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Antibiotics Increase Gut Metabolism and Antioxidant Proteins and Decrease Acute Phase Response and Necrotizing Enterocolitis in Preterm Neonates

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Abstract

Background: The appropriate use of antibiotics for preterm infants, which are highly susceptible to develop necrotizing enterocolitis (NEC), is not clear. While antibiotic therapy is commonly used in neonates with NEC symptoms and sepsis, it remains unknown how antibiotics may affect the intestine and NEC sensitivity. We hypothesized that broad-spectrum antibiotics, given immediately after preterm birth, would reduce NEC sensitivity and support intestinal protective mechanisms.

Methodology/Principal Findings: Preterm pigs were treated with antibiotics for 5 d (oral and systemic doses of gentamycin, ampicillin and metromidazole; AB group) and compared with untreated pigs. Only the untreated pigs showed evidence of NEC lesions and reduced digestive function, as indicated by lowered villus height and activity of brush border enzymes. In addition, 53 intestinal and 22 plasma proteins differed in expression between AB and untreated pigs. AB treatment increased the abundance of intestinal proteins related to carbohydrate and protein metabolism, actin filaments, iron homeostasis and antioxidants. Further, heat shock proteins and the complement system were affected suggesting that all these proteins were involved in the colonization-dependent early onset of NEC. In plasma, acute phase proteins (haptoglobin, complement proteins) decreased, while albumin, cleaved C3, ficolin and transferrin increased.

Conclusions/Significance: Depressed bacterial colonization following AB treatment increases mucosal integrity and reduces bacteria-associated inflammatory responses in preterm neonates. The plasma proteins C3, ficolin, and transferrin are potential biomarkers of the colonization-dependent NEC progression in preterm neonates.

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Introduction

Intestinal microbiota, prematurity and inappropriate enteral feeding are regarded as three key risk factors for the onset and progression of necrotizing enterocolitis (NEC), a serious intestinal inflammatory disease in preterm infants with high morbidity and mortality [1]. The crucial role of intestinal microbiota has been documented in many studies, including in our own studies on germ-free, fetal or postnatal immature pigs that are protected against NEC [2]. The intestinal microbiota in preterm neonates is less diverse than in term neonates, especially when delivered by caesarean section [2], and this may predispose the gut to pathogenic E. coli, Clostridium, Klebsiella and Bacteroides species [2–4]. Overgrowth of these pathogenic species triggers inappropriate inflammatory processes in the immature intestine which sensitizes to further translocation of pathogenic bacteria and toxins, leading to sepsis and necrosis. Although the intestinal commensal microbiota plays a crucial role in the onset and progression of NEC, no single causative pathogenic microbial species has been identified [5].

Antibiotic regimens in clinical neonatology are highly variable and empirical and mainly used with the aim to prevent and treat systemic sepsis. Antibiotics such as ampicillin plus cefotaxime or aminoglycoside, clindamycin and/or metronidazole have been recommended for NEC treatment in the USA [6,7], while penicillin, gentamicin and metronidazole are sometimes used in the UK [8]. Molecular profiling of infant fecal microbial communities after such antibiotics treatment shows dramatic reductions in the total bacterial densities and alterations in population composition [6].

The widespread use of broad-spectrum antibiotics in clinical neonatology has some obvious disadvantages. These include possible development of antibiotics-resistant microbes and the potential to induce an inappropriate delay in bacterial colonization and a microbiota composition that may predispose to NEC [4]. Despite these reservations, we believe that the widespread
therapeutic use of antibiotics in virtually all neonatology units justifies a renewed look at the possible benefits of a more controlled, prophylactic antibiotic treatment that delays gut microbial colonization. It is noteworthy that oral treatment with vancomycin or gentamycin has been associated with decreased incidence of NEC [9].

Studies in appropriate animal models of preterm birth and NEC may offer an opportunity to re-think the optimal time and mode of antibiotics treatment for newborn preterm infants. A high proportion of preterm pigs spontaneously develop diet- and colonization-dependent NEC lesions that are similar to those infants [11,12]. We hypothesized that immediate postnatal treatment of preterm pigs with broad-spectrum antibiotics would reduce the overall gut bacterial density and prevent bacterial-induced deficits in cellular proteins important for early NEC progression. In our previous studies, we adopted gel-based proteomics to detect the expression change of hundreds of different proteins in response to feeding, bacterial colonization and NEC [11,12]. These studies served as the background to make the interpretation of the proteomic data less meaningful and indicate intestinal proteome of NEC pathology rather than initial events of NEC progression. According to our macroscopic NEC criteria, untreated pigs showed higher NEC incidence than AB pigs (6/6 vs. 0/6, p<0.05) and higher tissue NEC score specifically in the middle intestine (median 2 vs. 1, Mann-Whitney test, p<0.05). Representative hematoxylin and eosin (HE) stained histological slides of the middle small intestine in the AB and the untreated pigs are shown in Figure 1. The healthier state of the AB intestines was indicated by higher villi, absence of hemorrhage and no separation of different layers (Figure 1C), whereas, the untreated pigs showed various features related to NEC in different individual pig from villous atrophy, hemorrhage (Figure 1A) to separation of mucosa layers (Figure 1B).

Small intestine weight (g) over body weight (kg) (Figure 2A), mucosa portion of intestinal segments (Figure 2B), villus height (Figure 2C) were significantly higher in AB pigs (p<0.01), whereas there was no significant difference in crypt depth between AB and untreated pigs (Figure 2D). Activities of lactase (p = 0.11), aminopeptidase N (ApN, p = 0.08, Figure 2E) and aminopeptidase A (ApA, p<0.01, Figure 2F) were higher, while maltase (p = 0.06) and dipeptidylpeptidase IV (DPPIV) activities were lowered in AB pigs. Significantly lower bacterial number (p<0.001) was observed in the caecum contents of AB pigs compared with untreated pigs, both aerobes (0.3±0.1 vs. 7500±1400, ×10⁶) and anaerobes (0.3±0.1 vs. 7600±1400 ×10⁶) using call blood agar culturing. All the bacteria found in the cultures were gram-positive species.

Intestinal Proteomics

Figure 3A and B shows representative intestinal proteomes of the AB and the untreated pigs. There were 53 differentially expressed protein spots that were successfully identified. Table 1 shows a descriptive summary of the identified proteins, including spot numbers (circled in Figure 3A, B), protein name, GeneInfo identifier, expression quantity, expression change the identified proteins. The spots were classified into 13 groups according to their major physiological functions, as related to heat shock proteins, pathogen response, antioxidant, complement system, protein synthesis, processing and degradation, carbohydrate metabolism, mRNA metabolism, amino acid metabolism, fatty acid metabolism, pyrimidine metabolism, iron homeostasis, intracellular traffic, ion channel, cytoskeleton and cell mobility, and secretory proteins. The biological functions of the identified proteins and their proposed role in mediating the physiological and clinical effects of AB treatment are discussed in the Discussion section.

Plasma Proteomics

Untreated pigs showed higher total protein content in plasma (p<0.05), likely reflecting a higher degree of intestinal water loss and dehydration during feeding, relative to AB pigs. Twenty-two protein spots were identified (Figure 3). Four proteins appeared at different positions on 2-DE gels, including complement component, haptoglobin, fibrinogen, and albumin. Descriptive information and the expression conditions of these spots are shown in Table 2 with positions of the spots indicated in Figure 3 C and D.

Western-blot

The expression change of four selected proteins was further validated by Western blot (Figure 4). Laminin receptor (Figure 4A), pyrophosphatase 1 (Figure 4B), HSPB1 (Figure 4C) and haptoglobin (Figure 4D) all showed significantly reduced levels in the AB pigs, relative to the untreated pigs (p<0.05).

Discussion

Treatment with systemic antibiotics is widely used for preterm infants as treatment against neonatal sepsis, or as a part of the medical intervention against NEC together with withdrawal of enteral feeding [6–9,13]. However, treatment protocols vary widely among clinics and there is currently no consensus regarding the optimal neonatal antibiotics regimen to simultaneously prevent sepsis, NEC, bacterial dyscolonization and growth of antibiotics-resistant bacteria [6–9,14,15]. Antibiotics are most commonly given intravenously because intestinal immaturity and dysmotility may impair absorption of orally administered antibiotics. Regardless of delivery route, antibiotics will affect both the circulation and the gut environment, albeit in a product- and time-dependent manner [5,9]. In this study, we chose to treat preterm pigs from birth with both intravenous and oral antibiotics to prove our hypothesis that depressed gut colonization would prevent the immature intestine from the potential damaging effects of a high density of colonizing bacteria. In our preterm pig model, we have consistently found that the sensitivity to NEC lesions increase shortly after the transition to full enteral formula feeding, concomitantly with a surge in bacterial density both in the
intestinal lumen and along mucosal surfaces [10,16]. We aimed to show benefits of reducing gut bacterial density at this critical time. Two days after the transition to full enteral feeding, we identified a large number of intestinal proteins that were differentially expressed between AB and the untreated pigs. Collectively, the nature of these proteins suggests that AB treatment supports changes in the expression of proteins related to tissue structure, function and microbial defense that may help to prevent NEC, at
least short term. Further, we identified some plasma proteins that changed in response to the AB treatment and thus, could act as circulating biomarkers for the gut microbiota-related NEC development. Our follow-up studies have shown that AB-treated preterm pigs remain NEC-resistant for at least another week after completing AB treatment on day 5 after birth (NEC incidence: 0/6 vs. 9/10 and NEC score: median 1 vs. 3 in AB vs. untreated, Mann-Whitney test). Further studies are required to investigate long term effects of different early AB regimes on NEC and the developing immune system.

As the adaptive immune system is immature in preterm neonates, defense against exogenous pathogens is primarily handled by the innate immune system [17]. Complement component 3 (C3, spot 8618, Table 1; spot 8512, 9101, 9507, Table 2) that was lowered in the AB pigs, is an important constituent of the complement system, a part of innate immune system. The action of C3 is correlated with toll-like receptor (TLR) 4 and with intestinal ischemia-reperfusion [18], both of which have been suggested to play key roles in the bacteria-mediated NEC-inflammatory processes in infants and animal models [19–21]. C3 was also lowered in the plasma and linked with another

Figure 3. 2-DE proteome graphs of the mid small intestine and blood plasma. Panel A: small intestine, untreated; Panel B, small intestine, AB. Panel C: plasma, untreated; Panel D, plasma, AB. Spot number was assigned by the analysis software and correlated with the ones presented in Tables 1 and 2.
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Table 1. Intestinal proteins identified with differential expression between the AB and the untreated pigs (p<0.05).

| Spotno* | Protein Name | GI Idb | Protein Scorec | Expression Leveld (AB) | Expression Leveld (Untreated) | Fold Change (AB/Untreated) |
|---------|--------------|---------|----------------|------------------------|-------------------------------|-----------------------------|
| **Heat shock proteins** | | | | | | |
| 0818    | heat shock protein 90B1 | gi|27807263 | 186 | 25.8±6.2 | 80.0±15.1 | -3.1 |
| 2720    | heat shock protein 70A2 | gi|296439628 | 111 | 9.9±1.4 | 0 | + |
| 4002    | heat shock protein B1 | gi|55926209 | 198 | 22.2±3.9 | 74.7±15.5 | -3.3 |
| 4020    | heat shock protein B1 | gi|50916342 | 207 | 42.5±10.9 | 0 | + |
| **Pathogen response** | | | | | | |
| 6009    | regenerating islet-derived protein 3γ | gi|221325622 | 153 | 0 | 113.6±32.0 | - |
| **Antioxidation** | | | | | | |
| 7607    | catalase | gi|50979303 | 479 | 93.2±11.7 | 46.8±5.8 | +2.0 |
| **Complement system** | | | | | | |
| 8618    | complement C3 | gi|47522844 | 76 | 4.1±1.0 | 7.8±0.9 | -1.9 |
| **Protein synthesis, processing and degradation** | | | | | | |
| 0301    | laminin receptor precursor | gi|161761214 | 325 | 33.7±5.3 | 92.8±11.4 | -2.8 |
| 1009    | elongation factor 1-γ | gi|74001912 | 171 | 117.4±9.3 | 31.8±5.8 | +3.7 |
| 1402    | protein disulfide isomerase-related protein 5 | gi|1710248 | 352 | 10.9±1.9 | 37.2±6.8 | -3.4 |
| 2009    | elf5A-1 isoform A | gi|219555707 | 152 | 97.7±12.9 | 37.0±7.1 | +2.6 |
| 5502    | leucine aminopeptidase 3 | gi|165905571 | 274 | 159.7±24.6 | 84.6±12.7 | +1.9 |
| 1724    | ubiquitin activating enzyme E1 | gi|35830 | 163 | 25.3±4.8 | 12.2±1.6 | +2.1 |
| 3013    | ubiquitin-conjugating enzyme E2 J1 | gi|123858322 | 102 | 22.9±3.2 | - | + |
| 8025    | chain B, ubiquitin-conjugating enzyme Ubch3b | gi|119389041 | 136 | 43.7±4.8 | 90.7±9.2 | -2.1 |
| **Carbohydrate metabolism** | | | | | | |
| 3512    | aldehyde dehydrogenase 2 | gi|187370719 | 186 | 53.0±11.5 | 26.0±4.2 | +2.0 |
| 4515    | α enolase | gi|4416381 | 78 | 32.7±5.3 | 15.1±0.9 | +2.2 |
| 6708    | glucuronidase, β precursor | gi|178056516 | 117 | 12.9±2.8 | 0 | + |
| 7208    | chain A, fructose-1,6-bisphosphatase | gi|24987565 | 308 | 78.4±11.4 | 37.6±9.2 | +2.1 |
| 7616    | phosphoglucomutase-1 | gi|116004023 | 319 | 16.2±2.0 | 8.5±1.2 | +1.9 |
| 8710    | phosphoenolpyruvate carboxykinase 2 | gi|194038870 | 568 | 116.0±19.2 | 40.4±4.6 | +2.9 |
| 9207    | quinone oxidoreductase | gi|113205780 | 226 | 20.7±1.6 | 8.9±3.5 | +2.3 |
| 9310    | fructose-bisphosphate aldolase A | gi|156120479 | 252 | 153.2±32.0 | 305.7±15.9 | -2.0 |
| **mRNA metabolism** | | | | | | |
| 4501    | tryptophanyl-tRNA synthetase isoform 2 | gi|109084884 | 188 | 53.3±12.3 | 20.1±1.9 | +2.6 |
| 2309    | heterogeneous nuclear ribonucleoprotein F isoform 1 | gi|57107167 | 137 | 6.0±1.5 | 11.9±0.6 | -2.0 |
| 5523    | heterogeneous nuclear ribonucleoprotein U | gi|55859526 | 98 | 26.1±3.4 | 12.3±2.1 | +2.1 |
| 8017    | heterogeneous nuclear ribonucleoprotein H1 | gi|48145673 | 343 | 44.4±6.2 | 83.8±12.5 | -1.9 |
| 8026    | heterogeneous nuclear ribonucleoprotein A2/B1 isoform A2 | gi|4504447 | 113 | 0 | 27.0±3.5 | - |
| 8122    | heterogeneous nuclear ribonucleoprotein A2/B1 isoform 2 | gi|73976092 | 116 | 0 | 40.6±5.5 | - |
| **Amino acid metabolism** | | | | | | |
| 6005    | asparaginase-like 1 protein | gi|57100467 | 164 | 132.8±27.2 | 56.3±17.6 | +2.4 |
| 6401    | L-arginine/glycine amidinotransferase | gi|194034805 | 272 | 17.9±2.9 | 0 | + |
| 7211    | D-amino acid oxidase | gi|47522948 | 144 | 66.5±5.0 | 29.1±7.5 | +2.3 |
| **Fatty acid metabolism** | | | | | | |
| 4102    | crystallin λ1 | gi|47523096 | 243 | 145.6±25.9 | 50.0±10.2 | +2.9 |
| 5703    | glycerol-3-phosphate dehydrogenase 2 | gi|62088378 | 132 | 6.8±0.7 | 12.4±1.4 | -1.8 |
identified protein, ficolin (spot 4107, Table 2). The ficolins form complexes with MBL-associated serine proteases (MASPs) in the circulation and recognize the conserved molecular patterns on the surface of pathogenic microbes. The MASP2 makes C3 convertase C4bC2b, which leads to the lysis of pathogens [17] and higher surface of pathogenic microbes. The MASP2 participates in the intestinal innate immunology, and modulates tight junction permeability [27]. The lower level of six different isoforms of haptoglobin in the AB pigs might be due to the less strong microbial attack following reduced density of the gut microbiota. These different isoforms may possess different functions during NEC progression and the individual levels, or the total haptoglobin level, may serve as a biomarker for the microbiota-related NEC progression.

Regenerating islet-derived protein 3-γ (Reg3γ, spot 6009, Table 1) is a protein whose expression is triggered by increased microbial-epithelial contact at mucosal surfaces involving activation of TLR–MyD88-mediated signals in small intestine [28,29]. The finding that the AB pigs showed lower intestinal expression of this protein corresponds with other results [30]. Similar to our findings, AB treatment with enrofloxacin and clindamycin also participated in the intestinal innate immunology, and modulates tight junction permeability [27]. The lower level of six different isoforms of haptoglobin in the AB pigs might be due to the less strong microbial attack following reduced density of the gut microbiota. These different isoforms may possess different functions during NEC progression and the individual levels, or the total haptoglobin level, may serve as a biomarker for the microbiota-related NEC progression.

Consistent with our previous studies on germ-free preterm pigs [12], several intestinal heat shock proteins (HSPB1 (spot 4002, 4020), HSP90B1 (spot 0818), HSPA2 (spot 2720), Table 1) were

### Table 1. Cont.

| Spotno* | Protein Name | GI Idb | Protein Scorec | Expression Leveld (AB) | Expression Leveld (Untreated) | Fold Change (AB/Untreated) |
|---------|--------------|--------|----------------|------------------------|-----------------------------|---------------------------|
| **Pyrimidine metabolism** | | | | | |
| 5610 | dihydropyrimidinase-related protein 2-like isoform 1 | gi|194041527 | 484 | 63.9±12.1 | 25.3±6.1 | +2.5 |
| **Iron homeostasis** | | | | | |
| 4006 | ferritin L subunit | gi|10304378 | 261 | 78.9±9.4 | 35.9±7.9 | +2.2 |
| 6801 | aconitate hydratase | gi|115497728 | 376 | 15.4±2.2 | 8.1±1.6 | +1.9 |
| **Intracellular traffic** | | | | | |
| 1006 | RAB1A, member RAS oncogene family | gi|119620325 | 305 | 99.6±14.7 | 42.8±14.6 | +2.3 |
| 1207 | protein SEC13 homolog isoform 7 | gi|109034613 | 382 | 43.6±4.9 | 75.8±11.0 | −1.8 |
| 2201 | pyrophosphatase 1 | gi|194042750 | 364 | 25.2±1.2 | 52.5±7.4 | −2.1 |
| **Ion channel** | | | | | |
| 8702 | Ca-activated chloride channel regulator 1 | gi|47523388 | 144 | 28.6±3.8 | 13.9±2.6 | +2.1 |
| **Cytoskeleton and cell mobility** | | | | | |
| 0514 | tubulin β4 | gi|73987242 | 380 | 52.5±8.8 | 141.1±29.6 | −2.7 |
| 1503 | β tubulin | gi|57209813 | 88 | 6.4±1.1 | 20.3±4.4 | −3.1 |
| 1010 | β actin | gi|118136261 | 115 | 105.3±15.2 | 49.9±3.4 | +2.1 |
| 1109 | actin γ2 | gi|49168516 | 130 | 41.0±5.5 | 19.1±1.0 | +2.2 |
| 2124 | α actin | gi|119612724 | 112 | 23.8±5.9 | 0 | + |
| 3306 | actin α2 | gi|4501883 | 380 | 52.5±8.8 | 141.1±29.6 | −2.7 |
| 4302 | actin α2 | gi|149632150 | 310 | 65.8±8.2 | 31.1±4.6 | +2.1 |
| 3102 | F-actin-capping protein subunit β | gi|148822609 | 313 | 41.9±4.5 | 93.2±19.4 | −2.2 |
| 2504 | keratin 8 | gi|227430407 | 372 | 45.3±2.8 | 18.6±1.8 | +2.4 |
| 3418 | keratin 10 | gi|186629 | 85 | 12.8±1.2 | 5.9±1.4 | +2.2 |
| 0309 | keratin 17 | gi|296202900 | 75 | 22.0±3.8 | 0 | + |
| 3412 | keratin 20 | gi|160011626 | 81 | 8.0±0.5 | 0 | + |
| 3809 | filamin A isoform 5 | gi|109132802 | 90 | 6.2±0.5 | 11.3±1.3 | −1.8 |
| **Secretory protein** | | | | | |
| 6003 | epididymal secretory protein E1 | gi|28373999 | 338 | 395.9±83.2 | 69.1±30.4 | +5.7 |

*Spot number consistent with those indicated in Figure 3.

†GI ID: Genbank identifier.

‡Protein score indicating the confidence of identification.

§Expression quantity defined as the sum of optical density for each pixel of spot area (mean ± SEM, ×10²).

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affected by the reduced gut microbiota following AB treatment. The altered production of HSPs mitigates the injurious actions of oxidant-induced stress, probably through regulating protein homeostasis via binding, stabilizing, or refolding cell-essential proteins [31]. HSPB1 showed overall lower expression level in the homeostasis via binding, stabilizing, or refolding cell-essential oxidant-induced stress, probably through regulating protein expression of HSPB1 in the completely healthy AB pigs, relative to germ free pigs in our earlier report [12].

| Spot no | Protein Name | GI Id | Protein Score | Expression Level (AB) | Expression Level (Untreated) | Fold Change (AB/Untreated) |
|---------|--------------|-------|---------------|------------------------|-----------------------------|---------------------------|
| 1207    | α 1s haptoglobin | gi|164614625 | 364 | 34.5±8.8 | 72.3±34.2 | –2.1 |
| 1209    | haptoglobin   | gi|189409353 | 181 | 15.1±1.9 | 107.4±7.4 | –7.1 |
| 1217    | haptoglobin   | gi|47522826  | 310 | 30.6± | 72.7±22.8 | –2.4 |
| 2011    | haptoglobin   | gi|114667507 | 91  | 32.4± | 292.7±68.1 | –9.1 |
| 2212    | haptoglobin   | gi|189409353 | 306 | ± | 100±34.3 | – |
| 3012    | haptoglobin   | gi|189409353 | 231 | 61.7± | 325.4±83.5 | –5.3 |

Table 2. Identified proteins in blood plasma with differential expression between AB-treated and untreated pigs (p<0.05).

Table 1

| Spot no | Protein Name | GI Id | Protein Score | Expression Level (AB) | Expression Level (Untreated) | Fold Change (AB/Untreated) |
|---------|--------------|-------|---------------|------------------------|-----------------------------|---------------------------|
| 6106    | albumin      | gi|833798  | 148 | 30.0±6.2 | 66±1.3 | +4.6 |
| 6406    | albumin      | gi|833798  | 117 | 51.8±15.1 | 9.2±1.6 | +5.6 |
| 1117    | COL1A1 protein | gi|13096810  | 167 | 37.6±6.7 | 6.8±2.2 | +5.6 |
| 4107    | ficolin 1     | gi|119608546 | 80  | 77.2±7.5 | – | + |
| 6106    | type I collagen | gi|30102  | 293 | 27.0±4.5 | 9.0±1.9 | +3.0 |
| 6615    | transferrin   | gi|189232884 | 219 | 18.2±3.1 | 8.7±2.1 | +2.1 |

Refer to Table 1 for the details of table head.
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Bacterial growth is very iron-dependent. Correspondingly, AB treatment affected intestinal iron homeostasis via iron regulatory proteins (IRPs). IRP1 (spot 6615, Table 1) is converted into aconitase when the iron level is high [37]. Intestinal aconitase was elevated in our AB pigs, probably reflecting higher iron availability. Similarly, higher levels of ferritin light chain (spot 6615, Table 1), the major intracellular iron storage protein [37], the major intracellular iron storage protein [37], the major intracellular iron storage protein [37], demonstrates that intestinal tissue binds more iron for metabolism when the bacterial load is largely removed by the AB treatment. Similarly, transferrin (spot 6615, Table 2), a major iron transporter protein in plasma [38], was also increased in the AB pigs. Excessive iron metabolism may cause damage as this would trigger the production of reactive oxygen species (ROS) [39]. The expression of cathespin (spot 7607, Table 1), an enzyme that is highly efficient in degrading H2O2, was increased in the AB pigs, suggesting the intestine from AB pigs may possess better capacity to cope with ROS production than untreated pigs.

Proteins related to protein synthesis, processing and degradation were also increased in the AB pigs. The identified proteins included a component of the translational machinery (laminin...
receptor, spot 0301, Table 1 [40], and also functions related to initiation of protein synthesis (eIF 5A-1 isoform A, spot 2009, Table 1) [41], transfer of aminocyl-tRNA to 80S ribosomes (elongation factor 1-γ isoform 3, spot 1009, Table 1) [42] as well as the formation, reduction and isomerization of disulfide bonds (protein disulfide isomerase-related protein 5, spot 1402, Table 1) [43]. Two proteins related to the transport of newly synthesized proteins from the endoplasmatic reticulum to Golgi apparatus were identified, namely SEC13 (spot 1207, Table 1) [44] and RAB1A (spot 1006, Table 1) [45], which is also influenced by the aforementioned HSP90 [46]. The AB treatment also affected the ubiquitination system, the major system of protein degradation. The ubiquitination enzymes identified were ubiquitin-activating enzyme E1 (spot 1724), ubiquitin-conjugating enzyme E2J1 (spot 3013), and ubch5b (spot 8025). The ubiquitin-activating enzyme E1 and ubiquitin-conjugating enzymes activate the ubiquitin, and consequently transfer it to the targeted protein [47]. Multi ubiquitinated target protein is then subjected to proteolysis in the proteasome. This system is also influenced by the aforementioned protein chaperones such as HSPs and bacterial infection [47]. Consistent with changed recycling of proteins by the AB treatment, five heterogeneous nuclear ribonucleoproteins (spot 2309, 5523, 8017, 8026, 8122, Table 1) influencing pre-mRNA processing, modification, transport and degradation [48] were also found with changed expression.

Aminopeptidases cleave amino acids from the amino terminus of protein or peptides. In this study, activities of two aminopeptidases, ApA and ApN, were higher in AB pigs (Figure 2E), which is consistent with previous studies on the effects of germ-free conditions for preterm pigs after formula-feeding. [1] Another aminopeptidase, leucine aminopeptidase 3 (spot 5502, Table 1) which removes the NH2-terminal L-prolyl residues from various peptides [49], also showed higher expression in the AB pigs, again supporting the conclusion that the AB-reduced microbial load might have increased intestinal protein digestion, protein synthesis pathways and amino acid metabolism in the immature intestine.

In previous studies, NEC progression significantly affected tissue proteins associated with carbohydrate and energy metabolism [11,12]. Most of the identified proteins in this study (7 of 9) showed higher expression level in AB versus the untreated pigs, suggesting a more active carbohydrate metabolism. Among the identified proteins, aldehyde dehydrogenase 2 transforms acetaldehyde to acetyl-CoA to enter the TCA cycle. Phosphoglucomutases 1 converts glucose-1-phosphate from a glycogen to glucose-6-phosphate, which goes into the glycolysis pathway. Aldolase A, glyceraldehyde-3-phosphate dehydrogenase 2 and enolase catalyze three different steps of glycolysis. Phosphoenolpyruvate carboxykinase 2 and glucuronidases are involved in gluconeogenesis. Inorganic pyrophosphatase plays roles in energy metabolism, provides a thermodynamic pull for many biosynthetic reactions [50].

In our previous proteomic studies on NEC, repeated identification of proteins related to cytoskeleton, cell integrity and cell mobility was a consistent observation associated with feeding and bacterial colonization [11,12]. Similarly in this study, two tubulins, six isoforms of actin, and four keratins were identified. Actins are crucial for cellular response and healing of mucosa defects after gram-negative bacterial attack and endotoxin exposure [51]. Keratin 8 has a role also in apoptosis of colonic cells [52]. The above structural cytoskeleton proteins are also associated with aforementioned identified proteins such as C3 [53], HSPB1 and HSPA2 [31,36].

Chloride secretion is the major driving force for intestinal fluid secretion and fluid hypersecretion induced by enterotoxin resulting in diarrhea and dehydration [54], the key features of NEC. We detected AB-induced increased abundance of Ca-activated chloride channel regulator 1 (spot 8702, Table 1) that is known to regulate the intercellular Cl− efflux and trans-epithelial Cl− secretion [55,56]. Hence, the AB-reduced bacterial load may be
associated with a more efficient regulation of intestinal Cl− secretion.

The optimal dose, timing, route of administration and product(s) of antibiotics in neonatology remain controversial. Using a preterm pig model of NEC, we now demonstrate very consistent beneficial effects of broad-spectrum antibiotics treatment for the first five days after birth during the difficult transition from parenteral to enteral nutrition. Our proteomic analyses indicate that the AB treatment might protect the intestine by the interacting effects of intestinal complement system, HSP protection, protein synthesis and degradation and the metabolism of iron, carbohydrates, fatty acids and amino acids. We also demonstrate that circulating levels of haptoglobin, Reg3γ, cleaved C3 and ficolin are related to these tissue effects, and therefore have a potential to act as biomarkers for the feeding- and microbiota-induced progression of NEC during the difficult first weeks of life after preterm birth. Such markers need to be validated in longitudinal studies on NEC and while our results demonstrate clear benefits of early broad-spectrum antibiotics on the preterm pig intestine, the optimal dose, product and route of delivery to provide short and long term benefits in both preterm pigs and infants remain to be defined.

Materials and Methods

Ethics Statement

All the procedures on animals were approved by the National Committee on Animal Experimentation in Denmark (permit no. 2009/561–1731). Surgical interventions were performed under anesthesia, and pigs were immediately euthanized if they showed extensive discomfort due to procedure- or disease-related reasons.

Animals and their Treatment

Delivery, and housing of the premature piglets were carried out as previously described [1]. Briefly, preterm piglets from two sows were delivered by caesarean section at 105–106 day (90%) gestation. All piglets were housed individually in incubators with regulated temperature, moisture, and oxygen. Immediately after birth, a vascular catheter (infant feeding tube 4F; Portex, Kent, UK) was inserted into the dorsal aorta via the umbilical cord of the anesthetized newborn pigs for parenteral nutrition, and an orogastric feeding tube (6F Portex) was provided for enteral feeding. After recovery from surgery, all piglets were given PN as well as minimal enteral nutrition (3 mL formula per 6 h) for 2 days. After that, all piglets were switched to total enteral nutrition (infant formula, 15 mL/kg/3 h) via the orogastric tube. The formula was composed of Peptide 2–0 (SHS, Liverpool, UK), 80 g, Laprodan 15 (ARLA, Aarhus, Denmark) 70 g, and 75 mL of Liquigen-MCT (SHS, Liverpool, UK) per L water, and designed to match the composition of sow’s milk during lactation.

Piglets were stratified between treatments according to sex and birth weight. Six piglets were given the antibiotic treatment daily (AB group), and six other piglets served as untreated controls and were given a corresponding volume of saline. The antibiotic treatment was 100 mg/kg per day ampicillin (Pentrexyl, Bristol-Myers Squibb, Bromma, Sweden, distributed equally between 50 mg i.m. and 50 mg i.g. daily doses), 2.5 mg/kg per day gentamycin (given i.m. and i.g., KU-LIFE Pharmacy, Copenhagen, Denmark) and 10 mg/kg per day metronidazole (Flagyl, Sanofi Aventis, Hursholm, Denmark and Metronidazole, Actavis, Hafnarfjordur, Island, given i.m and i.g., respectively). The product and doses were chosen based on the i.v. antibiotics regime generally used for septic infants at the Department of Neonatology, Copenhagen University Hospital (Copenhagen, Denmark).

Tissue Collection

If clinical signs of NEC were prior to the predetermined conclusion of the experiment on day 5 after delivery, the piglets were euthanized by sodium pentobarbital (200 mg/kg, i.a.). Otherwise the piglets were euthanized and sampled on the fifth day, 45–55 h after initiation of full enteral feeding. Just before euthanasia, a blood sample was collected from the arterial catheter, and plasma was separated and stored at −20°C for further analyses. Clinical signs of NEC was recorded according to our macroscopic NEC evaluation system [16], where 1 = absence of lesions, 2 = local hyperemia, inflammation, and edema, 3 = hyperemia, extensive edema, and local hemorrhage, 4 = extensive hemorrhage, 5 = local necrosis and pneumonia intestinalis, and 6 = extensive necrosis and pneumonia intestinalis. NEC was defined as a score of minimum 3 in minimum one intestinal region (proximal, middle, distal intestine, colon).

The gastrointestinal tract was immediately removed, and a 6 cm section of the middle small intestine was saved for histological analysis, brush border enzymatic activity assays and proteomic analysis. Tissue sections for histological analysis were fixed in 4% paraformaldehyde. Samples for enzymatic activity assays and proteomic analysis were frozen in liquid nitrogen and stored at −80°C. Another 10 cm section of the mid intestine was collected for determining the proportion of intestinal mucosa [16].

Villous Morphology, Brush-border Enzymes and Gut Microbiology

The paraformaldehyde fixed samples were embedded in paraffin and sectioned at 5 μm and stained with HE. All slides were checked with a light microscope (Ortholene, Leitz) and imagined by NIH Image J software (NIH, USA). Snap-frozen mid intestinal sections were homogenized in 1.0% Triton X-100 and the homogenates were assayed for activities of disaccharidases (lactase, maltase, sucrase) and peptidases (ApA, ApN, DPPIV) as described previously [57]. Densities of bacteria in luminal content obtained from the ceacum was enumerated by conventional culture-based microbiology [58]. The cultures for total aerobic and anaerobic bacteria were carried out on calf blood agar plates (SSI Diagnostika, Hillerod, Denmark). The number of colony forming units was then determined using serial dilutions, and enumerated on the highest countable dilution.

Gel-based Proteomics

Extraction of intestinal protein, 2-DE and protein identification was carried out as previously described [11,59]. Briefly, the tissue samples were disrupted with a tissue teaser (Biospec Products, OK, USA) in a cocktail buffer containing Triton X-100 and Protease Inhibitor Cocktail Set 3 (Bio-Rad, Hercules, CA, USA). The protein extracts were further purified with precipitation with trichloroacetic acid-acetonitrile solution. The purified protein was dissolved in a buffer containing 7 mol/L urea, 2 mol/L thiourea, 4% Chaps, 100 mmol/L dithiothreitol, and 5% glycerol. Protein concentration of the samples was determined by Bio-Rad Protein Assay (Bio-Rad).

Intestinal protein sample (100 μg), or heparin-treated blood plasma (5 μL) was mixed with rehydration buffer (9.5 mol/L urea, 2% Chaps, 0.28% dithiothreitol, 0.5% IPG Buffer pl 3–10) and applied onto one ReadyStrip IPG Strip (18 cm, pl 3–10 NL, Bio-Rad). The isoelectric focusing was carried out on an Ettan IPGphor 3 (GE Healthcare, Upssala, Sweden) with specific
running program after an active rehydration step. The SDS-PAGE of the focused gel strips were carried on 1.0 mm-thick 12.5% PAGE gels. After electrophoresis, gels were stained with SYPRO Ruby Protein Stain (Bio-Rad) according to the manufacturer’s guide. The stained gels were scanned with a Molecular Imager Pharo 6S Plus System (Bio-Rad) and analyzed by PDQuest 8.0 (Bio-Rad). Matched spots were assigned with numbers automatically.

Gel spots with significant abundance between the AB and untreated pigs (p<0.05) were manually cut out and applied to gel trypsin digestion. The peptide mixtures obtained were applied on a 4800 MALDI TOF/TOF Analyzer (Applied Biosystem, Carlsbad, CA, USA) for MALDI-TOF/TOF MS. Generated mass spectrum was used for the protein searching with searching taxonomy limited as Mammalia (mammals) against NCBI nr database. A protein match with a protein score > 71 was considered significant.

Western-blot Analysis

Briefly, 20 μg intestinal protein or 1 μL plasma was resolved by electrophoresis on a 12.5% SDS-PAGE gel. The expression of laminin receptor, pyrophosphatase 1, HSPB1 and haptoglobin were shown with specific antibody (ab65436, ab96099, ab12351, ab14248, Abcam, Cambridge, UK). The protein bands were visualized and the density of the protein bands was detected by Quantity One (Bio-Rad).

Statistical Analysis

The discrete NEC scores of the treatment groups were reported as medians, and the difference between groups evaluated with non-parametric Mann-Whitney test using GraphPad Prism 5 (GraphPad software, La Jolla, CA, USA). The abundance of proteins by proteomics and Western blot analysis were expressed as mean ± SEM and analyzed with two-tailed Student t test with Levene’s Test for equality of variances in SPSS 11.5. A p value less than 0.05 was considered significant.

Author Contributions

Conceived and designed the experiments: PJ JM-FW PTS. Performed the experiments: PJ MLJ MSC TT W-HS GLT. Analyzed the data: PJ MLJ MSC. Contributed reagents/materials/analysis tools: MLJ MSC TT W-HS GLT. Wrote the paper: PJ JM-FW PTS.

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