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1 **Effect of carbohydrate source on microbial nitrogen recycling in growing**
2 **rabbits**

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16
17

Abstract

18

19 In rabbits, caecal fermentation relies to a large extent on the type of substrate available
20 for bacteria. Therefore, in order to study the dietary effect of the source of carbohydrate
21 on microbial nitrogen (N) absorption, thirty-two New Zealand growing male rabbits
22 were randomly assigned to four diets formulated using two sources of structural
23 carbohydrates (fibre), alfalfa hay (AH) and sugar beet pulp (SBP), combined with two
24 sources of non-structural carbohydrates (starch), wheat or maize, at a constant
25 fibre/grain sources ratio (0.80/0.20). Microbial N intake was estimated by preventing
26 caecotrophy with a neck collar and, indirectly, by using urinary purine derivative (PD)
27 excretion and microbial ¹⁵N-lysine incorporation. No effect of diet on growth was
28 detected (average growth rate 26.6±0.69 g/d), although dry matter (DM) intake was
29 greater in animals fed diets with AH as main source of fibre than those receiving SBP
30 (100.2 vs 90.1 g/d; P<0.01). Nonetheless, the latter diets were better digested and no
31 significant differences were observed in digestible organic matter (OM) intake. Between
32 sources of starch, digestibility of DM, OM and N was greater with wheat than maize
33 (P<0.05). Microbial activity in the caecum was stimulated by SBP diets, as indicated by
34 a greater volatile fatty acid concentration (89.6 vs 67.5 mmol/L; P<0.01) and a lower
35 pH (5.7 vs 6.2; P<0.001). Significantly higher amino acid ¹⁵N-enrichments in both
36 caecotrophes and liver were observed with SBP diets and also in maize-fed rabbits
37 when SBP was the main fibre source. However, microbial contribution to tissue amino
38 acids (0.37±0.008) was not affected by the type of fibre.

39 *Keywords:* caecotrophy, caecum, fibre, lysine, starch, protein metabolism

40

41 **1. Introduction**

42 Monogastric herbivorous are hindgut fermenters, i.e. the fermentation compartment
43 is located after the enzymatic digestion area and thus microbial biomass synthesised in
44 the large intestine is mostly wasted with the faeces (Hörnigke, 1981). In order to recycle
45 this nutritious material, lagomorphs, such as rabbits have developed a physiological
46 mechanism, termed caecotrophy, involving ingestion of soft faeces (caecotrophes),
47 originating from a selective retention process actively performed in the main
48 fermentation compartment, the caecum, and proximal colon (Leng and Hornicke, 1976;
49 Fioramonti and Ruckebusch, 1976; Hornicke, 1981). Caecal fermentation may be
50 manipulated through the diet to improve the microbial contribution to rabbit protein
51 nutrition. Potential nutritional factors include dietary components able to resist digestion
52 in the small intestine and reach the caecum, such as structural carbohydrates (fibre) or
53 resistant starch (Gidenne, 1997; Belenguer et al., 2002).

54 Quantification of the contribution of caecotrophy to the host amino acid (AA)
55 metabolism has been limited by the accuracy of the methodology (Belenguer et al.,
56 2008). Conventional procedure involves preventing caecotrophy using a neck collar to
57 collect the soft faeces. Unfortunately, collar fitting in growing rabbits may alter dry
58 matter intake (Carabaño et al., 2000a) and caecotrophes production (Fioramonti and
59 Ruckebusch, 1976; Gidenne and Lebas, 1987; Gidenne and Lebas, 2006). Caecotrophy
60 reached 26% of feed intake when estimated without a neck collar, but only 12 to 15%
61 with the collar fitting procedure (Gidenne and Lebas, 2006). Another direct procedure, a
62 serial slaughtering protocol (Gidenne, 1987), or indirect methodologies based on
63 microbial markers utilization (internal - purine bases (PB), Balcells et al., 1998; or
64 external - microbial ¹⁵N-lysine, Belenguer et al., 2005) allow estimates of microbial-N

65 recycling *in vivo* without altering physiological behaviour, although the former
66 technique produces only mean values and not individual estimations.

67 This study aimed to examine the effect of the dietary inclusion of two types of
68 carbohydrates (starch or fibre), characterized by its high (wheat and sugar beet pulp
69 (SBP)) or low (maize and alfalfa hay (AH)) digestive utilization, on caecal fermentation
70 and microbial-N recycling, using either direct or indirect procedures.

71

72 **2. Material and methods**

73 Protocols and animal handling were approved by the “Comité Ético del Servicio de
74 Biomedicina y Biomateriales” of the University of Zaragoza.

75

76 *2.1. Animals and diets*

77 Thirty-two New Zealand White newly weaned male rabbits (35-45 days), with a
78 mean initial weight (W) of 0.91 ± 0.017 kg were used. Animals were randomised among
79 four experimental diets (8 animals per diet), housed individually in cages and submitted
80 to a 12:12 h light:dark schedule, starting the light period at 8:00.

81 The four experimental diets were formulated to contain a similar energy (11.9-13.1
82 MJ digestible energy/kg dry matter, DM, estimated as described by Villamide et al.,
83 2009), protein (170-185 g crude protein/kg DM), and lysine (10.2 mg/kg, estimated)
84 content, using two sources of structural carbohydrates (fibre), alfalfa hay (AH) and
85 sugar beet pulp (SBP). These fibrous ingredients were combined either with maize or
86 wheat grain, as sources of non-structural carbohydrates (starch), at a constant fibre/grain
87 sources ratio (0.80/0.20), i.e. containing about four times more fibre (SBP plus AH)
88 than grain (wheat or maize). Diets were supplemented with ^{15}N -labelled NH_4Cl (0.7 %;
89 $^{15}\text{NH}_4\text{Cl}$, 10^+ atom % ^{15}N ISOTECH, Inc USA) during the experimental period but not

90 during the adaptation period. Ingredients and composition of the four experimental diets
91 are presented in Table 1. Diets were offered at 8:00 in the morning at a constant level
92 (approximately 100 g/d; 90% *ad libitum* or 2.25 times maintenance requirements,
93 defined as 410 kJ metabolizable energy/kg $W^{0.75}$ /d; Xicatto and Trocino, 2010) for the
94 whole experimental period and animals had free access to drinking water.

95

96 2.2. *Experimental procedures*

97 Each experimental period lasted for 35 days, 28 days for dietary adaptation and
98 seven days for experimental measurements. Rabbits were penned individually during
99 the adaptation period and in metabolism cages for the experimental trial. The following
100 schedule was adopted on each experimental design: adaptation to the metabolic cage
101 (days 1-2), digestibility measurements and urine collection (days 3-6), and collar fitting
102 to prevent caecotrophy and allow collection of the soft faeces for the last 24 h (day 7),
103 according to the method of Carabaño et al. (2010). A wooden round neck collar (50 mm
104 i.d. and 270 mm e.d., weighing approximately 67 g) was fitted at 8:00 and maintained
105 for 24 h. Animals were weighed at the beginning of the experiment and then once a
106 week until the end of the trial when they were slaughtered between 9:00 and 12:00.

107

108 2.3. *Sample collection*

109 During the period of experimental measurements daily urine was collected
110 individually under 1 M H_2SO_4 (50 ml/L, final pH<3), weighed, diluted (to 1 L),
111 sampled (100 mL) and stored at $-20^{\circ}C$. Faeces were also collected daily, together with
112 caecotrophes on day 7, then weighed and immediately frozen at $-20^{\circ}C$.

113 Animals were slaughtered by cervical dislocation, dissected and the caecum excised
114 and weighed. Caecal content pH was measured with a glass electrode pH-meter.

115 Immediately afterwards, two samples of caecal contents were taken (1 g each), acidified
116 with either 0.2 M HCl or 0.5 M H₃PO₄, and both stored at -20°C for ammonia and
117 volatile fatty acid (VFA) determination, respectively. The remaining caecal contents
118 were weighed (20 to 50 g), diluted in a methylcellulose solution (9 g NaCl/L, 1 g
119 methylcellulose/L) and chilled at 4°C for 24 h to dislodge and isolate adherent bacteria
120 as previously described (Belenguer et al., 2005). The resultant microbial pellet was
121 frozen at -20°C and then freeze-dried for subsequent analysis. Samples of liver were
122 also taken and stored at -20°C for ¹⁵N-AA enrichment determination.

123

124 *2.4. Chemical analyses*

125 In feeds and faeces, either hard or soft, DM was determined by drying at 60°C to
126 constant weight. Organic matter (OM) was estimated by ashing samples at 550 °C for 8
127 h. Nitrogen (N) was measured by the Kjeldhal method. Neutral and acid detergent fibre
128 (NDF and ADF) and lignin were determined according to Van Soest et al. (1991) after
129 an amylase pre-treatment. Caecal volatile fatty acids (VFA) concentration was analysed
130 by gas chromatography, following the procedure described by Jouany (1982) and
131 ammonia concentration by the method proposed by Chaney and Marbach (1962).
132 Urinary purine derivatives (PD: allantoin, uric acid, hypoxanthine and xanthine) were
133 analysed by reverse-phase HPLC (Balcells et al., 1992). Purine bases (PB: adenine and
134 guanine) in feeds, bacterial extracts and soft faeces were determined by the same HPLC
135 technique, with the modifications proposed by Martín-Orúe et al. (1995).

136 Amino acid ¹⁵N-enrichments in caecotrophes and liver were measured by GC-C-
137 IRMS as described previously (Belenguer et al., 2005).

138

139 *2.5. Calculation and statistical analyses*

140 Duodenal flow of PB was estimated from the urinary excretion of PD following the
141 predictive model proposed by Balcells et al. (1998) as modified by Belenguer et al.
142 (2008). The microbial lysine intake and the contribution of microbes to tissue lysine
143 were estimated as described previously (Belenguer et al., 2005, 2008). Briefly, the
144 microbial lysine intake was estimated assuming a true ileal digestibility of 0.82
145 (Carabaño et al., 2000b) and 0.88 (Storm et al., 1983) for dietary and microbial lysine,
146 respectively. The microbial contribution to tissue lysine was calculated as the ratio of
147 ¹⁵N-enrichments in liver and microbial lysine. Data were analysed by ANOVA as a
148 complete randomised design, following a 2 x 2 factorial structure, with the source of
149 fibre (F; AH vs SBP), the source of starch (St; wheat vs maize) and their interaction as
150 main effects. Analyses of ¹⁵N-AA enrichment were done as a split-plot design,
151 comparing main plot factors (fibre, F and starch, St) against the animal error term (€1),
152 whereas ¹⁵N enrichment between substrates (Sub; liver and caecotrophes) nested within
153 animals (A) and their interactions were compared against the residual error term (€2).
154 The model was as follows:

$$155 \quad Y_{ijkl} = \mu + F_i + St_j + F \times St_{ij} + \epsilon_{1ijk} [A(F \times St)] + Sub_l + F \times Sub_{il} + St \times Sub_{jl} + \epsilon_{2ijkl}$$

156 When methodologies to estimate microbial N recycling were compared, data were
157 analyzed using a similar split-plot design with method (M) used instead of substrate.

158 Data were analyzed using the using the MIXED procedure of **the statistical software**
159 **SAS (2004)**. The level of statistical significance was set at P<0.05.

160

161 **3. Results**

162 No significant effect of the interaction between fibre and starch (F x St) was
163 observed in most studied parameters, and therefore only the effects of the main factors
164 (fibre and starch) are presented in the tables unless otherwise stated.

165

166 *3.1. Digestive parameters*

167 Average growth rate was 26.5 ± 0.69 g/d and final live weight was 1.90 ± 0.024 kg, and
168 no differences among experimental groups were recorded (Table 2). The lower dry
169 matter intake in animals fed SBP diets (-10%) than in those receiving AH diets ($P < 0.01$)
170 was counterbalanced by a higher DM and OM total tract apparent digestibility
171 ($P < 0.001$). In consequence, digestible organic matter intakes were similar, although
172 NDF and N were also better digested in SBP (0.53 and 0.78, respectively) than in AH
173 diets (0.43 and 0.74; $P < 0.001$).

174 Digestibility of DM, OM and N were higher for wheat than maize diets (0.70, 0.71
175 and 0.77 vs 0.68, 0.68 and 0.75, respectively; $P < 0.05$ for DM and OM, and $P < 0.01$ for
176 N), while there were no significant differences between starch sources for digestible
177 OM and N intake and NDF digestibility.

178

179 *3.2. Characterization of caecal fermentation*

180 Animals fed SBP had more fresh caecal contents (99.1 vs 80.6 g/d; $P < 0.05$) and
181 higher empty caecum weight than those receiving AH diets (37.1 vs 32.9; $P < 0.01$), but
182 there were no differences between starch sources (Table 2).

183 Rabbits with a larger caecum also showed higher total VFA concentrations (89.6 vs
184 67.5 mmol/L in rabbits fed SBP and AH diets, respectively; $P < 0.01$) and a lower pH
185 (5.69 vs 6.18; $P < 0.01$). Molar proportions of the main VFA did not differ between diets
186 (acetic, 0.79, butyric, 0.14, and propionic 0.06). Ammonia concentration averaged
187 3.90 ± 0.431 mg/dL, and was independent of dietary treatment.

188 Caecotrophes showed a two-fold higher protein concentration (335 vs 144 g/kg DM)
189 but only half the NDF concentration (297 vs 567 g/kg DM) of hard faeces.

190

191 3.3. Urinary excretion and duodenal flow of purine compounds

192 Urinary PD was composed almost entirely of allantoin and uric acid (92 and 8%)
193 with trace amounts of xanthine and hypoxanthine. Allantoin and uric acid excretions
194 averaged 839.5 ± 40.31 and 68.6 ± 4.22 $\mu\text{mol/kg W}^{0.75}$, respectively, with both affected by
195 diet. Total PD excretion was greater in rabbits fed AH than in those receiving SBP as
196 the main source of fibre (1035.4 vs 780.7 $\mu\text{mol/kg W}^{0.75}$, respectively; $P < 0.01$), but no
197 differences were detected between starch sources (Table 3). In addition, rabbits fed AH
198 diets showed a greater duodenal flow of PB than those fed SBP diets (1.55 vs 1.17
199 $\text{mmol/kg W}^{0.75}$; $P < 0.01$) due to both the greater ingestion of dietary PB (0.83 vs 0.62
200 mmol PB/d for AH and SBP-fed rabbits, respectively) and a higher estimated duodenal
201 flow of microbial PB (1.07 vs 0.81 $\text{mmol/kg W}^{0.75}$ for animals fed AH and SBP diets,
202 respectively; $P < 0.05$).

203

204 3.4. Microbial ^{15}N -lysine incorporation

205 Ingestion of the isotope (0.7 g/d $^{15}\text{NH}_4\text{Cl}$) resulted in enriched AA in caecotrophes
206 and liver (Table 4). For essential AA the isotope enrichments were always greater in
207 caecotrophes than in liver. With non-essential AA, however, there was no clear pattern,
208 with either lower (tyrosine, proline, aspartate, glutamate), similar (glycine), or higher
209 (alanine, serine) enrichments in liver.

210 The effect on ^{15}N -AA enrichment was always higher ($P < 0.05$) for both caecotrophes
211 and liver in animals fed SBP compared to those receiving AH as the main source of
212 fibre. Effects of starch type were less pronounced, but **for most amino acids, including**
213 **lysine, enrichments (atom % excess) were greater in maize-fed rabbits when SBP was**
214 **the main fibre source, whereas no significant differences were observed with AH, as**

215 indicated by the significant fibre x starch interaction. For instance, this occurred for
216 lysine either in caecotrophes (0.56 vs 0.50) or liver (0.22 vs 0.18; Table 4).

217 The contribution of microbial AA to tissues was estimated using lysine and
218 threonine, AA that do not undergo amination or transamination, as described by
219 Belenguer et al. (2005), although in the present study enrichments were measured in
220 caecotrophes rather than caecal bacteria. Microbial contributions to liver lysine and
221 threonine both averaged 0.37 (0.37 ± 0.008 and 0.37 ± 0.014 , for lysine and threonine,
222 respectively). Microbial lysine contribution to liver was not affected by the
223 experimental treatment (Figure 1).

224

225 3.5. Microbial N recycling

226 Dry matter and N excretion through the caecotrophy process and microbial N
227 recycling, estimated by the three approaches, are presented in Table 5. Average soft
228 faeces excretion, determined by caecotrophe collection, was 12.7 ± 0.71 g DM/d, with a
229 high interindividual variation (from 5.8 to 22.7 g/d), and was unaltered by the
230 experimental treatment.

231 Microbial N recycling values differed among estimation protocols, with the lower
232 values obtained by direct collection (collar method; 0.50 ± 0.032 g/d) compared to those
233 derived from PD excretion (1.22 ± 0.080 g/d) or ^{15}N -lysine incorporation (1.39 ± 0.064
234 g/d; $P<0.001$). The effect of either the source of fibre or starch was not significant for
235 any of the estimation methods. Residual variations (coefficient of variation, CV) were
236 37, 35 and 18%, for PD excretion, direct collection and microbial ^{15}N -lysine
237 incorporation, respectively.

238

239 **4. Discussion**

240 *4.1. Digestive and fermentation parameters*

241 Animals adapted well to the experimental treatments, although growth rate was
242 lower than in similar trials (26.6 ± 0.69 vs 30-38 g/d; de Blas and Villamide, 1990;
243 Gidenne and Bellier, 2000) where rabbits were fed *ad libitum*, while in our case feed
244 supply was restricted (90% of *ad libitum* intake), in order to minimize individual feed
245 intake variability.

246 SBP contains a greater proportion of hemicellulose plus water insoluble pectins
247 (Gidenne, 2003) than AH. The AH has a greater degree of lignification, which may
248 stimulate the transit of digesta through the digestive tract (Gidenne et al., 2001). These
249 differences may explain variations in intake and digestibility and the high fermentation
250 rates observed in SBP-fed rabbits (Gidenne et al., 2010), evidenced by a lower pH (-
251 8%) and a higher VFA concentration (+33%; Fraga et al., 1991; Gidenne, 1997).

252 Likewise, maize and wheat grains differ in the physical structure of the starch
253 granule. In maize the protein matrix that surrounds starch is thicker, which restricts the
254 enzyme accessibility and reduces digestibility compared to wheat (Rooney and
255 Pflugfelder, 1986; Blas and Gidenne, 2010).

256

257 *4.2. Indirect approaches to estimate microbial contribution*

258 PD excretion values were within the range described previously with similar animals
259 and diets (Belenguer et al., 2008), although lower than values derived from older and
260 heavier animals (Abecia et al., 2005). As previously observed (Belenguer et al., 2002),
261 urinary PD was greater with AH than in SBP-fed animals, due to a higher intake of
262 dietary PB. A similar effect was observed in total and microbial duodenal PB flow.

263 Ingestion of a ^{15}N -labelled NH_4Cl results in production of labelled microbial AA-N
264 (Belenguer et al., 2005) with a differential ^{15}N enrichment depending on metabolic
265 inflows from labelled or unlabelled sources (Atasoglu et al., 2004). In this regard, amino
266 acid enrichment in caecotrophes was greater in SBP-fed animals than in those animals
267 receiving AH diets. We might speculate that availability of dietary [non-labelled] N for
268 caecal microbes would be higher in AH-fed animals due to either more dietary resistant
269 protein (Gidenne and Ruckebusch, 1989) and/or greater protein ingestion. Alternatively,
270 SBP diets could have provided more fermentable fibre (such as hemicellulose) reaching
271 the caecum, which would elicit an increased level of microbial biosynthesis and
272 consequently recycling of endogenous labelled N sources.

273 Although starch is digested mainly in the small intestine (Merino and Carabaño,
274 1992; Carabaño et al., 1997), the resistant starch structure in maize granule (Blas and
275 Gidenne, 2010) may enhance the starch flow at the ileum (Gidenne et al., 2005) and the
276 microbial activity within the caecum. Thus caecotrophes seemed to show a higher level
277 of ^{15}N incorporation in maize than in wheat-fed rabbits, although this effect was
278 significant only with SBP as the main source of fibre (+12%), suggesting that the starch
279 effect could be enhanced by presence of fermentable fibre.

280 In tissues, the AA ^{15}N -enrichments rely on the contribution of microbial AA, derived
281 mostly from caecotrophy (Belenguer et al., 2005), plus amination/transamination
282 processes. Average tissue enrichments were lower in the essential AA, such as lysine,
283 that do not undergo transamination within tissues (Bender, 1985) and was then used to
284 estimate microbial contribution (mostly through caecotrophy) to AA absorption.

285 Differences in absolute AA enrichments in caecotrophes and tissues between fibre
286 sources (SBP vs AH, Table 4) were not reflected in the microbial contribution to liver
287 lysine, which seems to suggest that the ingested amount of caecotrophes relative to total

288 intake might be similar among treatments. If this is the case, variations between fibre
289 sources in ^{15}N -AA enrichments in caecotrophes may be due to differential $^{15}\text{N}/^{14}\text{N}$
290 availability from either labelled (ammonia, body proteins) or unlabelled (dietary)
291 sources in the caecum.

292 Regarding the source of starch, no significant effect was observed on microbial AA
293 contribution to tissue lysine (Figure 1), despite the greater microbial ^{15}N incorporation
294 in caecotrophes (and also in **liver**) in maize than in wheat-fed rabbits when SBP was the
295 main source of dietary fibre.

296 The use of ^{15}N -lysine enrichments in caecotrophes instead of caecal bacteria may
297 overestimate microbial contribution, since, as mentioned, ^{15}N -lysine enrichment in
298 caecotrophes are lower (-18%) than in caecal bacteria. Even applying such a correction,
299 the revised microbial contribution to tissue lysine (0.30) is still greater than values
300 previously reported either with the same method in growing rabbits (0.22; Belenguer et
301 al., 2005) and lactating does (0.23; Abecia et al., 2008), or with the caecotrophes
302 collection technique in lactating does (0.18; Nicodemus et al., 1999). Differences
303 among trials could be explained by different experimental conditions and in the present
304 experiment the limited feed (and N) supply might have also enhanced the ability of the
305 animals to recycle microbial protein.

306

307 *4.3. Microbial N recycling*

308 The average contribution of microbes to total protein intake differed among
309 methodologies (29.3 ± 1.47 , 33.3 ± 0.94 and $15.3\pm 0.84\%$ for PD, ^{15}N -lysine and
310 caecotrophe collection procedures, respectively), confirming previous results from our
311 group (Belenguer et al. 2005; Belenguer et al 2008). Similarly, the lowest values of
312 microbial OM recycling (20.1 ± 1.27 , 22.7 ± 0.90 and 11.3 ± 0.63 g/d for PD, ^{15}N -lysine
313 and caecotrophes collection procedures, respectively) or its contribution to total OM

314 intake (18.7 ± 1.05 , 21.2 ± 0.54 and $11.6 \pm 0.62\%$, respectively) were observed with the
315 conventional technique. Collar fitting may distress rabbits and reduce feed intake
316 (Belenguer et al., 2002) and caecotrophes excretion (Gidenne and Lebas 1987;
317 Belenguer et al., 2008), as a consequence of the altered nutritional behaviour. The DM
318 intake was more variable and decreased with the collar (-21%), suggesting a lack of
319 adaptation of the animals, which might explain the lower amount of caecotrophes
320 collected (12.7 g DM/d) and the smaller microbial contribution to total N intake
321 (15.3%) than the range reported by Villamide et al. (2010; 15-30 g DM/d or 17-29%).
322 The present study aimed, however, to investigate the effect of diet on microbial N
323 recycling. In this regard, a previous study from our group (Belenguer et al. 2002), using
324 similar diets (fibre/grain sources ratio, 0.80:0.20), showed an improvement of microbial
325 N recycling (g/d) with AH diets in relation to SBP, using the conventional and the PD
326 techniques, in rabbits fed *ad libitum*. Conversely, in the current study no significant
327 differences were detected in microbial N recycling between treatments and thus the
328 contribution of soft faeces to total DM (or N) was similar in all diets. Some aspects of
329 the PB metabolism are still unclear in rabbits (Belenguer et al., 2008), and as far as the
330 authors are aware, this is the first study of the effect of different sources of fibre on
331 microbial N recycling using the ^{15}N -lysine incorporation method. With the soft faeces
332 collection, different results on the effect of the type of fibre on microbial N excretion
333 have been reported, with no variations between alfalfa and soya bean hulls (Nicodemus
334 et al. 2007) or differences (from 0.34 to 0.83 g microbial N/day) using a range of
335 different fibre sources (paprika meal, olive leaves, alfalfa hay, NaOH-treated straw and
336 hull from soybean and sunflower) at different inclusion levels (NDF varied from 33.1 to
337 78.7 % of DM; García et al., 2000). In the last case, however, differences were mostly
338 explained by the low values obtained with straw and sunflower (0.34 g DM/d).

339

340 **5. Implications:** The utilization of two different sources of structural carbohydrates, AH
341 and SBP, or two types of starch, wheat and maize, did not result in significant variations
342 in microbial protein recycling. Nevertheless, **our results suggest that** the utilization of
343 SBP, especially in combination with maize, as **a** dietary source that may provide a
344 greater amount of carbohydrates to the hindgut, might increase microbial biosynthesis
345 in the caecum, **indicating** a potential to improve microbial protein contribution. Further
346 research would be necessary to elucidate this effect and make dietary recommendations
347 **for** these ingredients for growing rabbits.

348

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355

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479

480 **Table 1.** Ingredients (g/kg) and chemical composition (g/kg DM) of the experimental
 481 diets formulated using two sources of fibre (alfalfa hay or sugar beet pulp) and two
 482 sources of starch (maize or wheat), either labelled (Lab.; with $^{15}\text{NH}_4\text{Cl}$) or unlabelled
 483 (Unlab.).

Source of fibre Source of starch	Alfalfa hay				Sugar beet pulp			
	Maize		Wheat		Maize		Wheat	
	Unlab.	Lab.	Unlab.	Lab.	Unlab.	Lab.	Unlab.	Lab.
Ingredients								
Sugar beet pulp	196	195	185	184	478	475	485	482
Alfalfa hay	506	502	516	512	159	158	162	161
Maize grain	184	183	0	0	149	148	0	0
Wheat grain	0	0	196	195	0	0	165	164
Soya bean meal	107	107	97	97	161	160	146	145
Treated straw	5	5	0	0	51	51	41	41
Sunflower oil	0	0	4	4	0	0	0	0
Vit-min mix†	2	2	2	2	2	2	2	2
Composition								
Dry matter (g/kg)	909	910	912	910	906	917	910	913
Organic matter	899	900	899	900	920	917	922	920
Digestible energy (MJ/kg) ‡	11.9	11.9	12.2	12.2	12.7	12.7	13.1	13.1
Crude protein	181	191	184	195	170	184	174	182
Digestible crude protein	130	137	141	149	132	143	136	143
NDF	338	336	324	333	350	342	341	356
ADF	176	180	181	182	182	184	181	184
Lignin	46	41	41	44	28	24	26	22

484 CP, crude protein (N x 6.25).

485 † Composition of vitamin-mineral mix: 200 ppm Co (CoSO₄ 7 H₂O), 3000 ppm Cu (CuSO₄ 5 H₂O),
 486 20000 ppm Fe (FeSO₄ 1 H₂O), 8000 ppm Mn (MnO₂), 30000 ppm Zn (ZnO), 30 ppm Se (Na₂SeO₃), 500
 487 ppm I (KI), 4500000 IU/kg vit A, 550000 IU/kg vit D₃, 1100 ppm vit E, 250 ppm vit B₁, 1500 ppm vit B₂,
 488 100 ppm vit B₆, 6000 ppm vit B₁₂, 500 ppm vit K, 5000 ppm D-pantothenate, 12500 ppm niacin, 100000
 489 ppm choline chloride.

490 ‡ Estimated using the prediction equation: Digestible energy (MJ/kg) = 1.92 + 15.31 DM digestibility
 491 (Villamide et al., 2009).

492

493 **Table 2.** Effect of dietary inclusion of alfalfa hay (AH) or sugar beet pulp (SBP), and
 494 maize or wheat as sources of fibre and starch respectively on growth rate, dry matter
 495 intake, digestible organic matter (OM) intake, and total tract apparent digestibility of
 496 dry matter (DM), organic matter (OM), neutral detergent fibre (aNDFom) and nitrogen
 497 (N), and physical and chemical characteristics of caecal contents (pH, NH₃ and volatile
 498 fatty acid (VFA) concentrations, and proportions of acetic, propionic and butyric acids)
 499 in growing rabbits.

	AH	SBP	Maize	Wheat	SE	Statistical significance	
						Fibre	Starch
Productive parameters							
Growth rate (g/d)	26.9	26.3	26.1	27.0	1.44	NS	NS
Intake (g/d):							
Dry matter	100.2	90.1	94.1	96.3	3.23	**	NS
Digestible OM	59.6	60.0	58.0	61.6	1.96	NS	NS
Digestible N	2.29	2.06	2.10	2.25	0.732	**	NS
% N recycled by caecotrophes	14.4	16.0	13.8	16.7	1.68	NS	NS
Digestibility:							
DM	0.66	0.71	0.68	0.70	0.010	***	*
OM	0.66	0.73	0.68	0.71	0.010	***	*
aNDFom	0.43	0.53	0.46	0.50	0.018	***	NS
N	0.74	0.78	0.75	0.77	0.021427	***	**
Caecum characteristics							
Physical:							
Full weight (g)	114	136	124	126	8.5	*	NS
Empty viscera (g)	32.9	37.1	35.0	35.0	1.16	**	NS
Chemical:							
pH	6.18	5.69	5.85	6.02	0.125	**	NS
NH ₃ (mg/dL)	3.92	3.90	3.65	4.17	0.897	NS	NS
VFA (mmol/L)	67.5	89.6	82.3	74.8	7.54	**	NS
Acetic (mol/mol)	0.80	0.78	0.78	0.80	0.012	NS	NS
Propionic (mol/mol)	0.06	0.06	0.06	0.05	0.006	NS	NS
Butyric (mol/mol)	0.14	0.14	0.13	0.14	0.010	NS	NS

500 SE: Standard error of the treatment means; NS, non-significant; *, P<0.05; **, P<0.01; ***, P<0.001.

501

502 **Table 3.** Effect of dietary inclusion of alfalfa hay (AH) or sugar beet pulp (SBP), and
 503 maize or wheat as sources of fibre and starch, respectively, on the urinary excretion of
 504 purine derivatives (PD) and duodenal flow of purine bases (PB) in growing rabbits.

	AH	SBP	Maize	Wheat	SE	Statistical significance	
						Fibre	Starch
($\mu\text{mol}/\text{W}^{0.75}/\text{d}$)							
PD excretion							
Alantoin	956	723	783	896	69.2	**	NS
Uric acid	79.5	57.6	70.1	67.0	7.73	**	NS
Total PD	1035	781	853	963	72.6	**	NS
Duodenal flow of PB							
Total†	1.545	1.165	1.273	1.438	0.1083	**	NS
Dietary	0.525	0.392	0.451	0.465	0.0129	***	NS
Microbial‡	1.066	0.808	0.861	1.013	0.1148	*	NS

505 SE: Standard error of the treatment means; NS, non-significant; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$.

506 † Estimated from urinary excretion of PD using the model proposed by Balcells et al. (1998), modified by
 507 Belenguer et al. (2008).

508 ‡ Estimated by subtraction of dietary PB ingested, assuming digestibility of 0.913 (Chen et al., 1990),
 509 from total duodenal flow of PB.

510

511 **Table 4.** Effect of dietary inclusion of alfalfa hay (AH) or sugar beet pulp (SBP), and maize or wheat as sources of fibre and starch,
 512 respectively, on ¹⁵N-enrichments (atom % excess) in non-essential and essential amino acids in caecotrophes and liver in growing rabbits.

Amino acids	Caecotrophes				Liver				SE ₁	SE ₂	Statistical significance			
	AH		SBP		AH		SBP				Fibre	Starch	Substrate	Fibre x Starch
	Maize	Wheat	Maize	Wheat	Maize	Wheat	Maize	Wheat						
<i>Non-essential</i>														
Alanine	0.540	0.550	0.741	0.644	0.622	0.608	0.815	0.641	0.0190	0.0068	***	**	***	***
Glycine	0.411	0.389	0.597	0.488	0.467	0.434	0.630	0.516	0.0230	0.0162	***	**	NS	NS
Proline	0.165	0.187	0.239	0.236	0.118	0.115	0.182	0.136	0.0048	0.0051	***	NS	***	**
Serine	0.418	0.441	0.612	0.529	0.463	0.451	0.669	0.514	0.0154	0.0065	***	**	*	***
Aspartate	0.515	0.519	0.744	0.638	0.501	0.499	0.679	0.545	0.0137	0.0061	***	***	***	***
Glutamate	0.598	0.590	0.822	0.695	0.581	0.560	0.773	0.605	0.0171	0.0078	***	***	**	***
Tyrosine	0.446	0.459	0.565	0.528	0.202	0.197	0.303	0.205	0.0137	0.0101	***	*	***	*
<i>Essential</i>														
Valine	0.494	0.497	0.678	0.589	0.190	0.186	0.290	0.232	0.0125	0.0061	***	*	***	**
Leucine	0.502	0.505	0.692	0.594	0.202	0.199	0.312	0.238	0.0118	0.0061	***	**	***	***
Threonine	0.401	0.426	0.551	0.495	0.151	0.137	0.237	0.167	0.0103	0.0056	***	*	***	**
Phenylalanine	0.425	0.454	0.570	0.551	0.153	0.152	0.232	0.179	0.0122	0.0056	***	NS	***	**
Lysine	0.402	0.406	0.562	0.502	0.149	0.144	0.221	0.177	0.0100	0.0048	***	*	***	**

513 SE₁ and SE₂: standard errors of the animal effect and residual term in split-plot design; * NS, non-significant; *, P < 0.05; **, P < 0.01; ***, P < 0.001.

514

515 **Table 5.** Effect of dietary inclusion of alfalfa hay (AH) or sugar beet pulp (SBP), and
 516 maize or wheat as sources of fibre and starch, respectively, on caecotrophe dry matter
 517 (DM) and N production and microbial nitrogen (MN) recycling using the following
 518 methods (M): caecotrophy prevention by using neck collar (CC), urinary excretion of
 519 purine derivatives (PD), or microbial ¹⁵N-lysine incorporation (¹⁵N-lysine) in growing
 520 rabbits.

	AH	SBP	M	W	SE	Significance				
						Fibre	Starch			
Caecotrophes										
DM (g/d)	13.4	12.0	13.4	11.9	1.42	NS	NS			
N (g/d)	0.73	0.63	0.64	0.71	0.075	NS	NS			
	AH	SBP	M	W	SE ₁	SE ₂	Significance			
							Fibre	Starch	Method	Starch x M
MN recycling (g/d)					0.079	0.119	NS	NS	***	NS
CC	0.52	0.48	0.44	0.56						
PD	1.35	1.09	1.07	1.37						
¹⁵ N-lysine	1.37	1.39	1.46	1.30						

521 SE: Standard error of the treatment means; SE₁ and SE₂: standard errors of the animal effect and residual
 522 term in split-plot design; M, methodology; NS, non-significant; ***, P < 0.001.

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527 **Figure 1.** ¹⁵N-lysine enrichments (atom % excess) in caecotrophes and liver, and
528 contribution of caecotrophes to tissue lysine in growing rabbits fed diets formulated
529 based on alfalfa hay (AH) or sugar beet pulp (SBP) as main source of fibre, and those
530 receiving diets with the inclusion of maize (M) or wheat (W) as source of starch (NS,
531 non-significant; *, P < 0.05; ***, P < 0.001).

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