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8 Abstract

9 Heat stress (HS) during lactation poses a critical challenge in swine production, often impairing feed
10 intake, metabolic function, and reproductive performance in sows. This study aimed to evaluate the
11 effects of feed form (mash vs. pellet) and dietary electrolyte balance (dEB; 230 vs. 290 mEq/kg) adjusted
12 with sodium bicarbonate on sow performance, litter growth, immune response, antioxidant status, and gut
13 microbiota under HS conditions. A total of 40 multiparous sows were assigned to four treatments in a 2×2
14 factorial design: Mlow (mash + 230 mEq/kg), Mhigh (mash + 290 mEq/kg), Plow (pellet + 230 mEq/kg),
15 and Phigh (pellet + 290 mEq/kg). Each treatment contained 10 sows with 3-5 parity and their initial body
16 weight was 241.83 ± 16 kg at d 112 of lactation. The trial spanned from parturition to weaning (21 days)
17 during summer at an average temperature of 28.8°C. Results showed that sows fed pelleted diets (Plow,
18 Phigh) and higher dEB levels (Mhigh, Phigh) had higher ($p < 0.001$) average daily feed intake. Piglets
19 from Mhigh and Phigh sows had increased ($p = 0.001$) weaning weights. Dry matter digestibility was
20 increased ($p = 0.022$) in sows receiving pelleted diets. The tumour necrosis factor-alpha was lower ($p <$
21 0.001) in Plow, Phigh, and Mhigh ($p = 0.010$), with an interaction ($p = 0.013$) in feed forms and dEB. The
22 interleukin-1 β was lower ($p < 0.001$) in Plow and Phigh, with higher ($p < 0.001$) superoxide dismutase
23 activity in Phigh and Plow. Hair cortisol was lower ($p = 0.048$) in pelleted groups, suggesting lower
24 physiological stress. Although alpha diversity did not differ, beta diversity and relative abundance of
25 *Lactobacillus* and *Turicibacter* indicated microbial shifts influenced by feed form. In conclusion, pelleted
26 feed form and higher dEB, particularly the Phigh treatment, enhanced feed intake, litter performance, and
27 anti-inflammatory status without negatively affecting milk composition or gut integrity. These findings
28 support the integration of feed form and electrolyte strategies to improve sow productivity under HS
29 conditions.

30

31 Keywords:

32 Antioxidant status; Gut microbiota; Heat stress; Microbial diversity; Milk composition

33

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Introduction

35

36 Heat stress (HS) is a major challenge in swine production, particularly for lactating sows, as it
37 negatively affects overall reproductive performance [1,2]. High ambient temperatures interfere with
38 thermoregulation, leading to increased respiration rates, metabolic acidosis, and reduced voluntary feed
39 intake resulting in insufficient nutrients available for milk production [3]. The decline in feed
40 consumption and metabolic activity is a natural mechanism to lower metabolic heat production [4]. These
41 factors collectively lead to economic losses and reduced productivity in swine operations. Therefore,
42 effective nutritional strategies to mitigate HS effects in lactating sows are essential to maintain optimal
43 sow and litter performance.

44 Among various strategies, feed form is an important factor influencing nutrient utilization and
45 sow productivity [5]. The mash diet is a common feed type for lactating sows, primarily because it is cost-
46 effective, requires minimal processing, and is easy to produce [5,6]. However, during periods of HS,
47 lactating sows face additional physiological stress and reduced feed intake, making it challenging to meet
48 their elevated nutritional demands through mash diets alone. In this context, pelleted diets, though more
49 expensive, may provide tangible benefits. They improve feed intake and nutrient density due to increased
50 palatability, reduced wastage, enhanced hygienic quality, and prevention of selective feeding [11–13].
51 These attributes are particularly valuable under HS conditions, where maintaining high feed intake and
52 energy availability is crucial for sustaining sow and litter performance [11].

53 Despite their benefits, pelleted feeds also have limitations. The pelleting process reduces particle
54 size and increases starch gelatinization, leading to faster digestion and higher gastric acid secretion, which
55 may predispose sows to gastric ulcers [9,10]. This risk is exacerbated during HS, when digestive health is
56 more vulnerable [10]. To address this, sodium bicarbonate (NaHCO_3) supplementation has been explored
57 as a dietary buffer that helps stabilize gastric pH and reduce acidity [14]. Moreover, NaHCO_3 increases
58 dietary electrolyte balance (dEB), calculated as $\text{Na} + \text{K} - \text{Cl}$ (mEq/kg), which plays a crucial role in
59 maintaining acid-base equilibrium during HS [15,16]. A positive dEB has been shown to improve sow
60 performance and support a healthier digestive environment, possibly by modifying gut microbiota
61 composition [6,17,18]. Given these considerations, the combination of pelleted feed and sodium
62 bicarbonate supplementation may offer synergistic advantages. While pelleted feeds enhance feed intake
63 and nutrient utilization, sodium bicarbonate buffers gastric pH and improves dEB, potentially reducing
64 stress and supporting gut integrity. We hypothesized that the synergistic effect of pelleted feed and higher
65 dEB, achieved through sodium bicarbonate supplementation, may alleviate the risk of gastric ulcers by
66 promoting consistent feed intake, stabilizing gastric pH, and enhancing mucosal protection. Thus, the
67 objective of this study was to evaluate the effects of feed form (mash vs. pellet) and dEB levels (230
68 mEq/kg vs. 290 mEq/kg) on sow and litter performance, nutrient digestibility, milk composition,

69 inflammatory cytokines, antioxidant levels, gut integrity, hair cortisol, salivary pH, and gut microbiota
70 diversity under HS conditions.

71

72

Materials and Methods

73 **Animal ethics statement**

74 The Kangwon National University Institutional Animal Care and Use Committee approved all
75 protocols involving animal use, care and handling (protocol, KW-240722-4). The NaHCO₃ used in the
76 present study was purchased from (SOMA, Chungcheong do, Republic of Korea) with purity $\geq 99\%$.

77 **Experimental design, animals, and diets**

78 Forty multiparous sows (Landrace \times Yorkshire; average initial body weight of 241.83 ± 16 kg) at
79 d 112 of lactation were exposed to HS with an average temperature of 28.25°C . The 21-day (parturition-
80 weaning) experiment was carried out during the summer period of August in Haman-gun, Gyeongsang
81 province, South Korea. The sows were randomly distributed to four treatment diets based on parity in a
82 completely randomized design with 10 pigs per replicate and 1 pig per replicate per head as a 2×2
83 factorial arrangement with 2 feed forms (mash and pellet) and 2 dEB levels (low/230 mEq/kg and
84 high/290 mEq/kg). The treatments include (1) mash diet + 230 mEq/kg (Mlow), (2) mash diet + 290
85 mEq/kg (Mhigh), (3) pellet diet + 230 mEq/kg (Plow), and (4) pellet diet + 290 mEq/kg (Phigh). Sows
86 were fed every morning and evening, with a feed intake of 2.5 kg per day during gestation. After
87 farrowing, the allowance was gradually increased by 1 kg per day until reaching the maximum limit. All
88 diets were formulated using corn and soybean meal to meet or exceed the nutrient recommendations of
89 NRC [19] (Table 1) in accordance with a lactating sow feeding program. All precautions were taken to
90 ensure the reduced dEB does not compromise animal health and welfare as shown in the results. Sows
91 were housed in individual farrowing crates (2.14 m \times 2.15 m), each with designated spaces (2.14 m \times
92 2.15 m) on both sides for newborn piglets. Heat lamps were provided to keep the piglets warm. Standard
93 management procedures, including teeth clipping, tail docking, ear notching, and subcutaneous iron
94 dextran injections (1 mL per piglet) within 24 hours of birth, were followed. Sows had unrestricted access
95 to water throughout the experiment, while piglets were not provided with creep feed. Environmental
96 factors, including temperature and humidity, were monitored every five minutes using Tenmars
97 temperature/humidity data loggers (TM-305U, Tenmars Electronics Co., Neihu, Taiwan), which were
98 positioned at the level of the sow's head. The data loggers measured temperature with a tolerance of
99 $\pm 0.5^{\circ}\text{C}$ (resolution: 0.02°C) and humidity with an accuracy of $\pm 3.4\%$ (resolution: 0.2%). The
100 temperature humidity index (THI) was calculated as $\text{THI} = \text{temperature} - [0.55 - (0.0055 \times \text{humidity})] \times$
101 $(\text{temperature} - 14.5)$, and the THI and room temperature are shown in Fig. 1 and Fig. 2. The THI ranged
102 from 75.58 to 82.76 during the experimental period. Respiratory rates shown in Fig. 3 were measured by

103 observing flank movements over 60 second period and expressed as breaths per minute at 13:00,
104 following the methods of Brandt et al. [20].

105 **Sampling and chemical analysis**

106 **Sow and litter performance**

107 Each sow's body weight (BW) and backfat thickness were evaluated on d 112, at 24h postpartum,
108 and during weaning (d 133). The backfat thickness was also measured on the same days at 6.5 cm off the
109 midline at the 10th rib using an ultrasonic device (Agroscan A16, Angoulême, France). The leftover diets
110 in the feeder troughs were collected to calculate average daily feed intake (ADFI) during lactation,
111 farrowing, and at weaning to estrus intervals. Litter performance parameters, such as the number of
112 piglets born, number born alive, number weaned (day 21 of lactation), survivability percentage, litter
113 weight at birth, at weaning, as well as the piglet's weight at birth and weaning, were recorded.

114 **Diet and fecal analysis for nutrient digestibility**

115 One week before weaning, chromium oxide (0.24%) was incorporated into the diet as a non-
116 digestible inert marker. The diet was administered to all sows per replicate for 5 days, consisting of a 3-
117 days adaptation phase followed by 2 days of sampling, preceding nutrient evaluation on d 133. Faecal
118 samples were collected from each sow through gentle massage of the rectum. The harvested samples from
119 each pen were pooled and then dried using a forced-air drying oven at 60 °C for 72 h. The combined
120 samples were subsequently milled using a Thomas Model 4 Wiley Mill (Thomas Scientific, Swedesboro,
121 NJ, USA) with a 1-mm screen before being analyzed in triplicate for dry matter (DM) method 930.15,
122 AOAC 2007, crude protein (CP) method 990.03, AOAC 2007, ether extract (EE) method 942.05, AOAC
123 2007, calcium method 985.01, AOAC 2007, phosphorus method 975.03, AOAC 2007, and acid detergent
124 fiber method 973.18, AOAC 2007. Neutral detergent fiber content was determined by treating samples
125 with amylase, sodium sulfite, and a neutral detergent solution. The resulting residues were filtered using a
126 1.5 µm glass fiber filter. The chromium (Cr) concentration was analyzed using an automated
127 spectrophotometer (Jasco V-650, Jasco Corp., Tokyo, Japan) following the method described by Fenton
128 and Fenton [21]. Amino acid concentrations in feed samples were determined using high-performance
129 liquid chromatography (HPLC; Agilent 1260 series, Agilent Technologies, Waldbronn, Germany)
130 following acid hydrolysis, with methodological modifications based on Hosseindoust et al. [22]. Organic
131 matter was calculated by subtracting DM from ash content.

132 **Milk composition**

133 On the last day of the experiment (d 133), sows were given 1 mL of oxytocin (1 U/mL) to spur
134 milk production. Fresh milk samples of 20 mL were then manually collected from the functional teats of
135 all lactating sows in each replicate after wiping with alcohol ensuring no contamination from external
136 sources. The samples were immediately transferred to sterile containers and stored at 4°C. Prior to
137 analysis, each milk sample was thoroughly mixed to ensure homogeneity. A portion of the milk sample

138 (typically 15 mL) was then transferred into the sample cup of the Milko Scan 133B Analyser (Foss
139 Electric, Hillerød, Denmark). All samples were analyzed in duplicate to ensure accuracy and consistency
140 of results. The MilkoScan 133B Analyzer was calibrated according to the manufacturer's guidelines using
141 the provided standard calibration solutions for fat, protein, lactose, total solids, and solids-not-fat. Regular
142 calibration checks were performed to ensure the accuracy of the readings. The milk samples were placed
143 in the sample chamber of the Analyzer which uses near-infrared spectroscopy for measuring the milk
144 compositions. Each sample was measured individually, and the results were automatically recorded [23].

145 **Blood inflammatory cytokine, antioxidant status, and gut integrity**

146 On d 133, 15 mL blood samples were collected from all sows via jugular vein puncture between
147 08:30 and 09:30 using K₂ EDTA-coated vacutainer tubes (Becton Dickinson, Franklin, NJ, USA) to
148 prevent clotting and minimize cytokine release from blood cells. Immediately after collection, the tubes
149 were gently inverted 5–10 times to ensure proper mixing with the anticoagulant. Samples were then
150 placed on ice and transported to the laboratory for further processing. To obtain plasma, blood samples
151 were centrifuged at 3,000 × g for 15 minutes at 4°C within 30 minutes of collection. Following
152 centrifugation, the plasma was carefully pipetted into sterile microcentrifuge tubes, ensuring no
153 disturbance of the buffy coat to prevent contamination with cellular components. Part of the plasma was
154 used for evaluating tumour necrosis factor-alpha (TNF-α), Interleukin-10 (IL-10), and IL-1β determined
155 using ELISA kits (MBS262753, MBS2513043, and MBS260684, Mybiosource, San Diego, CA, USA)
156 according to the manufacturer's instructions. Part of the plasma was used for measuring total antioxidant
157 capacity (TAC), superoxide dismutase (SOD), and malondialdehyde (MDA) (MBS2611923, MBS265304
158 and MBS742540 Mybiosource, San Diego, CA, USA). The remaining plasma was employed for
159 evaluating zonulin and occluding, ELISA kits (MBS2607498, and MBS740246 Mybiosource) were
160 considered following the manufacturer's instructions. All the absorbance was measured at 450 nm using a
161 microplate reader.

162 **Hair cortisol**

163 The method for measuring hair cortisol was outlined by Tajudeen et al. [24]. Briefly, freshly
164 grown hair from individual sows was collected for cortisol analysis. Prior to this, a section of dorsal hair
165 from the sows was removed at d 133. The hair samples were washed three times with isopropanol and
166 then dried in a vacuum dryer at 35°C. They were then placed in an EML plastic tube containing steel
167 pellets and processed using a bead beater (tacoTMPrep, 50/60 Hz 2A, GeneReach, Taichung, Taiwan).
168 Cortisol was extracted from the hair by methanol following crushing at the Biotechnology Corp, Taiwan.
169 The cortisol concentration in the extracted samples was measured using an ELISA kit (ADI-900-071,
170 Enzo Life Sciences, Farmingdale, NY, USA).

171 **Salivary pH**

172 We started by calibrating the pH meter (Sevenmulti, Mettler Toledo, Columbus, Ohio) using pH
173 4, 7, and 10 buffers, following the manufacturer's instructions. The electrode was immersed in each

174 buffer, allowing the meter to stabilize and adjust the readings accordingly. After calibration, the probe
175 was rinsed with distilled water to avoid cross-contamination. Saliva samples were then collected from
176 each sow using a sterile method (from the oral cavity) and transferred into clean containers. Briefly, the
177 sow's oral cavity was gently swabbed using a sterile cotton swab, ensuring that the swab did not contact
178 external surfaces such as the snout or feeding trough to avoid contamination. The collected saliva was
179 immediately transferred into sterile polypropylene tubes and sealed to prevent environmental exposure.
180 All instruments and containers used were sterile and handled with disposable gloves to maintain sample
181 integrity. The pH probe was submerged into the saliva sample for 20 seconds to allow the pH to stabilize,
182 ensuring the probe was fully immersed but not in contact with the sides or bottom of the container. The
183 displayed pH value on the meter was recorded after stabilization.

184 **DNA extraction, 16S rRNA amplification and sequencing**

185 Faecal samples were obtained from all sows on lactation day 21 through rectal stimulation and
186 promptly preserved at -20°C in sterile 50 mL conical tubes. Genomic DNA was isolated from 250 μL of
187 each faecal sample using the QIAamp PowerFecal Pro DNA Kit (Qiagen, Hilden, Germany), adhering to
188 the manufacturer's guidelines to maximize yield and minimize contamination. The extracted DNA
189 samples were then stored at -20°C for subsequent analysis.

190 **16S rRNA Gene Amplification and Sequencing**

191 The V3–V4 hypervariable regions of the bacterial 16S rRNA gene were amplified using specific
192 primers and processed for sequencing according to the standard Illumina 16S metagenomic library
193 preparation protocol (Illumina, San Diego, CA, USA; Part No. 15044223 Rev. B). The resulting PCR
194 amplicons were purified, adjusted to equimolar concentrations, pooled, and sequenced on an Illumina
195 MiSeq platform using a 2×300 bp paired-end sequencing strategy.

196 **Sequence Processing and Taxonomic Classification**

197 Raw sequencing reads were assessed for quality, trimmed, and de-multiplexed using custom Perl
198 scripts to enhance read accuracy and reduce sequencing artifacts. Processed sequences were analysed
199 using Quantitative Insights into Microbial Ecology (QIIME2, version 2023.7). Amplicon Sequence
200 Variants (ASVs) were identified through DADA2, and taxonomic classification was conducted using the
201 SILVA 138-99 reference database. To account for variability in sequencing depth, a single rarefaction
202 was applied to normalize ASVs to 18,911 reads per sample. This ensured unbiased comparisons across
203 samples.

204 **Microbial Diversity and Statistical Analysis**

205 Alpha diversity metrics, including the Chao1 richness estimator and Shannon diversity index,
206 were calculated in QIIME2. Beta diversity was assessed using Bray-Curtis dissimilarity, unweighted
207 UniFrac, and weighted UniFrac distance metrics. Principal Coordinate Analysis (PCoA) was performed to
208 visualize microbial community differences and was plotted using EMPeror software. Relative abundance
209 at the phylum, family, and genus levels were analysed to assess microbiome composition. The differential

210 abundance of bacterial taxa was evaluated using linear discriminant analysis effect size (LEfSe) to
211 identify key microbial shifts [25.26].

212 **Statistical Analyses**

213 Data were compiled in Excel and analyzed using a 2×2 factorial arrangement of treatments within
214 a completely randomized design. The main effects of dietary feed forms, dEB levels, and their interaction
215 were evaluated using the MIXED procedure in SAS (version 9.1; SAS Institute, Cary, NC).

$$216 Y_{ijk} = \mu + A_i + B_j + (AB)_{ij} + R_k + \varepsilon_{ijk}$$

217 where Y_{ijk} is the observed response variable, μ is the overall mean, A_i is the fixed effect of feed
218 form, B_j is the fixed effect of dEB level, $(AB)_{ij}$ is the interaction between feed form and dEB, R_k is the
219 random effect of block (experimental week), and ε_{ijk} is the residual error assumed to be normally
220 distributed. Individual pigs were considered the experimental unit for all analyses.

221 Individual sows served as the experimental unit for all analyses. When data violated parametric
222 assumptions, nonparametric analyses were performed using the Kruskal–Wallis test, with Bonferroni
223 corrections applied to adjust for multiple comparisons and minimize type I errors. ASV (Amplicon
224 Sequence Variant) features were statistically analysed using STAMP software (version 2.1.3, available at
225 <https://beikolab.cs.dal.ca/software/STAMP>). β -diversity analysis was conducted through Principal
226 Coordinate Analysis (PCoA) based on Bray–Curtis distance matrices to visually represent group
227 differences. Microbial community structures were compared using permutational multivariate analysis of
228 variance (PERMANOVA). Variations in individual ASVs across taxonomic levels were identified
229 through pairwise Kruskal-Wallis H-tests in STAMP and visualized using graphical representations.

230

231 **Results**

232 **Sow performance**

233 The effects of feed forms and dEB levels on sow performance are presented in Table 2. There
234 were no significant differences in sow BW and backfat thickness during d 112, 24h postpartum, and at
235 weaning in all the dietary treatments. However, sows fed pellet feed forms Plow and Phigh, and higher
236 dEB Mhigh and Phigh in diet had increased ($p < 0.001$) ADFI compared with Mlow.

237 **Litter performance**

238 The effects of feed forms and dEB levels on litter performance are presented in Table 3. There
239 was no significant difference in litter size including total born, born alive, weaned, and survivability
240 percentage. There was also no significant difference in litter weight at birth, at weaning, and piglet weight
241 at birth. However, piglet weight at weaning was higher ($p = 0.001$) in Mhigh and Phigh compared with
242 Mlow and Plow.

243 **Nutrient digestibility and milk composition**

244 The effects of feed forms and dEB levels on nutrient digestibility and milk composition of sows
245 are presented in Table 4 and Table 5. The digestibility of DM was higher ($p = 0.022$) in feed forms Plow
246 and Phigh compared with Mlow and Mhigh. There was no significant difference in CP and EE in all
247 dietary treatments (Table 4). In Table 5, there was no significant difference in milk fat, protein, lactose,
248 total solid, and solid not fat composition in all the dietary treatments.

249 **Inflammatory cytokine and antioxidant**

250 The effects of feed forms and dEB levels on inflammatory cytokine and antioxidants of sows are
251 presented in Table 6 and Table 7. The TNF- α was lower ($p < 0.001$) in pellet feed forms Plow, Phigh, and
252 higher dEB Mhigh and Phigh ($p = 0.010$), compared with Mlow, with significant interactions ($p = 0.013$)
253 in feed forms and dEB. The IL-1 β was lower ($p < 0.001$) in pellet feed forms Plow and Phigh compared
254 with Mlow and Mhigh. There was no significant difference in IL-10 (Table 6). In Table 7, SOD was
255 higher ($p < 0.001$) in pellet feed forms Plow and Phigh compared with Mlow and Mhigh. There was no
256 significant difference in TAC and MDA in all dietary treatments.

257 **Gut integrity, hair cortisol, and salivary pH**

258 The effects of feed forms and dEB levels on gut integrity, hair cortisol, and salivary pH of sows
259 are presented in Table 8, Table 9, and Table 10. There was no significant difference in the zonulin and
260 occludin of sows (Table 8) in all treatments. In Table 9, the sow's hair cortisol was lower ($p = 0.048$) in
261 pellet feed forms Plow and Phigh compared with Mlow and Mhigh. In Table 10, there was no significant
262 difference in salivary pH of sows in all dietary treatments.

263 **Heat indicators**

264 The ambient temperature (blue line) ranged from 26.0 °C to 31.1 °C with an average value of
265 28.8 °C, while the THI (orange line) was below 70 °C (Fig. 1). There was no significant difference in
266 rectal temperature (Fig. 2), and respiratory rate (Fig. 3) throughout the experimental period.

267 **Alterations of gut microbiota diversity**

268 The effect of feed forms and dEB levels on alpha diversity (within-sample diversity) in lactating
269 sows is shown in Fig. 4. There was no significant difference observed in Chao1 and Shannon in all
270 treatments. In Fig. 5, there was a significant difference ($p = 0.027$) in Mlow vs Plow in the Unweighted
271 UniFrac (between-sample diversity). Lastly, as illustrated in Fig. 6, the relative abundance of microbial
272 taxa in the phylum level showed no difference in *Firmicutes*, *Bacteroidetes*, and *Spirochaetota*. The
273 microbial taxa at the family level showed higher *Lactobacillaceae* in Mhigh, while Phigh and Plow
274 followed the same trend. *Clostridiaceae*, *Erysipelotrichaceae*, *Peptostreptococcaceae*, *Lachnospiraceae*,
275 *Prevotellaceae*, *Christensenellaceae*, *Oscillospiraceae*, *Ruminococcaceae*, and *Spirochaetaceae* were not
276 affected by the treatments. In the genus level, *Lactobacillus* was higher in Mhigh, with Phigh and Plow
277 following the same trend. *Turicibacter* was higher in Mlow, while *Prevotella* was more obvious in Plow,

278 and lower in Phigh, Mhigh, and Mlow. *Clostridium*, *Romboutsia*, *Terrisporobacter*, *Christensenellaceae*,
279 *Treponema*, *NK4A214* group, and *Ruminococcus* were not affected.

280

281

Discussion

282 This study evaluated the effects of feed form and dEB levels on sow performance, immune status,
283 gut health, and microbiota composition during lactation. While sow BW and backfat thickness remained
284 unaffected, sows fed pelleted diets (Plow and Phigh) and those receiving higher dEB (Mhigh and Phigh)
285 exhibited significantly greater ADFI, suggesting nutrient partitioning during lactation. Even though
286 pelleted diets and higher dEB improved ADFI, the additional nutrients were likely directed toward
287 sustaining milk production and supporting piglet growth rather than maternal tissue retention. Under HS
288 conditions, sows mobilize body reserves to meet the high energy demands of lactation, and this metabolic
289 prioritization often prevents detectable differences in body weight and backfat thickness despite higher
290 feed intake [4, 27, 33]. Thus, the benefits of improved intake were manifested primarily in litter
291 performance and physiological resilience rather than in maternal body condition. In addition, higher feed
292 intake during lactation is important, as it directly influences maternal energy status and nutrient
293 availability [23]. Consistent with improved maternal intake, piglets from the Mhigh and Phigh groups had
294 significantly higher weaning weights, despite the indifferences in litter size or birth weights. This
295 indicates that the elevated dEB in lactation diets may have enhanced nutrient transfer to offspring,
296 potentially by improving nutrient absorption and flow [27]. Although milk composition (fat, protein,
297 lactose, and solids) did not differ among treatments, greater DM digestibility was observed in sows fed
298 pelleted diets (Plow and Phigh), which may explain the improved growth performance of piglets. The
299 improved nutrient digestibility likely enhanced the efficiency of nutrient transfer to offspring during
300 lactation. Feed form is known to influence nutrient utilization, with pelleted diets often enhancing nutrient
301 availability through reduced sorting and improved digestibility [28]. The lack of variation in milk
302 composition suggests that while feed form and dEB levels may influence the quantity of milk or its
303 physiological impact as reflected in piglet growth, they do not significantly alter its nutritional profile.
304 Such stability in milk composition is beneficial, as it ensures that piglets receive consistent nutrient
305 profiles during the suckling phase, regardless of maternal dietary modifications. Taken together, our
306 findings indicate that both feed form (pelleting) and higher dEB effectively improved sow performance
307 and feed intake under HS. The tendency for interactive effects on ADFI and piglet weaning weight
308 highlights the potential benefits of combining pelleted diets with higher dEB.

309 The immune-modulating effects of the dietary interventions were demonstrated by the reduced
310 levels of pro-inflammatory cytokines TNF- α and IL-1 β in sows fed pelleted diets and those receiving
311 higher dEB. As key mediators of inflammation, the downregulation of these cytokines is typically linked
312 to a more regulated immune response, improved gut integrity, and reduced oxidative stress [29,30]. These

313 effects may be attributed to the combined physiological benefits of pellet processing and electrolyte
314 balance. High dEB diets enhance systemic buffering capacity, potentially reducing gastric acidity that
315 protects the non-glandular region of the stomach, where ulcers commonly occur [17,18,31]. Concurrently,
316 pelleted diets promote consistent feed intake and uniform gastric emptying, helping to minimize
317 fermentation-induced acid accumulation and mucosal irritation [13,28]. Such anti-inflammatory state may
318 support improved nutrient absorption and productivity during the metabolically demanding HS and
319 lactation period. This is further supported by increased SOD activity in sows fed pelleted diets, indicating
320 enhanced antioxidant defense. Moreover, the significant interaction observed for TNF- α suggests a
321 synergistic effect when pelleted feed is combined with higher dEB.

322 Although markers of gut barrier integrity (zonulin and occludin) were not significantly affected,
323 sows fed pelleted diets had lower hair cortisol concentrations, which may reflect reduced chronic stress
324 during lactation. Our findings align with improved feed intake and inflammatory status in pelleted feed
325 which could have practical implications for sow welfare [32]. While direct studies on pelleted feed
326 reducing stress in lactating sows are limited, it is recognized that improved feed intake and nutrient
327 digestibility can alleviate metabolic stress [33]. Enhanced nutrient absorption supports better energy
328 balance, which may contribute to reduced physiological stress responses [34,35]. For lactating sows, a
329 THI value below 72 is generally considered thermoneutral, 72–78 indicates mild heat stress, 79–88
330 indicates moderate stress, and values above 88 indicate severe stress [20]. During the experimental period,
331 the THI ranged from 75.58 to 82.76, which corresponds to mild to moderate heat stress conditions.
332 Salivary pH and physiological heat stress indicators (rectal temperature and respiratory rate) did not differ
333 between treatments, and the ambient THI remained within the thermoneutral range, indicating that
334 environmental heat load was unlikely to confound treatment effects. The tendency for interactive effects
335 observed in hair cortisol further indicates a synergistic benefit of combining pelleted feed with higher
336 dEB.

337 Microbial diversity is a crucial aspect of animal nutrition as it is linked to better overall health,
338 including nutrient absorption, immune function, and disease prevention [36]. Our microbial diversity
339 analysis revealed no significant differences in alpha diversity across treatments, suggesting that microbial
340 richness and evenness were maintained. However, beta diversity analysis (Unweighted UniFrac) revealed
341 distinct microbial compositions between Mlow and Plow, suggesting that feed form influenced microbial
342 structure even in the absence of major diversity shifts. At the family and genus levels, the relative
343 abundance of *Lactobacillaceae* and *Lactobacillus* was higher in Mhigh, with similar trends in Phigh and
344 Plow, possibly contributing to improved gut health and anti-inflammatory responses [37]. *Turicibacter*,
345 which has been associated with immune activation and oxidative stress [38,39], was elevated in Mlow,
346 aligning with higher inflammatory markers in this group. Conversely, *Prevotella* was most abundant in
347 Plow, a genus often linked to fiber fermentation and carbohydrate metabolism [40], although its role is
348 context-dependent and requires species-level interpretation.

349 In conclusion, these findings suggest that the interaction between pelleted feed form and higher dEB
350 levels (Phigh) emerged as the most effective result during lactation by improving feed intake, litter
351 performance, anti-inflammatory responses, antioxidant status, and influence gut microbial composition
352 without negatively impacting milk composition or gut integrity. These outcomes support the use of pellet
353 processing and high dEB as complementary strategies to enhance sow productivity and health in lactation
354 period during heat stress.

355

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Tables

Table 1. Formula and chemical composition of experimental basal diets (as-fed basis)

dEB	Mlow	Plow	Mhigh	Phigh
Ingredient (%)				
Corn	57.99	57.99	57.73	57.73
Soybean meal	28.14	28.14	28.27	28.27
Wheat	5.00	5.00	5.00	5.00
Sugar	3.00	3.00	3.00	3.00
Animal fat	3.30	3.30	3.42	3.42
Choline	0.05	0.05	0.05	0.05
Limestone	0.78	0.78	0.78	0.78
Di calcium phosphate	0.87	0.87	0.87	0.87
Salt	0.52	0.52	-	-
NaHCO ₃	-	-	0.53	0.53
Vitamin premix ¹	0.15	0.15	0.15	0.15
Mineral premix ²	0.15	0.15	0.15	0.15
Phytase	0.05	0.05	0.05	0.05
Total	100	100	100	100
Chemical composition³				
Metabolizable energy ⁴ , (kcal/kg)	3,300	3,300	3,300	3,300
Crude protein (%)	18.00	18.00	18.00	18.00
Ether extract (%)	5.35	5.35	5.43	5.43
Lysine	1.00	1.00	1.00	1.00
Methionine + Cysteine	0.58	0.58	0.58	0.58
Threonine	0.68	0.68	0.68	0.68
Tryptophan	0.20	0.20	0.20	0.20
Calcium (%)	0.76	0.76	0.76	0.76
Phosphorus (%)	0.65	0.65	0.65	0.65
Potassium (%)	0.95	0.95	0.96	0.96
Sodium (%)	0.20	0.20	0.20	0.20
Chlorine (%)	0.28	0.28	0.14	0.14
EB (mEq/kg)	258	258	250	250
dEB (mEq/kg)	230	230	290	290
Analyzed composition⁵				
Gross energy (kcal/kg)	4,352	4,376	4,354	4,350
Crude protein (%)	18.11	18.32	18.24	18.22
Ether extract (%)	5.42	5.45	5.50	5.49
Neutral detergent fiber	10.45	10.58	10.26	10.85
Acid detergent fiber	3.76	4.01	3.69	3.85
Ash	5.13	5.21	5.06	5.13
Lysine	1.05	1.10	1.06	1.04
Methionine + Cysteine	0.59	0.60	0.58	0.61
Threonine	0.69	0.72	0.74	0.72
Tryptophan	0.23	0.22	0.21	0.24
Calcium (%)	0.80	0.79	0.81	0.82
Phosphorus (%)	0.65	0.67	0.69	0.66

Mlow, mash diet + 230 mEq/kg; Plow, pellet diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

¹Supplied per kilogram of vitamin premix: 12,000,000 IU vitamin A, 2,400,000 IU vitamin D3, 132,000 IU vitamin E, 1,500 mg vitamin

K3, 3,000 mg vitamin B1, 11,250 mg vitamin B2, 3,000 mg vitamin B6, 45 mg vitamin B12, 36,000 mg pantothenic acid, 30,000 mg

niacin, 600 mg biotin, 4,000 mg folic acid.

²Supplied per kilogram of mineral premix: 80,000 mg Fe, 170 mg Co, 8,500 mg Cu, 25,000 mg Mn, 95,000 mg Zn, 140 mg I, 150 mg Se

³The presented numbers were calculated based on NRC (2012)

⁴The metabolizable energy (ME) was calculated based on NRC (2012).

⁵Based on AOAC (2007) and HPLC

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Table 2. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on sow performance in lactating sows under heat stress

Feed form	Mash		Pellet		SEM	Feed	<i>p</i> -value	
	Mlow	Mhigh	Plow	Phigh			dEB	Interaction
BW, kg								
D 112	245.53	238.84	243.06	239.89	5.18	0.846	0.186	0.634
24h postpartum	224.12	220.87	223.50	214.77	5.43	0.387	0.127	0.480
Weaning (D 133)	206.65	204.10	206.69	197.87	5.35	0.418	0.142	0.413
Loss during lactation	17.47	16.76	16.81	16.89	0.81	0.652	0.582	0.494
BF, mm								
D 112	21.44	21.88	21.73	21.44	0.36	0.790	0.775	0.159
24h postpartum	21.34	21.73	21.59	21.18	0.36	0.567	0.976	0.124
Weaning (D 133)	18.47	18.72	18.60	18.12	0.35	0.346	0.654	0.147
Loss during lactation	2.86	3.00	2.99	3.06	0.11	0.250	0.180	0.645
ADFI, kg/d								
During lactation	5.40	5.47	5.61	5.89	0.08	<0.001	<0.001	0.079
Farrowing duration, h								
	4.48	4.53	4.46	4.54	0.12	0.925	0.441	0.900
WEI, d								
	6.50	5.70	5.90	5.80	0.60	0.560	0.297	0.416

SEM, standard error of means; BW, body weight; BF, backfat thickness; ADFI, average daily feed intake; WEI, weaning to estrus intervals.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

Table 3. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on litter performance in lactating sows under heat stress

Feed form	Mash		Pellet		SEM	Feed	<i>p</i> -value	
	Mlow	Mhigh	Plow	Phigh			dEB	Interaction
Litter size, n								
Total born	12.40	12.10	12.50	12.30	0.62	0.736	0.574	0.910
Born alive	11.20	11.00	11.00	10.90	0.45	0.640	0.640	0.876
Weaned	10.50	10.20	10.30	10.20	0.35	0.687	0.422	0.687
Survivability of piglets, %	93.84	92.85	93.94	93.85	1.86	0.677	0.684	0.735
Litter weight, kg								
At birth	14.91	14.46	14.50	14.34	0.46	0.422	0.345	0.648
At weaning	59.19	58.26	57.96	60.26	1.85	0.771	0.601	0.223
Piglet weight, kg								
At birth	1.33	1.32	1.32	1.32	0.03	0.788	0.767	0.804
At weaning	5.64	5.71	5.63	5.92	0.08	0.071	0.001	0.051

SEM, standard error of means.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

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Table 4. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on nutrient digestibility in lactating sows under heat stress

Feed form	Mash		Pellet		SEM	<i>p</i> -value		
	Mlow	Mhigh	Plow	Phigh		Feed	dEB	Interaction
DM	86.86	86.73	88.58	88.62	1.07	0.022	0.949	0.908
CP	87.22	87.16	89.05	89.15	1.54	0.088	0.983	0.940
EE	84.78	84.81	86.69	86.25	1.26	0.068	0.819	0.797

SEM, standard error of means; DM, dry matter; CP, crude protein; EE, ether extract.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

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Table 5. The effects of feed processing and sodium bicarbonate (NaHCO_3) supplementation on milk composition in lactating sows under heat stress.

Feed form	Mash		Pellet		SEM	<i>p</i> -value		
	Mlow	Mhigh	Plow	Phigh		Feed	dEB	Interaction
Fat	7.48	7.65	7.72	7.61	0.15	0.378	0.795	0.206
Protein	4.87	5.06	4.95	4.89	0.22	0.765	0.698	0.417
Lactose	8.43	8.58	8.75	8.60	0.61	0.693	0.992	0.727
Total solid	18.28	18.40	18.06	18.21	0.32	0.370	0.564	0.959
Solid not fat	11.31	11.89	11.86	11.51	0.37	0.746	0.653	0.184

SEM, standard error of means.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

Table 6. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on inflammatory cytokine in lactating sows under heat stress

Feed form dEB	Mash		Pellet		SEM	<i>p</i> -value		
	Mlow	Mhigh	Plow	Phigh		Feed	dEB	Interaction
TNF- α , pg/mL	120.19	119.89	110.78	96.70	3.71	<0.001	0.010	0.013
IL-10, pg/mL	64.61	62.16	63.21	64.06	2.16	0.871	0.603	0.287
IL-1 β , pg/mL	51.07	51.93	47.98	45.29	1.78	<0.001	0.473	0.167

SEM, standard error of means; TNF- α , tumour necrosis factor- α ; IL-10, interleukin-10; IL-1 β , interleukin-1 β .

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

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Table 7. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on antioxidant in lactating sows under heat stress

Feed form	Mash		Pellet		SEM	<i>p</i> -value		
	Mlow	Mhigh	Plow	Phigh		Feed	dEB	Interaction
TAC, mmol/L	0.49	0.50	0.47	0.48	0.08	0.737	0.792	0.993
SOD, ng/mL	33.61	33.10	35.97	38.15	1.37	<0.001	0.398	0.174
MDA, nmol/mL	1.48	1.47	1.53	1.46	0.09	0.810	0.573	0.671

SEM, standard error of means; TAC, total antioxidant capacity; SOD, superoxide dismutase; MDA, malondialdehyde.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

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Table 8. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on gut integrity in lactating sows under heat stress

Feed form	Mash		Pellet		SEM	<i>p</i> -value		
	Mlow	Mhigh	Plow	Phigh		Feed	dEB	Interaction
Zonulin, ng/mL	33.23	34.36	34.84	33.57	1.56	0.713	0.950	0.285
Occludin, ng/mL	5.45	5.55	5.51	5.28	0.51	0.783	0.864	0.654

SEM, standard error of means.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

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ACCEPTED

Table 9. The effects of feed processing and sodium bicarbonate (NaHCO_3) supplementation on hair cortisol in lactating sows under heat stress

Feed form dEB	Mash		Pellet		SEM	<i>p</i> -value		
	Mlow	Mhigh	Plow	Phigh		Feed	dEB	Interaction
Hair cortisol, pg/mg	165.71	161.32	154.67	151.85	7.08	0.048	0.013	0.090

SEM, standard error of means.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

ACCEPTED

Table 10. The effects of feed processing and sodium bicarbonate (NaHCO_3) supplementation on salivary pH in lactating sows under heat stress

Feed form dEB	Mash		Pellet		SEM	<i>p</i> -value		
	Mlow	Mhigh	Plow	Phigh		Feed	dEB	Interaction
Salivary pH	7.46	7.47	7.48	7.48	0.02	0.669	0.974	0.767

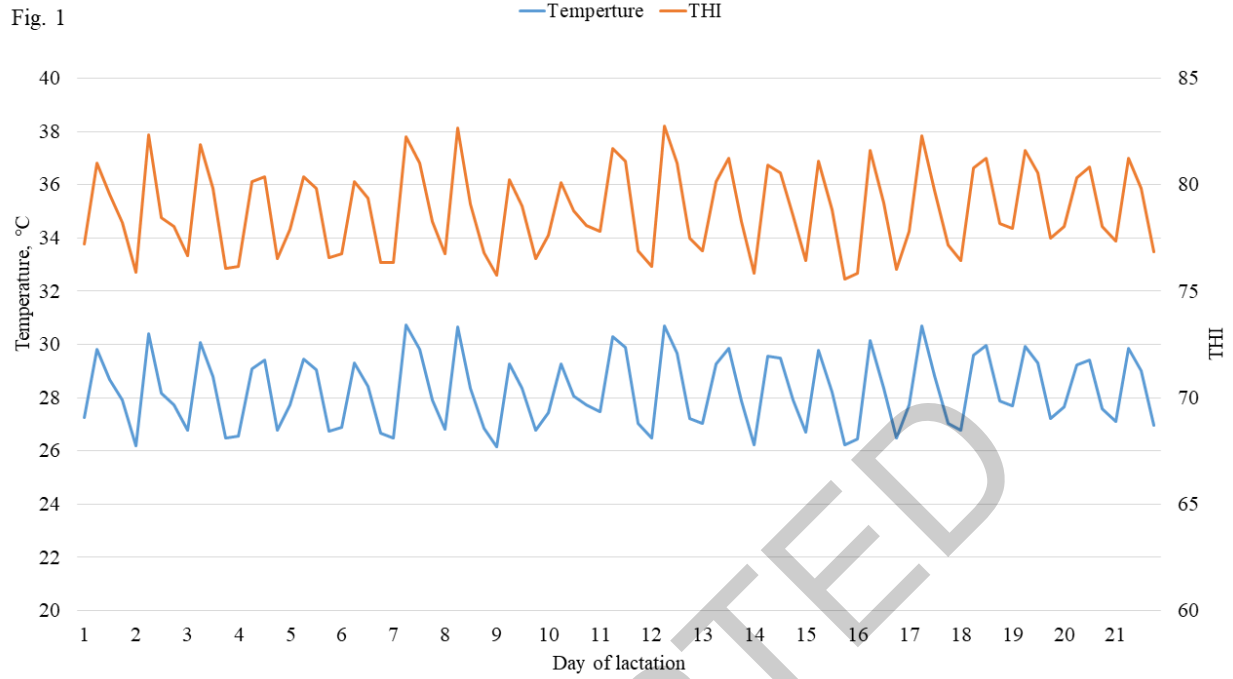
SEM, standard error of means.

Mlow, mash diet + 230 mEq/kg; Mhigh, mash diet + 290 mEq/kg; Plow, pellet diet + 230 mEq/kg; Phigh, pellet diet + 290 mEq/kg.

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Figure legends



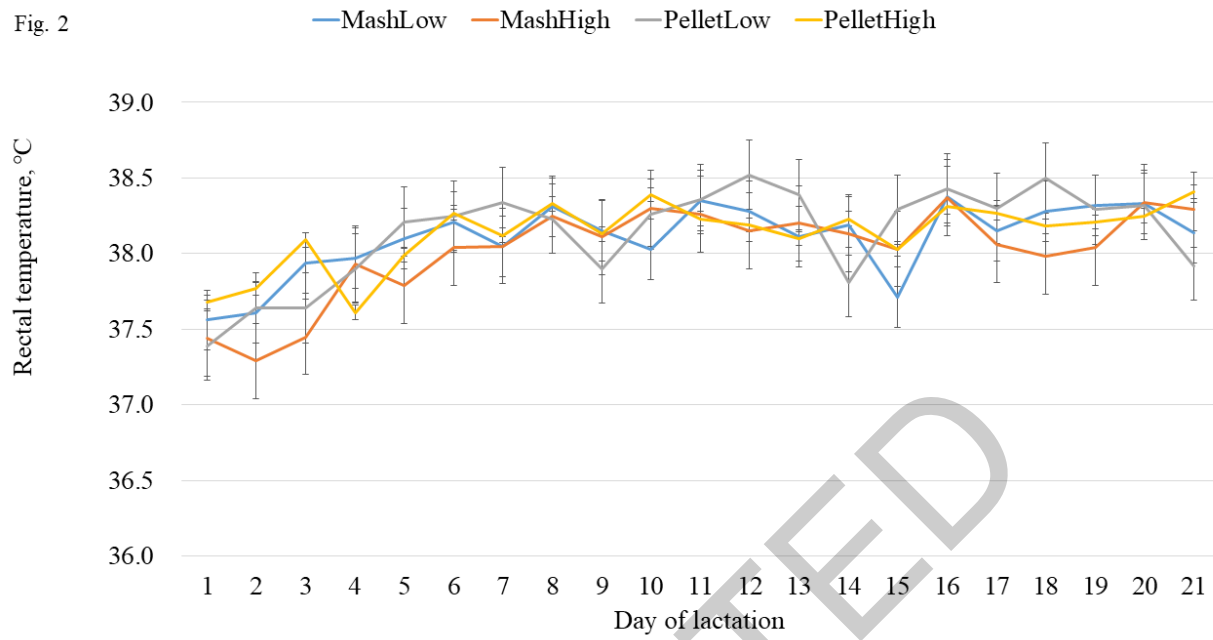
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Fig. 1. Ambient temperature (blue line) and temperature-humidity index (THI) (Orange line) during experimental period.

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Fig. 2



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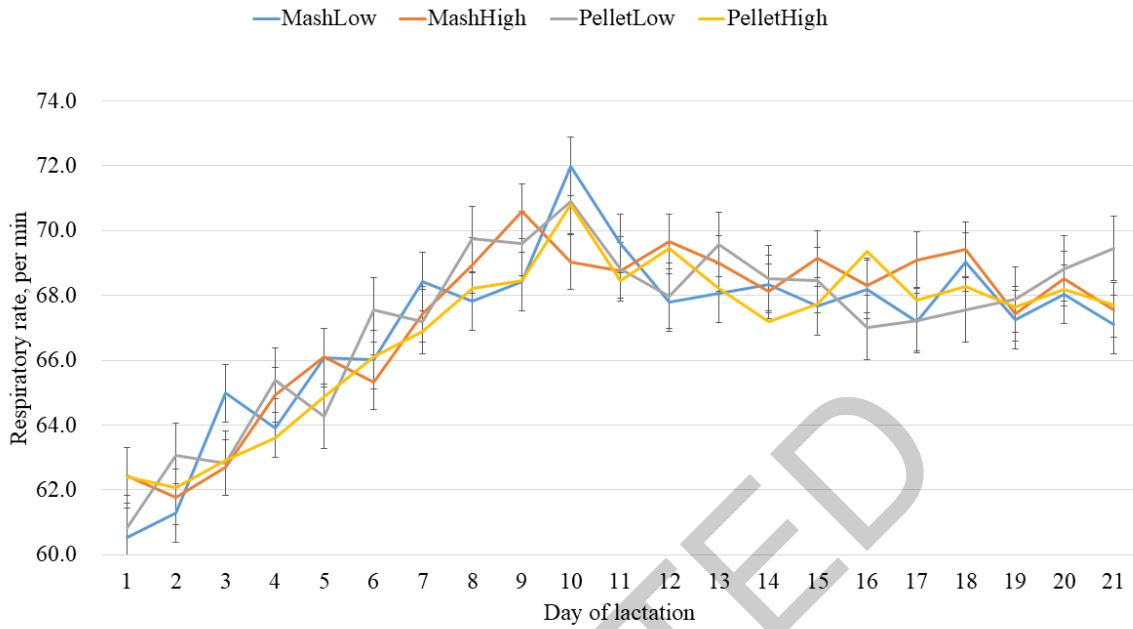
553 Fig. 2. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on
554 rectal temperature in lactating sows under heat stress. Asterisks (*) indicate statistical
555 significance ($p < 0.05$).

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Fig. 3



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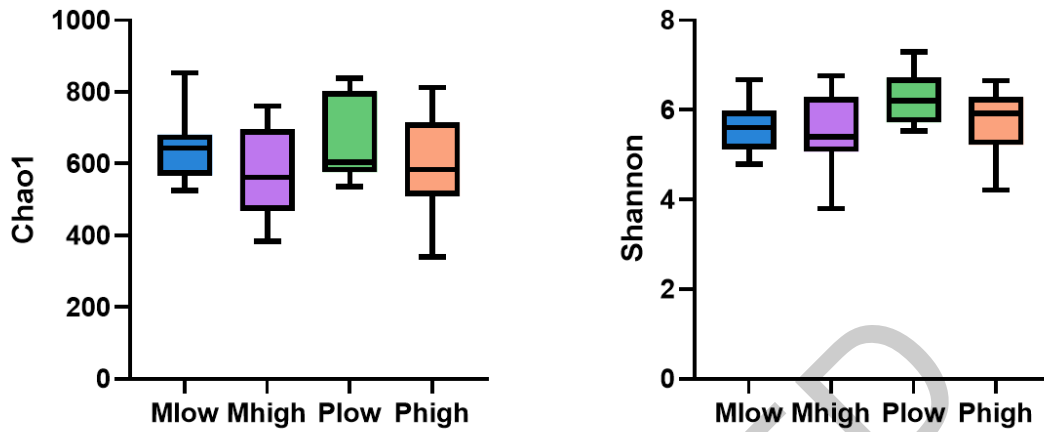
560 Fig. 3. The effects of feed processing and sodium bicarbonate (NaHCO_3) supplementation on
561 respiratory rate in lactating sows under heat stress. Asterisks (*) indicate statistical significance
562 ($p < 0.05$).

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564

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Fig. 4



Feed form	Mash		Pellet		SEM	Feed	<i>p</i> -value	
	Low	High	Low	High			dEB	Interaction
Chao1	641.18	584.96	664.30	592.37	56.44	0.704	0.118	0.845
Shannon	5.58	5.55	6.25	5.75	0.33	0.071	0.267	0.330

SEM, standard error of means; DM, dry matter; CP, crude protein; EE, ether extract.

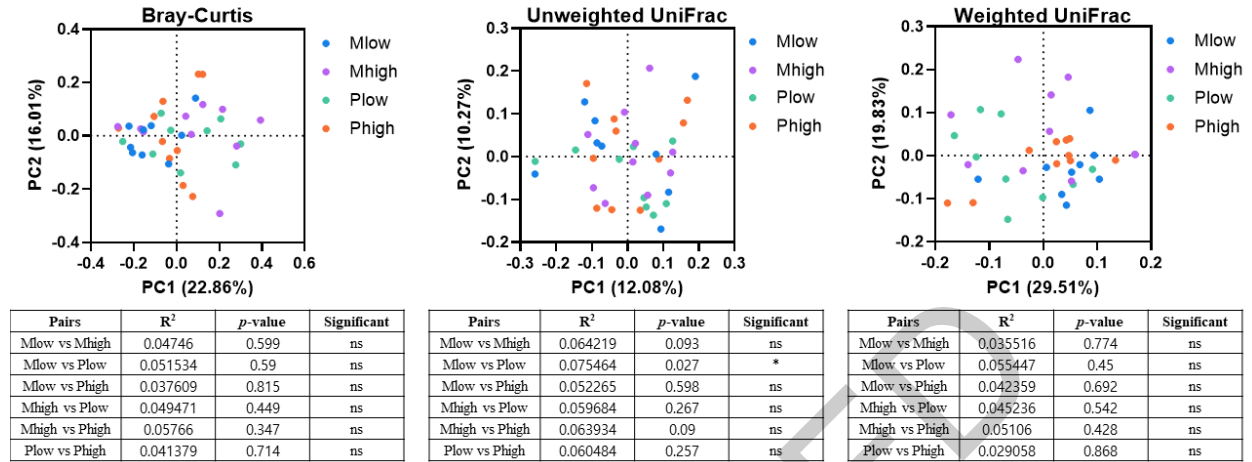
566

567 Fig. 4. The effects of feed processing and sodium bicarbonate (NaHCO₃) supplementation on

568 alpha diversity in lactating sows under heat stress

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Fig. 5

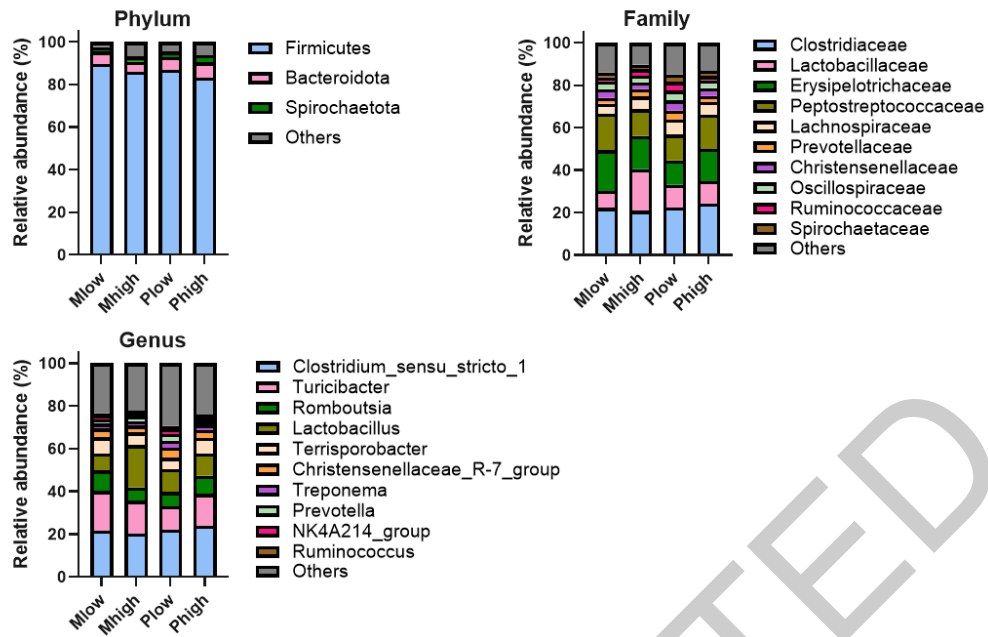


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572 Fig. 5. The effect of feed forms and dEB levels on the Unweighted UniFrac (between-sample
 573 diversity) in lactating sows

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Fig. 6



576

577 Fig. 6. The effect of feed forms and dEB levels on the relative abundance of microbial taxa in the
 578 phylum, family, and genus level in lactating sows

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