The dried samples were dissolved
230 in 80 μ L mixture containing methoxyamine hydrochloride in pyridine (20 mg/mL), incubated at
231 30 °C for 60 min and sonicated at 30 °C for 30 min. In addition, 80 μ L of N-methyl-N-
232 (trimethylsilyl) trifluoroacetamide were added and kept at 37 °C for 30 min. The derivatized
233 samples were transferred into glass autosampler vials with insert and aliquot of 1 μ L was injected.
234 The analysis was performed on GC–MS (1310-ISQ QD single quadrupole GC–MS instrument
235 from Thermo Fisher) equipped with a capillary column (CP9012 VF-5ms 30 m, ID 0.25 mm and
236 0.25 μ m film thickness with 5m EZ-Guard, Agilent), at 1 mL/min flow rate of helium. The
237 temperature of injector was held at 250 °C. The GC temperature program: 70 °C for 5 min, ramped
238 at 5 °C/min until 310 °C. Analysis time was 60 min. Ions were generated in an electron ionization
239 source by a 70 eV electron beam. The source temperature was 250 °C, and the recorded mass range
240 was m/z 50–700. MS files from Chromeleon software (v7.2; Thermo Fisher Scientific) were
241 exported in the netCDF format (Thermo Scientific Xcalibur, v4.1.50) to GC/MS Agilent
242 Translator.

243 Identification of metabolites was performed in MassHunter Qualitative Analysis (B.07.00,
244 Agilent) using NIST17 (National Institute of Standards and Technology, Gaithersburg, MD, USA)
245 with \geq 70% mass spectral match. Mass spectra of identified compounds were confirmed using
246 GOLM metabolome database (Max-Planck Institute for Molecular Plant Physiology, Golm,

247 Germany). Compounds that were not present in at least 50% of samples from one dietary treatment
248 were removed from the data set. The internal standard was used for data quality control and
249 semiquantification of identified metabolites. External alkane standard mix (C₈-C₂₀) was used to
250 calculate retention index (RI) of metabolites. RI of compounds that eluted after C₂₀ was
251 extrapolated.

252

253 *2.7. Sensory profiling*

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255 Meat (n = 4/dietary treatment) for sensory testing was defrosted during 2 days at 2 °C. Whole loins
256 in vacuum bags were heated for 2 h at 70 °C in an oven (Rational CombiMaster, mod CM 101)
257 with steam (100% moisture). Thirty min after cooking samples were sliced in 3 × 0.5 cm pieces
258 and served to assessors. Serving temperature was 30 ± 5 °C. The sensory test was performed on 4
259 samples per diet in a standardised sensory laboratory at Nortura (ISO 8589:2007). The recruited
260 assessors (N = 8; 5 males and 3 females, 32-60 years old) were Nortura's employees, semi-trained,
261 but experienced in sensory evaluation (flavor and texture) of pork meat by the partial napping
262 method (Perrin et al., 2007). Prior to testing, all assessors were re-introduced to the napping
263 principles by using additional 4 samples. During training, they were given a set of words to
264 describe the samples. The assessors were asked to place the samples on an A3 paper according to
265 perceived sensory difference, followed by an Ultra-Flash Profiling (UFP) where the samples were
266 described with sensory attributes (Perrin et al., 2008). X and Y coordinates were then recorded for
267 each sample along with the frequencies of each attribute used to describe the samples. In order to
268 measure the degree of reproducibility of the assessors, one replicate sample was included in each
269 test.

270

271 *2.8. Statistical analyses*

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273 Statistical analyses on animal performance and carcass characteristics were performed using the
274 GLM procedure of SAS (1990) for a complete randomized block design with individual pig as the
275 experimental unit. Fatty acid composition (mg/100 g of meat) and TBARS were analyzed using
276 one-way ANOVA (Minitab, version 16 from Minitab Inc., State College, PA, USA) to define the
277 differences between dietary treatments.

278 The effect of diet and chilled storage on metabolite abundance in pork meat from the two dietary
279 treatments was investigated using one-way ANOVA, multivariate ANOVA (MANOVA),
280 principal component analysis (PCA) and fold change analysis. One-way ANOVA was performed
281 using Minitab 16 (Minitab Inc., State College, PA, USA) to show the effect of diet on metabolite
282 abundance (mg/kg) in *pre rigor* muscle (N = 39 samples) and chilled stored meat (N = 24 samples).
283 To investigate the effect of diet on overall metabolite profile, 50-50 MANOVA (Windows version,
284 Prediktor, 2016) was applied. Further interpretation of metabolomics data from MassHunter Qual
285 was carried out with Mass Profiler Professional 15.0 (Agilent Technologies). The abundance of
286 identified metabolites was log₂ transformed. Fold change analysis (threshold: FC > 2.0), applying
287 Benjamini-Hochberg multiple test corrections, and principal component analysis were carried out
288 to monitor the effect of storage on metabolite abundance in both diet groups. For comparison of
289 pork muscle and chilled meat metabolite profiles, the same 24 carcasses were used to avoid
290 individual differences between animals.

291 Napping analysis was done using the multiple Procrustean factor analysis function of the
292 SensoMineR package (<http://sensominer.free.fr/napping-data.html>). Napping is a sensory
293 technique used to obtain differences more easily although quantitative data, as in profiling, is
294 sacrificed.

295

296 **3. Results and discussion**

297

298 ***3.1. Growth performance and carcass characteristics***

299

300 In general, growth performance of pigs fed rapeseed meal and faba bean (RSM/FB) diets during
301 the total period was not significantly ($P > 0.05$) different from pigs fed the SBM diet, except for a
302 higher feed conversion ratio ($P = 0.04$) during the finishing period in pigs fed the RSM/FB diet
303 (Table 3). Skugor et al. (2019) reported that the inclusion of 20% commercial expeller pressed
304 RSM in pig diet reduced growth performance of growing-finishing pigs while Hansen et al. (2020)
305 reported only minor effects on growth performance of growing-finishing pig fed increasing levels
306 of RSM when fed a nutritionally balanced diets.

307 The poorer feed conversion ratio in the finishing period could be related to antinutritive factors
308 present in RSM and FB. Both RSM and FB have a higher fibre content, compared with SBM and

309 they contain several antinutritive factors that might reduce feed utilization. RSM contain
310 glucosinolates and their breakdown products have shown to reduce feed intake and to alter thyroid
311 function by inhibiting production of thyroid hormones (Mejicanos et al., 2016) and consequently
312 affecting metabolism and performance. Phenolic compounds such as tannins in RSM and FB for
313 instance can reduce protein digestibility and interfere with protein metabolism (Jansman et al.,
314 1995) and thus reduce feed conversion ratio.

315

316 **3.2. Cutting traits and meat quality**

317

318 There was no effect of dietary treatment ($P > 0.05$) on cutting traits of growing-finishing pigs and
319 physio-chemical properties of pork muscle (Table 4). These results are in agreement with previous
320 studies that examined the effect of legume and rapeseed cake in pig diet on carcass and meat
321 quality (Hanczakowska & Swiatkiewicz, 2013; Hanczakowska & Swiatkiewicz, 2014; Partanen et
322 al., 2003).

323 Replacing SBM with RSM/FB in diets for pig resulted in darker meat. Pigs fed RSM/FB had
324 significantly ($P < 0.05$) lower Minolta L^* (lightness) and b^* (yellowness) values than pigs fed
325 SBM. Reduced L^* of pork meat could be associated with slightly lower fat % (Table 4). In
326 addition, lower values for lightness of meat may indicate abundance of deoxymyoglobin (DMb)
327 on the meat surface (Phung, 2012). DMb has a purple-red color immediately after cutting or in
328 vacuum packed meat (Renerre, 1990). Inclusion of RSM in pigs' diet increased haem pigment
329 level, darkness and redness of meat compared to SBM (Dransfield, Nute, Mottram, Rowan, &
330 Lawrence, 1985). Additionally, L^* values lower than 48 could be considered as darker meat having
331 better visual scores (Partanen et al., 2003). In addition, the differences found in meat color (L^* and
332 b^* parameters) might not be detrimental for meat quality.

333 In general, RSM/FB diet reduced ($P = 0.13$) fat % of the *longissimus thoracis* muscle compared
334 with SBM (Table 4). The fatty acid composition of pork muscle from two dietary treatment is
335 given in Table 5. The diet supplemented with RSM/FB significantly reduced ($P < 0.05$) the content
336 of arachidic acid (C20:0) and eicosapentaenoic acid (EPA, C20:5n-3). In addition, a tendency for
337 decrease in linoleic acid (C18:2n-6; $P = 0.07$) content was observed in the muscle when feeding
338 RSM/FB. Skoufos et al. (2016) observed similar results when SBM (10%) was completely
339 replaced with RSM (14.7%) in growing-finishing pigs. In general, with increase of double-bounds

340 in fatty acids, oxidative stability of meat declines and induce flavor changes (Wood et al., 2008).
341 Therefore, lower PUFA content in RSM/FB pork meat might have reduced susceptibility to lipid
342 oxidation and off-flavor intensity in cooked meat.

343 In general, complete replacement of SBM with RSM/FB and lower inclusion of tallow in pig's
344 diet, when digestible energy was balanced, had no significant effect on total content of SFA,
345 MUFA and PUFA in the muscle. However, a tendency for increase of PUFA level in intramuscular
346 fat of SBM fed pig is in agreement with Okrouhlá, Stupka, Čítek, Lebedová, & Zadinová (2018),
347 that showed an increase of PUFA in pork back fat.

348

349 **3.3. The effect of diet on metabolite status of muscle in pre rigor phase and meat after 7 d storage**

350

351 Metabolite profiles of pork muscle from *pre rigor* phase and pork meat after 7 d chill storage were
352 significantly affected by dietary treatment and storage time. In total, forty-six compounds were
353 quantified in *longissimus thoracis* muscle obtained in *pre rigor* phase and 44 in meat after chilled
354 storage (7 days at 4 °C) from the two dietary treatments (Table 6). “Multivariate analysis” of semi-
355 quantified compounds showed clear separation between *pre rigor* metabolite profile and after
356 chilled storage (Fig. 1). The PCA plot explained 46% of variance, where the first component
357 separated the two sets of samples. Thus, overall metabolite profile of *pre rigor* muscle was
358 significantly (50-50 MANOVA; $P < 0.001$) different compared with 7 d chilled meat.

359 Dietary treatment had an effect on metabolite status of pigs in growing-finishing phase as
360 measured at the time of slaughter. β -alanine and glucose were enriched ($P = 0.022$ and $P = 0.003$,
361 respectively) in SBM muscle of 39 animals (Fig.2A). To date, the metabolic benefit of β -alanine
362 is attributed to carnosine biosynthesis (Quinn, Boldyrev, & Formazuyk, 1992). Carnosine
363 synthesis in skeletal muscle cell is dependent on the uptake of L-histidine and β -alanine from blood
364 stream into muscle cell (Drozak, Veiga-da-Cunha, Vertommen, Stroobant, & Van Schaftingen,
365 2010). Moreover, endogenous synthesis of carnosine is catalyzed by carnosine synthetase in
366 skeletal muscle (Artioli, Gualano, Smith, Stout, & Lancha, 2010). Because the affinity of carnosine
367 synthase is greater for L-histidine than for β -alanine, higher concentration of β -alanine is needed
368 for carnosine *in vivo* synthesis (Harris et al., 2006). Therefore, we speculated that elevated
369 concentration of β -alanine in muscle from SBM diet indicates failure of endogenous synthesis of
370 carnosine. In addition, muscle of pigs fed with SBM containing higher content of rendered fat

371 showed two times higher glucose level in muscle compared with RSM/FB. There are multiple
372 possible reasons for increased glucose level in muscle from SBM fed animals. Glucose storage
373 and uptake, lipid and protein synthesis are regulated by a number of genes that control the insulin
374 signaling pathway (Chang, Chiang, & Saltiel, 2004). Study by Park et al. (2012) demonstrated
375 close relation of lipid metabolism with insulin regulation, the type of dietary fat affected insulin-
376 related gene expression in pork muscle. Higher inclusion of rendered fat in rat diet reduced the
377 efficiency of glucose metabolism due to decreased number of insulin receptors and activity of
378 glucose transport system (Dobbins et al., 2002; Kraegen, James, Storlien, Burleigh, & Chisholm,
379 1986; Olefsky & Saekow, 1978). In addition, the difference in muscle glucose level between the
380 two dietary treatments in our study may be partly attributed to the antinutrients present in FB.
381 Fernández-Quintela, Barrio, Macarulla, & Martínez (1998) reported a lower glucose concentration
382 in plasma of rats fed with faba beans compared with soybeans and peas. However, carbohydrate
383 metabolism is to a large extent regulated by thyroid hormones (Brenta, 2011). Feeding the
384 growing-finishing pigs with 6-10% of 00-RSM resulted in higher weight of thyroid gland, but
385 normal concentration of thyroid hormones (Svetina, Jerković, Vrabac, & Ćurić, 2003). Depending
386 on the nature and concentration, breakdown products of glucosinolates from RSM may inhibit
387 hormone production by the thyroid gland (Mejicanos, Sanjayan, Kim, & Nyachoti, 2016). Pérez
388 de Nanclares et al. (2017) reported increased weight of thyroid gland in pigs fed with RSM, with
389 total glucosinolates below recommended limit of 2.1 mmol/kg. An increased intake of
390 glucosinolates by castrated boars decreased thyroid hormones in blood having no effect on the
391 growth rate (Spiegel, Bestetti, Rossi, & Blum, 1993). Furthermore, Skugor et al. (2019) showed
392 upregulation of several muscle genes (ODK4, UCP3, ESRRG and ESRRB) involved in glucose
393 metabolism in RSM pigs suggesting increased glucose uptake for energy homeostasis. However,
394 we speculate that RSM/FB dietary treatment with lower amount of tallow has provided less
395 available energy and possibly had an effect on upregulated glucose utilization. In addition, reduced
396 abundance of oxidized metabolites (glycine and pyroglutamic acid) in muscle from RSM/FB group
397 suggested lower oxidative stress in the muscle cell. The observed nominal decrease of glycine (P
398 = 0.332) and pyroglutamic acid (P = 0.058) provided by RSM/FB could suggest glutathione
399 synthesis efficiency and improved cellular defense system. This is in agreement with Skugor et al.
400 (2019) that reported upregulation of genes involved in antioxidant defense and ROS reduction in
401 the RSM pigs. On the contrary, Chen et al. (2018) found that metabolite markers of oxidative stress

402 (pyroglutamic acid and butanal) were upregulated in liver of RSM fed pigs. These results indicate
403 that dietary treatment had different effect on muscle and liver metabolite profiles. Regarding meat
404 eating quality the RMS/FB diet may actually have some beneficial effects. However, the present
405 study demonstrates scarce effect of diet on metabolite pathways in the *pre rigor* muscle.
406 Metabolite profile of meat (n = 24) after chill storage for 7 d was significantly affected by diet.
407 The level of glycine (P = 0.01), glyceric acid (P = 0.04), serine (P = 0.04), creatinine (P = 0.04),
408 glutamine (P = 0.01) and myo-inositol (P = 0.04) increased in meat from animals fed the RSM/FB
409 diet (Fig. 2B). Higher concentration of sugar-related compounds (glyceric acid, myo-inositol) in
410 our study could be related with higher glycogen content and its degradation during optimal storage
411 period (Koutsidis et al., 2008). In addition, accumulation of free amino acids (glycine, serine,
412 glutamine) in the RSM/FB *pre rigor* muscle suggested increased proteolytic activity and
413 hydrolysis of glycoproteins.

414

415 **3.4 Metabolite profiles after chilled storage**

416

417 Fold change analysis of identified metabolites showed changes that occurred during conversion of
418 *pre rigor* muscle into meat (n = 24) under optimal storage conditions (Table 6). To the best of our
419 knowledge, it has not been previously reported in the literature the effect of different diets on the
420 abundance of metabolites in *pre rigor* pork muscle vs chill stored meat. The set of 24 metabolites
421 were down-regulated (P < 0.05; FC > 2.0) in SBM chill stored meat and 23 were up-regulated
422 compared to *pre rigor* muscle. In RSM/FB, 24 metabolites were down-regulated and 30 up-
423 regulated in chilled meat compared to *pre rigor* muscle. In addition, semi-quantitative data of three
424 metabolites (mannose, palmitic acid, 9,12-octadecadienoic acid) do not coincides with their log-
425 fold-changes presented in Table 6. Thus, fold change analysis indicated differences between *pre*
426 *rigor* muscle and chilled meat when metabolite abundance was used, but semiquantitation based
427 on internal standard is possibly less precise and do not show clear differences of metabolite
428 concentration. The content of lactic acid and sugar-related compounds (sugar and sugar-
429 phosphates) significantly increased after chill storage. Conversion of muscle into meat and
430 activation of glycolysis has been attributed to increase lactic acid in *pre rigor* phase. Furthermore,
431 the increased lactic acid may be affected by the number of gram-positive bacteria in stored vacuum
432 packed meat (Pothakos, Devlieghere, Villani, Björkroth, & Ercolini, 2015). On the other hand,

433 chill stored meat exhibited lower levels of glutamate, pyroglutamic acid, and galactose. This
434 finding might reflect enhanced mitochondria related metabolism in muscle cell in early *post*
435 *mortem* phase (Aguer et al., 2011). Storage had a negative effect on Krebs cycle substrates (*i.e.*
436 fumaric acid, citric acid, malic acid), that may indicate the utilization of substrates to maintain cell
437 function both in *pre rigor* and early *post mortem* phase. Succinic acid, a complex II substrate
438 involved in formation and elimination of reactive oxygen species, increased in chill stored meat
439 possibly due to an incomplete function of the Krebs cycle. Abraham, Dillwith, Mafi,
440 VanOverbeke, & Ramanathan (2017) reported that increased succinic acid indicates either lower
441 mitochondrial consumption or conversion of glutamic acid. In addition, RSM/FB chilled stored
442 meat showed an increase in urea level compared with SBM, probably related to a higher *post*
443 *mortem* production of ammonia through increased protein breakdown. An increase of free amino
444 acids in RSM/FB chilled stored meat is possibly linked with antioxidants in RSM that assured
445 suppression of reactive oxygen species stimulating prolonged endogenous protease activity in
446 early *post mortem* conditions. As shown in Table 6, generally RSM/FB diet increased flavor
447 precursors independent of thresholds and maintained proteolytic activity, *i.e.* as previously
448 reported for RSM (Skugor et al., 2019). Metabolite data suggest adaption of RSM/FB muscle to
449 meet essential biological functions and nominally induced transformation to a more oxidative
450 metabolism.

451

452 ***3.5. Sensory properties of pork from two dietary treatments***

453

454 The multiple factor analysis (MFA) plot maps 8 loin samples on two axes based on the terms used
455 to describe their flavor and texture properties (Fig.3A and B). The plot showed clear separation
456 between SBM and RSM/FB based on flavor attributes given by panelists in the napping session
457 (Fig.3A). The first two dimensions explain 59% of variability between the two groups (41.44%
458 PC1 and 18.04% PC2), after the panelist's tablecloths have been aligned by rotation and scaling.
459 According to panellists, SBM pork was described as tame, with a weak (right amount of) smell,
460 and a round aftertaste. Higher inclusion of rendered fat in SBM diet resulted in a nominally higher
461 fat % that may have an impact on changes in fatty acid composition and possibly intensified round
462 aftertaste note. Frank, Appelqvist, Piyasiri, Wooster, & Delahunty (2011) reported more balanced
463 perception of flavor with increased inclusion of fat in the emulsion system. Moreover, SBM pork

464 was also described with the attributes liver taste, off taste and chemical/old attributes. The meat
465 samples selected for metabolite analysis were subjected to an accelerated oxidation test (warmed-
466 over flavor; WOF) development. SBM pork produced more WOF (0.34 mg MDA/kg) compared
467 to RSM/FB (0.27 mg MDA/kg) that may reflect nominally higher oxidation of unsaturated fatty
468 acids (i.e. C18:2n-6) that give characteristic aroma volatiles and enhance unpleasant flavor
469 (Ramalingam et al., 2019). However, the oxidative flavor was below flavor threshold (0.5 mg
470 MDA/kg of meat; Wood et al., 2008) indicating that taste-active metabolites were playing a key
471 role in modulation of pork flavor. In general, free amino acids in meat are significant constituents
472 that markedly affect the meat flavor (Ramalingam et al., 2019). RSM/FB pork was located on
473 positive side of the first and second dimension of the MFA plot, described with attributes as fresh,
474 powerful smell, long flavor, meaty flavor, round and sweet taste. Glycine and glutamine were
475 present in a concentration above flavor threshold (see Table 6) while the other metabolites that
476 increased during storage may also contribute to the flavor profile of RSM/FB meat. Bitter-related
477 amino acids (valine, isoleucine, leucine and phenylalanine) were present at higher concentrations
478 in meat from RSM/FB together with ornithine that might had a bitterness-suppression effect. The
479 concentration of sweet-related glycine, serine, threonine, and sugar related compounds increased
480 with storage and generally contributed to sweet taste of pork meat from RSM/FB. Moreover, these
481 amino acids and sugars are important flavor-precursors in the development of meaty, roasty, and
482 boiled flavor properties when meat is strongly heated (barbequed). Napping test showed large
483 texture variations (Fig.3B) between the samples from RSM/FB group and metabolite analysis
484 higher concentration of free amino acids indicating possible inconsistent proteolytic activity. The
485 SBM samples clustered more clearly together.

486

487 **4. Conclusion**

488

489 Overall, feeding a local diet containing rapeseed meal and faba beans, when replacing soybean
490 meal in pig diets gave no differences in growth rate, feed intake or carcass traits. Feeding the local
491 diet improved color of pork meat and increased the concentration of free amino acids, and sweet
492 tasting metabolites, leading to reduced warmed-over flavor and flavor attributes. The results, thus,
493 show desirable properties of feeding rapeseed meal and faba beans on pork meat.

494

495 **Conflict of interest**

496

497 All authors declare that they have no conflict of interest.

498

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500

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513

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793

794

795 **Figure Captions**

796

797 **Fig. 1.** PCA scores plot of metabolites ($P < 0.05$; $FC > 2.0$) identified in *pre rigor* muscle ($n = 24$)
798 and chilled meat at 4 °C during 7 d ($n = 24$) from SBM and RSM/FB dietary treatments.

799

800 **Fig. 2.** Replacement of SBM with RSM/FB showed significant ($P < 0.05$) effect on metabolite
801 profile of *longissimus thoracis* muscle. A) metabolites isolated from *pre rigor* muscle ($N = 20$
802 from SBM; $N = 19$ from RSM/FB). B) metabolites isolated from chilled meat ($n = 12$ / diet). Orange
803 bars for SBM and green bars for RSM/FB group. The significant difference detected by ANOVA
804 ($P < 0.05$; Tukey's test) is marked with *.

805

806 **Fig. 3.** Partial napping evaluation of SBM and RSM/FB pork meat by semi-trained panellists. A)
807 Flavor individual factor map. B) Texture individual factor map. C) Attributes used for at least 2
808 samples/diet to describe the flavor of pork meat.

809

810 **Table 1.**

811 Ingredient and chemical composition (g/kg) of Control diet based on soybean meal (SBM) and
 812 Local diet produced from rapeseed meal/ faba bean (RSM/FB) produced in Norway and Europe

Ingredients	Diet	
	SBM	RSM/FB
Barley	585.4	456.0
Oats	150.0	150.0
Soybean meal (SBM) (45% CP)	142.6	0.0
Rapeseed meal (RSM) (Mestilla)	60.0	180.0
Faba beans (Columbo)	0.0	161.12
Rendered fat ^a	23.0	16.5
Molasses	10.0	10.0
Limestone	9.7	8.7
Monocalcium phosphate	3.2	1.4
Salt	6.31	6.37
L-lysine HCl (98%)	3.25	3.04
L-threonine	1.28	1.39
L-methionine	0.98	0.97
L-tryptophan	0.07	0.31
Axtra phytase 5000T	0.02	0.02
Vitamin E (50%)	0.15	0.15
Premix ^b	3.87	3.86
Calculated contents		
Net energy, MJ/kg (FUn/kg)	9.42 (1.07)	9.42 (1.07)
SID ^c lysine, g/kg	8.99	8.99
SID methionine + cysteine, g/kg	5.56	5.57
SID threonine, g/kg	5.93	5.93
SID tryptophan, g/kg	1.75	1.75
Calcium, g/kg	6.65	6.54
ATTD ^d phosphorus, g/kg	4.46	4.76
Analyzed content, g/kg		
DM	868	870
Crude protein	153	158
Crude fat	40	51
Starch	424	422
Neutral detergent fibre (NDF)	165	173
Ash	45	44
Gross energy, MJ/kg	16.4	16.6

813 ^a In Norway this fat source often consists of 65-70% lard and 30-35% tallow, with possible variations with the season

814 ^b Provided the following amounts per kg of diet: Zn 72 mg, Fe 96 mg, Mn 48 mg, Cu 17 mg, I 20.48 mg, Se 0.27 mg,

815 Vitamin A 6500 IU, Cholecalciferol 1500 IU, dl- α -tocopheryl acetate 75 mg, menadione 4.63 mg, Riboflavin 5.625

- 816 mg, D-pantothenic acid 15 mg, Cyanocobalamine 15 µg, Niacin 45 mg, Biotin 0.30 mg, Folic acid 1.69 mg, Choline
817 2300 mg (SBM) and 1605 mg (RSM/FB).
818 ^c Standardized ileal digestible.
819 ^d Apparent total tract digestible.

820 **Table 2.**

821 Fatty acid composition of experimental diets

Fatty acids (mg/kg)	Diet	
	SBM	RSM/FB
C12:0	17.94	13.17
C14:0	213.07	146.29
C15:0	37.94	29.11
C16:0	3142.33	2569.65
C17:0	69.24	49.58
C18:0	1302.24	931.21
C20:0	50.14	20.32
C21:0	9.25	9.64
C22:0	23.92	28.98
C24:0	21.73	16.53
C14:1n-3	16.98	12.27
C16:1n-7	186.35	146.61
C17:1n-7	4.27	5.05
C18:1n-9t	197.38	136.46
C18:1n-9	4777.36	5602.44
C20:1n-9	455.83	606.98
C22:1n-9	72.92	74.03
C24:1n-9	8.60	16.17
C18:2n-6t	19.42	12.16
C18:2n-6	4579.01	4846.05
C18:3n-6	3.39	3.01
C18:3n-3	300.28	399.85
C20:2n-6	32.02	25.58
C20:3n-3	4.81	4.89
C20:4n-6	12.16	8.68
SFA (g/100 g)	4.89	3.81
MUFA (g/100 g)	5.71	6.58
PUFA (g/100 g)	4.96	5.32

822 SBM = soybean meal; RSM/FB = rapeseed meal and faba beans

823

824 **Table 3.**

825 The effect of SBM and RSM/FB diets on growth performance and carcass characteristics

Item	Diet		SEM	P-value
	SBM (n = 20)	RSM/FB (n = 19)		
Initial weight, kg	27.69	27.82	0.66	0.89
Final weight, kg	108.93	108.53	1.03	0.78
Growing period				
ADG ^a , kg	0.90	0.93	0.02	0.13
ADFI ^b , kg	1.55	1.61	0.02	0.08
F:G ^c , kg/kg	1.73	1.72	0.02	0.87
Finishing period				
ADG, kg	1.30	1.24	0.02	0.09
ADFI, kg	3.02	3.03	0.04	0.82
F:G, kg/kg	2.33	2.44	0.04	0.04
Overall period				
ADG, kg	1.09	1.08	0.01	0.71
ADFI, kg	2.24	2.27	0.02	0.25
F:G, kg/kg	2.06	2.12	0.02	0.12
Hot carcass weight, kg	70.39	70.31	0.69	0.94
Dressing percentage	64.62	64.79	0.40	0.76
Percentage carcass lean, %	59.75	59.91	0.47	0.80

826 ^a ADG: daily weight gain.827 ^b ADFI: average daily feed intake.828 ^c F:G: feed conversion ratio.

829

830 **Table 4.**

831 The effect of SBM and RSM/FB diets on cutting traits and physical characteristics of meat

Item	Diet		SEM	P-value
	SBM (n = 15)	RSM/FB (n = 16)		
Carcass characteristics				
Hot carcass weight, kg	70.41	70.59	0.68	0.85
Dressing percentage, %	64.57	65.04	0.49	0.50
Lean percentage, GP7	59.49	60.19	0.50	0.35
Backfat thickness, mm	13.05	12.14	0.63	0.32
Carcass lean, primal cuts, %	61.91	61.61	0.45	0.63
Frontpart, %	31.24	31.32	0.24	0.82
Midtpart, %	34.87	34.47	0.27	0.30
Backpart, %	33.88	34.21	0.21	0.28
Meat characteristics				
Fat, %	1.81	1.66	0.07	0.13
Protein, %	23.47	22.88	0.44	0.34
Collagen, %	0.36	0.35	0.01	0.65
Moisture, %	74.39	74.39	0.10	0.98
Drip loss, %	5.85	5.40	0.36	0.38
pH _u	5.41	5.45	0.02	0.10
Meat color				
Minolta L*	49.26	47.93	0.39	0.02
Minolta a*	7.26	7.11	0.15	0.47
Minolta b*	2.63	1.84	0.18	0.004

832

833 **Table 5.**

834 Fatty acid composition of *longissimus thoracis* muscle from pigs fed with SBM and RSM/FB.

	Fatty acids	SBM	RSM/FB	SEM ^a	P-values ^b
		(n = 15)	(n = 16)		
SFA (mg/100 g)	C12:0	9.8	7.9	0.84	0.13
	C14:0	144.3	110.0	15.26	0.12
	C16:0	2570.3	2009.6	257.91	0.13
	C17:0	33.2	25.3	3.12	0.08
	C18:0	1530.9	1135.7	156.87	0.08
	C20:0	18.2	11.9	1.67	0.01
MUFA (mg/100 g)	C16:1n-7	248.0	211.3	26.38	0.33
	C17:1n-7	44.1	42.1	1.71	0.42
	C18:1n-9t	30.2	24.2	3.08	0.18
	C18:1n-9	3884.6	3117.1	393.73	0.18
	C20:1n-9	35.0	26.9	3.45	0.10
	C22:1n-9	1.2	1.1	0.13	0.46
PUFA (mg/100 g)	C18:2n-6	1182.2	945.5	90.38	0.07
	C18:3n-6	8.2	7.4	0.39	0.17
	C18:3n-3	29.4	22.6	2.89	0.10
	C20:2n-6	35.8	28.2	3.37	0.12
	C20:3n-6	21.0	19.0	1.07	0.19
	C20:3n-3	6.8	5.2	0.67	0.09
	C20:4n-6	153.9	144.8	6.78	0.35
	C20:5n-3	14.7	12.6	0.69	0.03
	C22:6n-3	12.8	13.3	0.71	0.62
	Total (g/100 g)	SFA ^c	4.32	3.31	0.44
MUFA ^d		4.25	3.43	0.43	0.18
PUFA ^e		1.46	1.20	0.10	0.08
n-6 PUFA		1.40	1.14	0.01	0.08
n-3 PUFA		0.06	0.05	0.004	0.09
n-6/n-3 ^f		22.01	21.22	0.55	0.32

835 ^a SEM = standard error of mean

836 ^b Probability of significant effect due to type of diet

837 ^c SFA = C10:0 + C12:0 + C14:0 + C15:0 + C16:0 + C17:0 + C18:0 + C20:0

838 ^d MUFA = C14:1 cis 9+C16:1 cis 9+C17:1 cis 9+C18:1 trans 9+C18:1 cis 9+C20:1 cis 11+ C22:1 cis 13

839 ^e PUFA = C18:2 cis 9,12+C18:3 cis 6,9,12+C18:3 cis 9,12,15+C20:2 cis 11,14+C20:3 cis 8,11,14+C20:3 cis 11,14,17+C20:4 cis 5,8,11,14+C20:5 cis 5,8,11,14,17+C22:6 cis 4,7,10,13,16,19 cis

841 ^f n-6 : n-3 = n-6 PUFA : n-3 PUFA

842 **Table 6.**

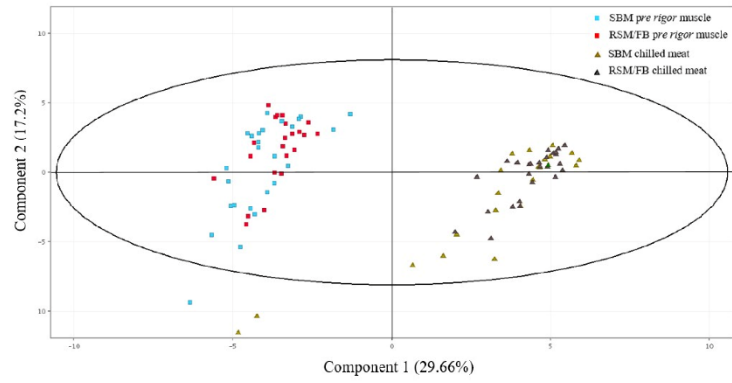
843 The semi-quantified metabolites (mg/kg) in *pre rigor* (n = 24) and 7 d chill stored (n = 24) *longissimus thoracis* pork muscle from
 844 animals fed with SBM and RSM/FB

RI	RT	Items	SBM			RSM/FB			Flavor threshold in water (mg L ⁻¹) / fat-oil (mg kg ⁻¹)	Odor / Taste
			Pre-rigor ^a	7 d ^b	Fold change 7 d vs pre- rigor ^c	Pre-rigor	7 d	Fold change 7 d vs pre- rigor		
<i>Amino acids</i>										
1098.13	11.67	alanine	26.98	12.87		14.75	16.64	↑	600 ¹ / 135 ²	sweet ²
1205.87	15.19	valine	1.81	1.11		1.16	1.24	↑	188 ³ / n.a.	sweet, bitter ⁴
1246.3	17.47	isoleucine	0.44	0.32		0.29	0.43	↑	900 ¹ / n.a.	bitter ⁵
1248.14	17.59	proline	1.73	0.31		1.00	0.43	↓	> 1,000 ⁶	characteristic odor with slight sweet taste ⁷
1352.02	17.81	glycine	61.36	17.37	↓	43.18	31.21	↓	3.9 – 35.67 ⁸ / n.a.	odorless ² /oily, bitter with a fatty, nutty aftertaste, slightly sweet ⁹
1378.62	19.32	serine	2.13	0.66	↓	1.70	1.02	↓	0.2 ¹⁰ / n.a.	sweet, umami, sour ¹¹
1390.42	19.99	threonine	3.53	1.12	↓	1.87	1.52	↓	1250 ¹² / n.a.	sweet ¹³
1423.18	21.13	β-alanine	16.12	19.33	↑	6.85	22.32	↑	107 ¹⁴ / n.a.	slight sweet taste ¹⁵
1615.66	25.88	glutamic acid	10.53	1.11	↓	6.72	1.50	↓	9.2 ¹⁶ / n.a.	high strength, roasted type ¹⁷ /umami, sour ¹⁷
1621.35	26.01	phenylalanine	0.91	0.66	↓	0.27	0.67	↑	530 ¹⁸ / n.a.	slight bitter taste ¹⁵
1769.18	29.31	glutamine	35.94	1.85	↓	23.07	5.66	↓	0.14 ¹⁹ / n.a.	sweet, umami ¹¹
1809.23	30.17	ornithine	n.a.	0.38	↑	n.a.	0.42	↑	460 ⁵ / n.a.	sweet ⁵
1913.76	32.32	lysine	3.17	1.04	↓	1.37	1.53	↑	104-327 ¹⁹ / n.a.	odorless ¹⁵ / bitter ¹⁴
1932.05	32.68	tyrosine	0.20	0.23		0.11	0.26	↑	725 ⁵ / n.a.	odorless/bland taste ¹⁵
<i>Acids</i>										
1058.83	10.41	lactic acid	57.00	69.13	↑	68.37	78.13	↑	10 ²⁰	odourless, sour ²¹
1074.42	10.91	glycolic acid	n.a.	0.09	↑	n.a.	0.09	↑	> 2000 ²² / n.a.	odourless, very mild buttery ²¹
1157.88	13.54	3-hydroxybutyric acid	0.12	0.36		0.13	0.48	↑	n.a. / n.a.	n.a.
1212.56	15.57	4-hydroxybutanoic acid	0.08	n.a.	↓	0.13	n.a.	↓	n.a.	n.a.
1357.13	18.10	succinic acid	1.82	8.76	↑	1.07	10.85	↑	200 ²³	odourless, sour ²¹
1363.11	18.44	glyceric acid	n.a.	1.44	↑	n.a.	2.26	↑	10.6 ²⁴ / n.a.	n.a.
1387.07	19.80	fumaric acid	0.37	n.a.	↓	0.25	n.a.	↓	n.a.	odourless ²¹
1483.86	22.69	malic acid	11.14	1.63	↓	10.03	3.46	↓	9.6-99 ²⁵ / n.a.	nearly odorless, sometimes a faint, acrid ¹⁵ /tart, acidic, nonpungent ¹⁵
1497.47	23.04	aspartic acid	5.36	n.a.	↓	0.70	n.a.	↓	30 ²⁶ / n.a.	n.a. / umami ²⁶
1497.86	23.05	2-aminomalonic acid	0.37	n.a.	↓	0.09	n.a.	↓	n.a.	n.a.
1973.48	31.50	citric acid	0.99	n.a.	↓	0.60	n.a.	↓	n.a.	n.a. / tart, delivers a “burst” of tartness ²⁷
1983.85	33.70	gluconic acid	n.a.	0.41	↑	n.a.	0.53	↑	75 ²⁸ / n.a.	refreshing sour ²⁹ , bitter, metallic ²⁸
<i>Alcohols</i>										
1798.48	30.05	9H-purin-6-ol	0.79	1.21	↑	0.85	1.72	↑	n.a.	n.a.
1901.57	32.08	sorbitol	0.41	15.31	↑	0.33	13.16	↑	n.a.	odourless, sweet, caramel ²¹

2112.80	34.27	scyllo-inositol	0.67	0.09	↓	0.42	0.16	↓	n.a.	n.a.
2172.73	35.45	myo-inositol	40.48	11.30		27.92	17.94	↓	3190 ³⁰ / n.a.	sweet ³⁰
Sugars										
1858.99	31.20	fructose	0.32	6.39	↑	0.24	7.22	↑	160 ³¹ / n.a.	sweet ³²
1873.96	31.51	mannose	3.80	8.77	↑	4.85	4.42	↑	n.a.	sweet with a bitter aftertaste ³³
1884.11	31.72	glucose	70.87	59.73		30.42	73.81	↑	700 – 1000 ³⁴ / n.a.	sweet ³⁵
1969.63	33.42	glucopyranose	n.a.	1.42	↑	n.a.	2.29	↑	n.a.	n.a.
1976.74	33.56	galactose	7.48	n.a.	↓	6.60	n.a.	↓	n.a.	n.a.
2688.22	45.60	maltose	n.a.	1.42	↑	n.a.	2.29	↑	15103 ⁶ / n.a.	sweet ²²
2699.90	45.83	lactose	0.15	5.41	↑	3.89	5.20	↑	n.a.	sweet ³⁶
Phosphates										
2365.72	39.25	fructose-6-phosphate	n.a.	25.86	↑	n.a.	25.89	↑	570 ¹³ / n.a.	Sweet ¹³
2375.88	39.45	mannose-6-phosphate	3.54	34.23	↑	1.72	40.15	↑	25 ²⁸ / n.a.	sweet, metallic tomatoes ²⁸
2436.31	40.64	glucose-6-phosphate	4.21	25.90	↑	0.27	34.66	↑	360 ¹³ / n.a.	sweet ¹³
Lipids										
2143.27	34.87	palmitic acid	6.56	6.57	↓	5.81	5.90		n.a./ 10 000 ³⁸	rancid, wax odor ³⁷ , waxy, creamy fatty, soapy with a crisco like fatty, lard and tallow like mouth feel and a dairy nuance ³⁹
2295.63	37.87	octadecadienoic acid, 9,12-(Z,Z)-(18:2)	1.06	1.06	↑	1.71	0.90	↓	n.a. / 4000 ⁴⁰	bitter ⁴¹
2322.04	38.39	stearic acid	3.73	4.14		4.98	3.68	↓	n.a./15 000 ³⁸	odourless, mild, fatty ²¹
2390.60	39.74	oleic acid	0.06	n.a.	↓	0.88	n.a.	↓	n.a.	n.a.
Other N-containing compounds										
842.48	4.35	2-butanedioic acid (Z)-, dimethyl ester	0.94	n.a.	↓	0.82	n.a.	↓	n.a.	n.a.
1115.99	12.23	hydroxylamine	0.03	n.a.	↓	0.04	n.a.	↓	n.a.	n.a.
1174.51	14.06	phosphoric acid, monomethyl ester	n.a.	5.46	↑	n.a.	7.58	↑	n.a.	n.a.
1230.53	16.59	urea	19.08	11.32		9.85	14.31	↑	0.19 – 6610 ⁴² / n.a.	almost odorless ⁴³ / cooling, saline taste ⁴⁴
1481.52	22.63	niacin	n.a.	1.74	↑	n.a.	2.25	↑	n.a.	n.a.
1517.17	23.52	niacinamide	1.67	n.a.	↓	1.31	n.a.	↓	n.a.	odorless ²¹ / n.a.
1518.82	23.56	pyroglutamic acid	41.55	6.04	↓	23.12	9.13	↓	n.a.	n.a.
1547.79	24.26	creatinine	16.94	4.62	↓	19.77	9.84	↓	n.a.	bitter ⁴⁵
1752.60	28.95	phosphoric acid, 2,3-propyl ester	n.a.	0.09	↑	n.a.	0.10	↑	n.a.	n.a.
1836.28	30.73	phosphorylethanolamine	0.05	n.a.	↓	0.07	n.a.	↓	n.a.	n.a.
2163.08	35.26	panthotenic acid	0.18	n.a.	↓	0.10	n.a.	↓	n.a.	n.a.
2591.21	43.69	inosine	10.61	47.86	↑	5.68	48.19	↑	60-250 ⁴⁶ / n.a.	bitter ⁴⁷
2936.57	50.49	adenosine-5-phosphate	n.a.	29.33	↑	n.a.	27.73	↑	n.a.	n.a.

846 ^a Significantly different ($P < 0.05$) metabolites between SBM and RSM/FB in *pre rigor* muscle are presented in Fig.2A.
847 ^b Significantly different ($P < 0.05$) metabolites between SBM and RSM/FB in 7 days chilled meat are presented in Fig.2B.
848 ^c Fold changes of metabolites ($P < 0.05$; $FC > 2.0$) between *pre rigor* muscle and 7 days chilled meat.
849 ¹Yoshida et al. (1966); ²Hofmann et al. (2005); ³Haefeli et al. (1990); ⁴Ishibashi et al. (1988); ⁵Scharbert et al. (2005); ⁶Harrison et al. (1968); ⁷Burdock (2016);
850 ⁸Hahn et al. (1948); ⁹Drauz et al. (2007); ¹⁰Schiffman et al. (1981); ¹¹Kawai et al. (2012); ¹²Faurion et al. (1992); ¹³Sonntag et al. (2010); ¹⁴Stark et al. (2006);
851 ¹⁵Burdock (2005); ¹⁶Graham et al. (1995); ¹⁷Kirk-Othmer Encyclopedia of Chem. Technology (1992); ¹⁸Tanimura et al. (1993); ¹⁹Schiffman et al. (1979); ²⁰Rothe
852 et al. (1972); ²¹<http://www.thegoodscentcompany.com>; ²²Meilgaard (1982); ²³Engan (1974); ²⁴Hidaka et al. (1992); ²⁵Stevens (1997); ²⁶Yimdee et al. (2016);
853 ²⁷Gardner (1977); ²⁸Grabež et al. (2019); ²⁹Ramachandran et al. (2006); ³⁰Hufnagel et al. (2008); ³¹Pangborn (1963); ³²Watkins et al. (2013); ³³Rudrum et al. (1965);
854 ³⁴Rothe et al. (1963); ³⁵Nagai et al. (2006); ³⁶Brittain et al. (1991); ³⁷<https://www.vcf-online.nl/VcfCompounds.cfm>; ³⁸Woo et al. (1983); ³⁹Mosciano et al. (2001);
855 ⁴⁰Ledahudec et al. (1991); ⁴¹Grosch et al. (1984); ⁴²Hahn et al. (1938); ⁴³Lewis (1997); ⁴⁴Budavari (1996); ⁴⁵Haseleu et al. (2014); ⁴⁶Kuchiba-Manabe et al. (1991);
856 ⁴⁷Dunkel et al. (2009).
857

Fig.1.



858
859

Fig.2A

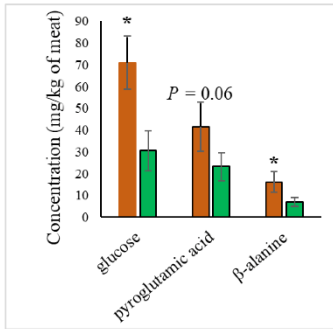
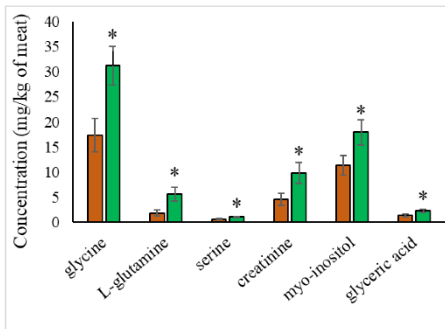


Fig.2B



860
861

Fig.3A

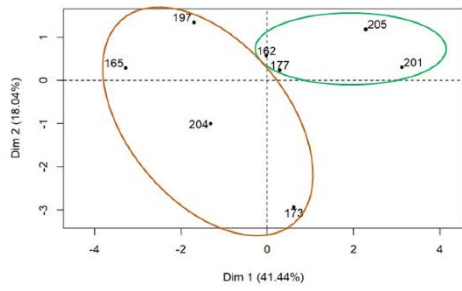


Fig.3B

