

**Expression of Digestive Enzymes and Nutrient Transporters in the Intestine  
of *Eimeria*-challenged Chickens**

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### ABSTRACT

Avian coccidiosis is caused by the intestinal protozoa *Eimeria*. The parasite's site of infection in the intestine is site specific. *Eimeria acervulina* infects the duodenum, *E. maxima* the jejunum, and *E. tenella* the ceca. Lesions in the intestinal mucosa cause reduced feed efficiency and body weight gain in *Eimeria*-challenged chickens. The growth reduction may be due to changes in expression of digestive enzymes and nutrient transporters in the intestine. The objective of this thesis was to examine the expression of digestive enzymes: APN and SI, peptide and amino acid transporters: Pept1, ASCT1, b<sup>0,+</sup>AT/rBAT, B<sup>0</sup>AT, CAT1/2, EAAT3, LAT1 and y<sup>+</sup>LAT1/2, sugar transporters: GLUT1, GLUT2, GLUT5 and SGLT1, mineral transporter: ZNT1 and an immune factor: LEAP2 in the duodenum, jejunum, ileum and ceca of *Eimeria*-challenged layers and broilers. Comparisons were made between *E. acervulina*-challenged layers and broilers and *E. acervulina*, *E. maxima* and *E. tenella*-challenged broilers to examine the effect of chicken breeds and *Eimeria* species, respectively, on digestive enzymes and nutrient transporter expression. *E. acervulina*-challenged layers and broilers showed downregulation of APN, b<sup>0,+</sup>AT/rBAT, B<sup>0</sup>AT, CAT2, EAAT3, GLUT2, SI, ZNT1 and LEAP2 in the duodenum, but not in the jejunum and ileum. *E. acervulina*-challenged duodenum, *E. maxima*-challenged jejunum and *E. tenella*-challenged ceca samples showed common downregulation of APN, GLUT5 and ZNT1. These results demonstrate that there are common changes in intestinal gene expression in response to *E. acervulina* in broilers and layers, and common changes in response to challenge by different *Eimeria* species in broilers.

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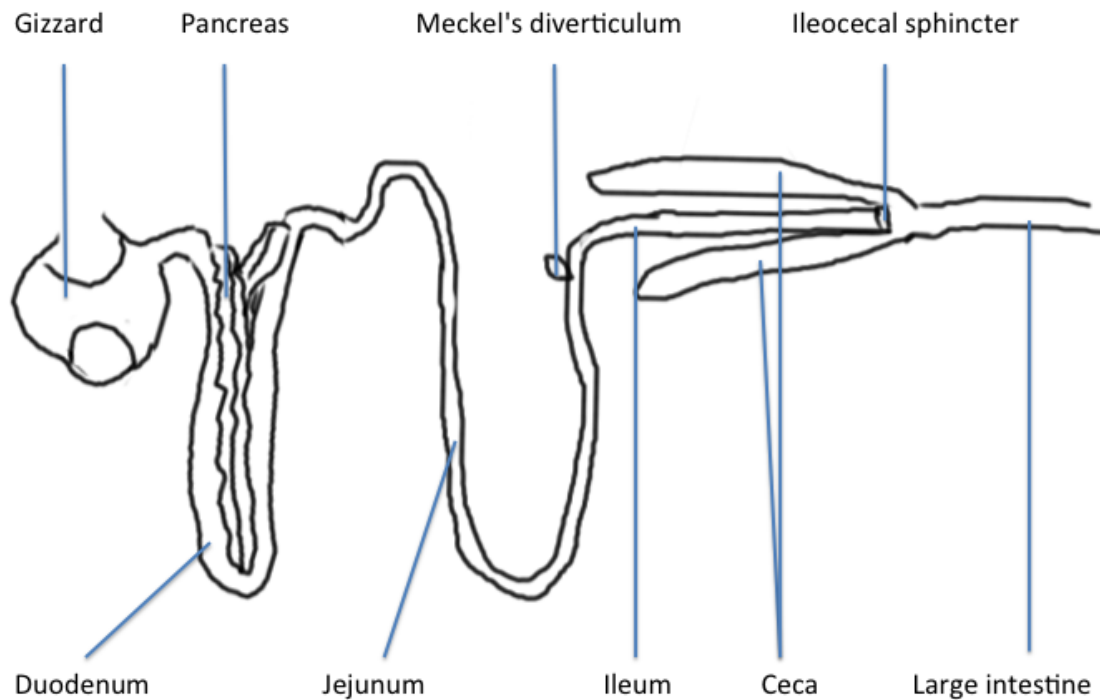


## CHAPTER I. REVIEW OF LITERATURE

### Morphology of the intestine

#### Sections of the gastrointestinal tract

The majority of nutrient absorption occurs in the small intestine (Leeson, et al., 2001). Structures such as plicae circularis (mucosal folds), villi and microvilli present at the small intestine increase the surface for absorption. In an adult chicken, the small intestine is about 1.3m in length and can be divided into three sections: duodenum, jejunum and ileum. Figure I-1. illustrates the anatomical structure of part of the chicken digestive system.



**Figure I-1. Anatomy of the chicken digestive system.** (not drawn to scale) (Su, 2013).

The duodenum is the first section of the small intestine (Figure I-1). The duodenum loops around the pancreas, which is called the duodenal loop. The primary function of the duodenum is to mix food chyme with digestive enzymes secreted from the liver, pancreas and the duodenal wall, this process also results in neutralizing the acid in the food chyme from the stomach (Smith and Morton, 2010). The duodenal section is larger in diameter compared with the other regions of the small intestine.

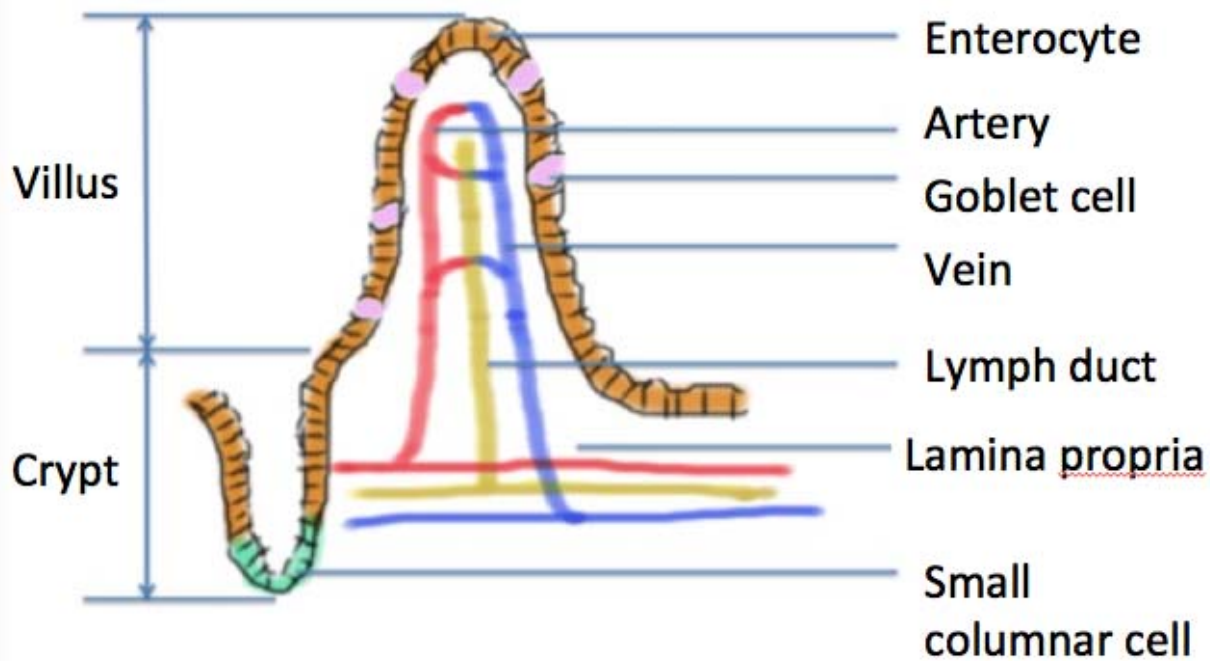
The jejunum has a very similar anatomical structure to the duodenum, but there is a reduction of the mucosal folds compared to the duodenum (Smith and Morton, 2010). The jejunum makes up about 40% in human and up to 90% in other species of the total small intestine length (Twietmeyer and McCracken, 2001). In many species there is no distinct anatomical feature that separates the jejunum and the ileum. In chicken, Meckel's diverticulum marks the end of the jejunum and the start of the ileum (Noy and Sklan, 2001). Right before hatch, the yolk sac is absorbed into the naval cavity of the chicken embryo, and the residual tiny yolk sac stalk is Meckel's diverticulum.

There is further reduction of the mucosal folds in the ileum, the distal part of the small intestine. The mucosal folds are absent at the end of the ileum. The ileum section has abundant lymph node like structures, called Peyer's patches, which are located in the mucosa and submucosal layer of the ileum (Smith and Morton, 2010). The ileocecal sphincter separates the ileum and the large intestine, which functions in reduction of reflux from the colon (Smith and Morton, 2010). In addition to nutrients, the ileum also absorbs bile acid, vitamin B12 and other intrinsic factors to be recycled in the body (Lazaridis, et al., 1997; Shaw, et al., 1989).

Birds have two ceca located below the junction of the small intestine and the large intestine (Moreto and Planas, 1989; Smith and Morton, 2010). The wall of the ceca has mucosal folds but not villus structures. The main function of the ceca is fermentation of dietary fiber, absorption of water, sugar and amino acids (Salanitro, et al., 1976; Whittow, 2000).

### **Structure of the intestinal wall**

**Villus.** The mucosal side of the intestine is covered with tiny projections, known as villi. The villus is considered the unit of absorption. In an adult chicken, the height of a villus is about 1mm, which varies depending on its location in the small intestine. The villi present in the duodenum are longer and tongue shaped. In the jejunum and ileum, there are reduced number and size of villi and more finger shaped villi (Smith and Morton, 2010).



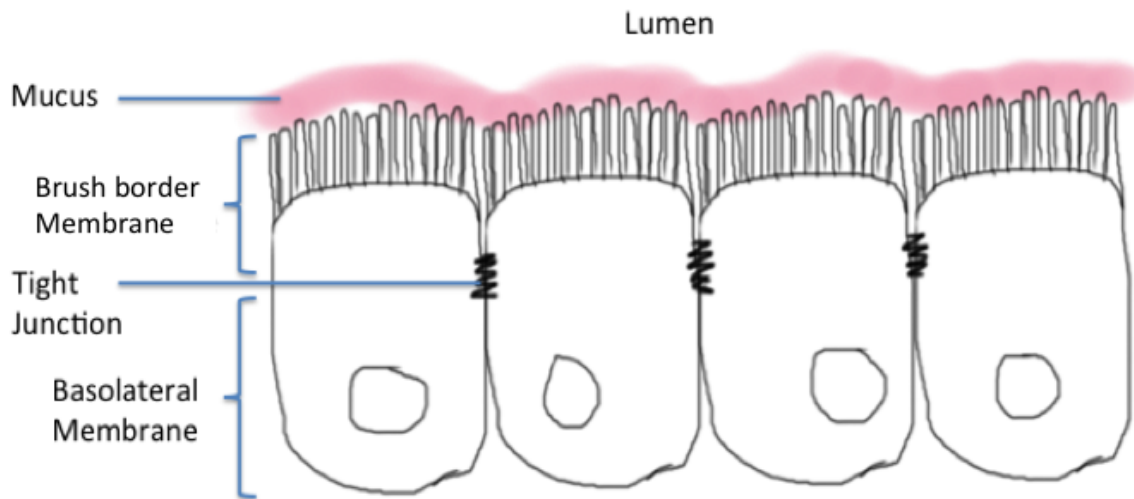
**Figure I-2. Structure of an intestinal villus and crypt.** (not drawn to scale) (Su, 2013).

A single simple columnar epithelium layer covers the villi (Figure I-2.) (Smith and Morton, 2010). Most of these cells are enterocytes with numerous cytoplasmic extensions, known as the microvilli, for nutrient digestion and absorption. Most of the rest of the cells are goblet cells and about less than 0.5% are endocrine cells. The goblet cells produce mucus, which serves as the primary barrier between the luminal environment and the epithelial layer. Tight junctions between the cells also form a physical barrier that is impermeable to fluids, nutrients and waste and thus protect the body from the harmful environment (Ivanov, 2012). The entero-endocrine cells are sensors of the luminal contents and regulate postprandial secretion and motility of the small intestine (Moran, et al., 2008). Underneath the epithelial cells, there is a layer of mucosa tissue called the lamina propria, which contains the capillary network and a sac like lymph vessel (Smith and Morton, 2010).

**Crypts of Lieberkuhn.** Between adjacent villi, there are cell depressions into the lamina propria that form the crypts of Lieberkuhn. The cells in the crypts are the only cells of the villus that undergo cell division. They gave rise to enterocytes, goblet cells, entero-endocrine cells, and paneth cells (Green and Greene, 1984). Paneth cells stay within the crypts; they secrete lysozyme by releasing granules into the lumen by exocytosis (Smith and Morton, 2010). The other three

types of cells migrate up the villus to replace the extruded old cells at the villus tip. The replacement time (cell turnover) is dependent on the age of the animal, section of the intestine and height of the villus (Green and Greene, 1984; Reece and Reece, 2005; Smith and Morton, 2010). In chicken, this process takes about 3 to 4 d (Uni, et al., 2000).

**Enterocyte.** The enterocytes are highly specialized and polarized cells (Figure I-3). Like other polarized cells, cell type specific proteins are expressed at the brush border membrane, while non-cell type specific proteins are expressed at the basolateral membrane (Van Beers, et al., 1995). The tight junction formed between adjacent enterocytes separates these two types of membranes. The specialized brush border membrane contains many cytoplasmic extensions, which characterize the brush border membrane and is essential for nutrient digestion and absorption (Van Beers, et al., 1995). Membrane bound glycoproteins like mucins at the brush border membrane protect the host against intestinal pathogens (Belley, et al., 1999).



**Figure I-3. Tight junction between enterocytes.** (Su, 2013).

### **Nutrient digestion and absorption at enterocyte**

The process of digestion, chemical breakdown of food by digestive enzymes, begins in the mouth. The final stage of digestion and nutrient absorption takes place in the intestinal lumen at the enterocyte surface (Johnson, 2007). At the brush border membrane, disaccharides are degraded into monosaccharides by saccharidases, and small peptides are further broken down to di- and tri-peptides or amino acids by peptidases (Van Beers, et al., 1995). Digestion is accomplished by hydrolysis by membrane bound enzymes produced by enterocytes. Transporters

located at the brush border mediate absorption of monosaccharides, amino acids and di- and tri-peptides (Johnson, 2007). Only a small fraction of the absorbed nutrients is used within the enterocyte. Most of the nutrients exit the cell via transporters located at the basolateral membrane. Once the nutrients are passed into the blood, they are exported via the portal vein to the liver and the rest of the body (Van Beers, et al., 1995).

### **Protein digestion and absorption**

Dietary protein is required to supply the essential amino acids, which the body cannot produce or cannot synthesize rapidly enough, and replace nitrogen lost in the urine (Smith and Morton, 2010). Degradation of protein into di- and tri-peptides and free amino acids is accomplished by two kinds of proteolytic enzymes: endopeptidases and exopeptidases. Endopeptidases are digestive enzymes like pepsin produced by the stomach and pancreas secreted trypsin, chymotrypsin and elastase. These proteases secreted by the pancreas cleave peptide bonds in the center of the peptides. Exopeptidases cleave peptide bonds at the ends of the peptides, while carboxypeptidases break the peptide bond at the C-terminus and aminopeptidases at the N-terminus.

Di- and tri-peptides are transported across the brush border membrane via peptide transporters (SLC15 family members) (Daniel and Kottra, 2004). Most of the small peptides that enter the enterocyte are hydrolyzed by intracellular peptidases, and transported out of the cell via amino acid transporters at the basolateral membrane. Free amino acids cross the brush border membrane via different types of transporters depending on the size and the electrical property of the amino acids. Most amino acids that enter the enterocyte are transported out of the cell via different types of amino acid transporters, except glutamate is retained and mainly used by the enterocyte as an energy source (Smith and Morton, 2010). Transporters, their location and function discussed in this review are summarized in Table I-1.

Abbreviation	Gene full name	Location	Function
APN	Aminopeptidase N	Brush border	Final digestion of peptides by N terminus cleavage
ASCT1	Alanine, serine, cysteine and threonine transporter (SLC1A4)	Basolateral	Na <sup>+</sup> -dependent neutral amino acid transporter
b <sup>0+</sup> AT	Solute carrier family 7, member 9 (SLC7A9)	Brush border	Na <sup>+</sup> -independent neutral/cystine, cationic amino acid exchanger
B <sup>0</sup> AT	Solute carrier family 6, member 14 (SLC4A14)	Brush border	Na <sup>+</sup> -dependent neutral amino acid transporter
CAT1	Cationic amino acid transporter-1 (SLC7A1)	Basolateral	Transport lysine, arginine and histidine
CAT2	Cationic amino acid transporter-2 (SLC7A2)	Basolateral	Transport lysine, arginine and histidine
EAAT3	Excitatory amino acid transporter 3 (SLC1A1)	Brush border	Transport aspartate, glutamate and cysteine
GLUT1	Glucose transporter-1 (SLC2A1)	Basolateral	Transport glucose, galactose, mannose and glucosamine
GLUT2	Glucose transporter-2 (SLC2A2)	Basolateral	Transport fructose, mannose, galactose, glucose and glucosamine
GLUT5	Glucose transporter-5 (SLC2A5)	Brush border	Transport fructose
LAT1	L type amino acid transporter-1 (SLC7A5)	Basolateral	Transport hydrophobic amino acids
LEAP2	Liver-expressed antimicrobial peptide-2	Cytosol	Innate immune factor
Pept1	Peptide transporter-1 (SLC15A1)	Brush border	Transport di- and tripeptides
rBAT	Solute carrier family 3, member1 (SLC3A1)	Brush border	Dimerize with b <sup>0+</sup> AT
SGLT1	Sodium glucose transporter-1 (SLC5A1)	Brush border	Transport low concentrations of d-glucose
SI	Sucrase isomaltase	Brush border	Hydrolysis of sucrose and isomaltose
y <sup>+</sup> LAT1	y <sup>+</sup> L amino acid transporter-1 (SLC7A7)	Basolateral	Na <sup>+</sup> -dependent neutral/cationic amino acid exchanger
y <sup>+</sup> LAT2	y <sup>+</sup> L amino acid transporter-2 (SLC7A6)	Basolateral	Na <sup>+</sup> -dependent neutral/cationic amino acid exchanger
ZNT1	Zinc transporter-1	Basolateral	Efflux of Zn <sup>2+</sup>

**Table I-1. Summary of intestinal genes in these studies. SLC=Solute carrier.**

***Aminopeptidase N (APN).*** The APN/CD13 is a type II metalloprotease that belongs to the M1 family of the Metallopeptidase, clan MA(E). There are two types of APN: the membrane bound aminopeptidase N and the soluble aminopeptidase N, each of which have many isoforms with different functions (Luan and Xu, 2007). APN cleaves neutral amino acids from the N-terminus of oligopeptides (Danziger, 2008). Besides its function as a digestive enzyme, APN is also involved in the trimming of antigens and in the process of antigen presentation (Luan and Xu, 2007).

***Peptide transporter 1 (PepT1).*** The PepT1 (SLC15A1) belongs to the proton-coupled oligopeptide transporter (POT) family (Hu, et al., 2008) and is a low-affinity, high-capacity di- and tri-peptide transporter (Gilbert, et al., 2008b; Hu, et al., 2008; Jappar, et al., 2010). PepT1 is responsible for absorption of most di- and tri- peptides and peptide-like drugs from the small intestinal lumen into the enterocytes (Hu, et al., 2008). Many tissues express PepT1, but the greatest level is found in the small intestine in both pre- and post-hatch chickens. Ceca and large intestine have much reduced expression. Very little expression of PepT1 is detected in other tissue and cell types (Zwarycz and Wong, 2013).

***b<sup>0+</sup>AT and rBAT transporter complex.*** The b<sup>0+</sup>AT (SLC7A9) and rBAT (SLC3A1) form a heteromeric amino acid transporter (HAT) by a disulfide bridge (Fotiadis, et al., 2013; Palacin and Kanai, 2004; Verrey, et al., 2004; Wagner, et al., 2001). The b<sup>0+</sup>AT is the light subunit, which has transporter function. rBAT is the heavy subunit, which is essential for trafficking the complex to the cell membrane (Palacin and Kanai, 2004; Verrey, et al., 2004). Transport activity of this complex is Na<sup>+</sup>-independent and exchanges extracellular cationic amino acids and cystine for intracellular neutral amino acids (Fotiadis, et al., 2013). b<sup>0+</sup>AT has high-affinity transport of L-cystine and cationic amino acids and lower affinity transport of neutral amino acids (Verrey, et al., 2004).

***Na<sup>+</sup>-dependent neutral amino acid transporter (B<sup>0</sup>AT).*** The B<sup>0</sup>AT (SLC6A19) transports a broad range of neutral amino acids into the cell (Broer, et al., 2004; Romeo, et al., 2006). Some of these neutral amino acids are used by b<sup>0+</sup>AT in exchange for cationic amino acids and cysteine (Fotiadis, et al., 2013). Transport of amino acids via B<sup>0</sup>AT is driven by the membrane potential. The most preferred substrate for B<sup>0</sup>AT is leucine in a pH-dependent manner, which

strongly increases with alkaline pH (Broer, et al., 2004). B<sup>0</sup>AT is highly expressed in the brush border membrane in the small intestine (Broer, et al., 2004; Terada, et al., 2005).

***Excitatory amino acid transporter 3 (EAAT3).*** EAAT3 (SLC1A1), also known as EAAC1, belongs to the X<sub>AG</sub><sup>-</sup> system, which is a Na<sup>+</sup>-dependent transporter of anionic amino acids such as aspartate and glutamate and is located at the brush border membrane of enterocytes (Gilbert, et al., 2007; Kanai and Hediger, 1992; Speier, et al., 2012). Glutamate is one of the most abundant amino acids in dietary protein, but the blood concentration is quite low. This is because in the small intestine, glutamate is the energy source of the enterocytes (Iwanaga, et al., 2005) (Fan, et al., 2004), and is also used by the enterocytes to synthesize other amino acids (Blachier, et al., 2009). Fan et al., (2004) showed that EAAT3 is the major L-glutamate transporter. Expression of EAAT3 can be detected along the crypt-villus axis, but there is higher capacity and lower affinity transport activity in crypt than in villus cells (Fan, et al., 2004). In chickens, expression of EAAT3 is greatest in the ileum, which indicates higher uptake of glutamate in the lower part of the small intestine (Gilbert, et al., 2007).

***Alanine, serine, cysteine and threonine transporter (ASCT1).*** The ASCT1 (SLC1A4) is a Na<sup>+</sup>-dependent neutral amino acid transporter. It was discovered by screening for expressed sequences similar to the sodium-coupled glutamate transporter GLAST1. Unlike the GLAST-related transporter family, ASCT1 does not transport glutamate or aspartate but alanine, serine, cysteine, and threonine (Hofmann, et al., 1994). The activity of ASCT1 requires extracellular Na<sup>+</sup>, but does not need countertransport of K<sup>+</sup> as other GLASTs (Zerangue and Kavanaugh, 1996).

***Cationic amino acid transporters (CAT1/CAT2).*** The CATs (SLC7A) family members are transmembrane glycoprotein-associated amino acid transporters (Verrey, et al., 2004). CAT1 is a high-affinity, low-capacity transporter, while CAT2 is a low-affinity, high-capacity transporter. They are both located at the basolateral membrane of the intestinal enterocyte and are responsible for the efflux of cationic amino acids (Fotiadis, et al., 2013; Verrey, et al., 2004). CATs also play a key role in nitric oxide synthesis by delivering L-arginine for nitric oxide synthase in certain cells (Fotiadis, et al., 2013).

***L-type amino acid transporter 1 (LAT1).*** LAT1 (SLC7A5) was the first cloned light subunit of HATs (Kanai, et al., 1998). It heterodimerizes with the heavy chain 4F2hC protein and mediates



the Na<sup>+</sup>-independent exchange of large neutral amino acids across the basolateral membrane (Verrey, et al., 2004). Like rBAT, 4F2hC functions to translocate the complex to the cell membrane (Fotiadis, et al., 2013; Verrey, et al., 2004; Wagner, et al., 2001). LAT1 is an obligatory exchanger with a 1:1 ratio (Fotiadis, et al., 2013; Wagner, et al., 2001). The affinity for amino acids is up to 100-fold higher at the extracellular side when compared to the cytosolic side of the transporter. Transport sidedness also affects substrate selectivity, L-leucine, L-isoleucine and L-methionine are better efflux than influx substrates (Fotiadis, et al., 2013).

***y<sup>+</sup>L amino acid transporters (y<sup>+</sup>LATs).*** y<sup>+</sup>LAT1 (SLC7A7) and y<sup>+</sup>LAT2 (SLC7A6) both heterodimerize with 4F2hC protein, and function as obligatory exchangers of cationic amino acids (Na<sup>+</sup>-independent) and neutral amino acids (Na<sup>+</sup>-dependent) (Fotiadis, et al., 2013). They both function in cationic amino acid efflux in the kidney and small intestine at the basolateral membrane (Broer, et al., 2000; Fotiadis, et al., 2013). But y<sup>+</sup>LAT2 preferentially mediates the efflux of L-arginine in exchange for L-glutamine and Na<sup>+</sup>. Also y<sup>+</sup>LAT2 has a broader tissue distribution than y<sup>+</sup>LAT1 (Broer, et al., 2000).

### **Carbohydrate digestion and absorption**

In chicken, the major source of carbohydrates is starch in grains. Digestion of carbohydrates provides an energy source for the body. There are several enzymes in the gastrointestinal tract that degrade starch and glycogen. Sucrase isomaltase secreted by the intestinal cells are responsible for the major part of the final digestion of polysaccharides. Hydrolyzed monosaccharides such as glucose, galactose, mannose and fructose are transported into the enterocyte by the Na<sup>+</sup>-dependent glucose transporter 1 (SGLT1) and glucose transporter 5 (GLUT5), and exit the cell via glucose transporter 2 (GLUT2) and glucose transporter 1 (GLUT1)(Smith and Morton, 2010). SGLT1, GLUT5 and GLUT2 are the most abundant monosaccharide transporters in the small intestine compared with other hexose carriers (Yoshikawa, et al., 2011).

***Sucrase isomaltase (SI).*** SI is an enzyme complex that is responsible for 80% of the maltase activity in the small intestine (Van Beers et al., 1995). The sucrase subunit hydrolyzes sucrose, but not α(1-6) glucosidic bonds. The isomaltase subunit hydrolyzes α(1-6) glucosidic bonds but not sucrose. Both subunits hydrolyze maltose, maltotriose and hydrophobic aryl- α-glucopyranosides. The complex has no activity towards polysaccharides like starch (Van Beers

et al., 1995). SI is highly expressed in the small intestine, which accounts for 10% of the brush border membrane protein. In chicken, expression of SI has been reported in embryonic and post-hatch intestine (Sklan et al., 2003). Very low expression of SI has been detected in the embryonic yolk sac membrane (Yadgary et al., 2011).

***Sodium-dependent glucose transporter-1 (SGLT1).*** SGLT1 (SLC5A1) is a Na<sup>+</sup>-dependent glucose cotransporter at the brush border membrane, which was the first cotransporter protein identified using rabbit intestine (Wright and Turk, 2004). SGLT1 is a uniporter, i.e., it pumps one glucose molecule into the cell along with 2 Na<sup>+</sup> ions (Hediger and Rhoads, 1994). Expression of SGLT1 can be found at the plasma membrane of cells located at the small intestine, trachea, kidney and heart (Wright and Turk, 2004). SGLT1 is highly expressed in the duodenum, and the expression level decreases in the distal part of the small intestine in mice (Yoshikawa, et al., 2011). In chickens, SGLT1 expression level is higher in the jejunum and ileum than duodenum (Gilbert, et al., 2007).

***Glucose transporter-5 (GLUT5).*** The GLUT5 (SLC2A5) is a Na<sup>+</sup>-independent high-affinity fructose transporter. It has no glucose transport activity in human and limited glucose transport in rat (Garriga, et al., 2004; Uldry and Thorens, 2004). GLUT5 is located at the brush border membrane of the enterocyte and transports fructose from the intestinal lumen into the cell (Le Gall, et al., 2007). GLUT5 is expressed in many tissues and organs (Yang, et al., 2002). Like SGLT1, GLUT5 has higher expression level in the duodenum in mice (Yoshikawa, et al., 2011), but higher expression in the jejunum and ileum in chickens (Gilbert, et al., 2007).

***Glucose transporter-1 (GLUT1).*** The GLUT1 (SLC2A1) is a Na<sup>+</sup>-independent transporter for glucose, galactose, mannose and glucosamine (Zhao and Keating, 2007). It was the first glucose transporter to be identified (Boyer, et al., 1996). The expression of GLUT1 in the small intestine is not as abundant as in the stomach and large intestine (Yoshikawa, et al., 2011). GLUT1 normally can only be detected at the basolateral membrane of the enterocytes, but it is present in the brush border membrane in diabetic rats (Boyer, et al., 1996).

***Glucose transporter-2 (GLUT2).*** The GLUT2 (SLC2A2) transporter is located at the basolateral membrane, mediates the Na<sup>+</sup>-independent, low-affinity transport of glucose, galactose, mannose and fructose, and high-affinity transport of glucosamine (Uldry and Thorens, 2004). GLUT2

translocation to the brush border membrane has also been reported (Mithieux, 2005). In mice, GLUT2 is highly expressed in the proximal half of the small intestine (Yoshikawa, et al., 2011).

### **Mineral absorption**

Absorption of ion minerals and trace elements occurs in the jejunum and ileum. Calcium, magnesium and phosphate can be absorbed by passive diffusion, but also can be transported across the membrane by active transporters like other ions such as sodium and zinc (Leeson, et al., 2001). The rate of absorption depends on pH, membrane potential, transporters and the presence of other minerals (Leeson, et al., 2001). The body requires minerals in many physiological processes (Smith and Morton, 2010). Calcium is important in bone development and cellular signaling pathways. Magnesium is an important co-factor for many enzymes. Phosphate is also involved in bone formation, acid-base balance and nucleic acid synthesis. Sodium is the key element in maintaining and changing membrane potential, and is also required for many nutrient co-transporters as discussed above. Zinc is a trace mineral, which functions as a cofactor of enzymes, nuclear factors and hormones (Devergnas, et al., 2004).

***Zinc transporter 1 (ZNT1)***. The ZNT proteins are members of the cation diffusion facilitator family. They function in transporting zinc out of the cells or contained in cellular compartments (Tako, et al., 2005). ZNTs are expressed in a tissue-specific manner, ZNT1 is ubiquitously expressed in the body, but is most abundant at the basolateral membrane of enterocytes in the duodenum and jejunum (McMahon and Cousins, 1998). Expression of ZNT1 in the small intestine can be induced by increasing dietary zinc, which was first found in rat (McMahon and Cousins, 1998) and later confirmed in chicken (Tako, et al., 2005).

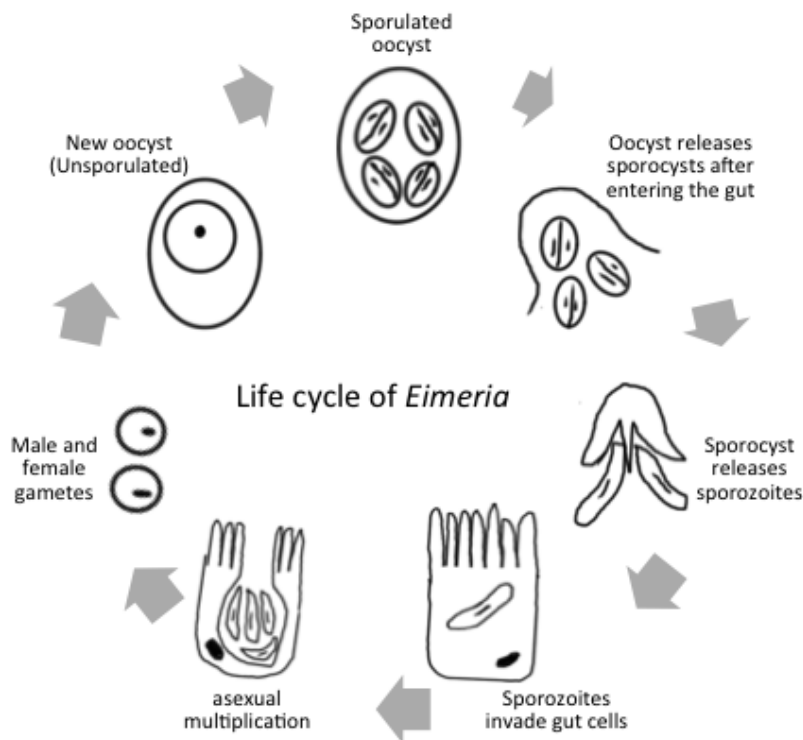
### **Avian coccidiosis and *Eimeria***

Coccidiosis is a major disease of poultry caused by the intestinal protozoa *Eimeria* (Conway and McKenzie, 2007). Lesions in the intestinal mucosa reduce feed efficiency and body weight gain. A damaged intestinal barrier leads to bacterial infection, which can increase mortality in birds. Coccidiosis is responsible for the loss of billions of dollars in the poultry industry worldwide (Dalloul, et al., 2007). The common treatment for coccidiosis is use of anticoccidial drugs, but large-scale and long-term use of these drugs has led to the worldwide development of resistance against most of these drugs. Live attenuated and non-attenuated anticoccidial vaccines have

shown positive results in preventing coccidiosis. Highly efficient and low-cost anticoccidial vaccines could potentially replace anticoccidial drugs in the future (Peek and Landman, 2011).

### Life cycle of *Eimeria*

The life cycle of *Eimeria* takes about 4 to 7d to complete. The bird can pick up oocysts from the environment by swallowing infected litter. The life cycle of *Eimeria* is shown in Figure I-4. An oocyst contains 4 sporocysts, which each contains 2 sporozoites. Oocysts are generally ovoid to ellipsoid in shape, and range from 10-40µm in length by 10-30µm in width. The wall of the oocyst contains peptide, lipid and carbohydrate. The likely physical arrangement of the components places the lipid in a 10 nm thick outer layer, covering a 90 nm thick layer of glycoprotein (Stotish, et al., 1978). After the bird consumes the oocyst, 8 sporozoites will be released into the digestive system. The sporozoites will invade the intestinal epithelial cells, and use the host cell as a nutrient supply for replication. After several generations of asexual multiplication, a sexual stage occurs in which male and female gametes unite and form new oocysts that are protected by a thick wall. These oocysts are shed in the feces, to be picked up by other animals (Allen and Fetterer, 2002).



**Figure I-4. Life cycle of *Eimeria*.** (not drawn to scale) (Su, 2013).

### ***Eimeria* infection in chicken**

*Eimeria* infection is species- and site-specific. The species of *Eimeria* that infect chickens are different from those that infect turkeys. In the U.S., the three species of *Eimeria* that most impact the poultry industry are *E. acervulina*, *E. maxima* and *E. tenella*. *E. acervulina* infects the duodenum, *E. maxima* the jejunum, and *E. tenella* the ceca (Lillehoj and Trout, 1996). Lesions in the intestinal mucosa can be measured on a scale of 0 to 4. A score of 0 shows no lesions, and a score of 4 shows many lesions (Johnson and Reid, 1970). Chickens challenged with *E. maxima* oocysts yield the same lesion score as chickens challenged with a higher dose of *E. acervulina* or *E. tenella* oocysts. A study conducted to compare the relative sensitivities of *E. acervulina*, *E. maxima*, and *E. tenella* oocysts to desiccation showed that *E. maxima* oocysts have greater resistance to drying compared to *E. acervulina* and *E. tenella* (Jenkins, et al., 2013).

### **Immune response to *Eimeria* challenge in chicken**

The mucosal immune system is composed of the mucosal associated lymphoid tissues (MALT) that attacks the pathogen at its site of entry (Yun, et al., 2000a). Gut associated lymphoid tissues (GALT) are the largest component of MALT. Unlike mammals, chickens do not have lymph nodes, they have lymphoid structures such as the bursa of Fabricius, cecal tonsils, Meckel's diverticulum and Peyer's patches (PP) (Lillehoj and Trout, 1996). Microfold cells at the PP present antigens to T lymphocytes at the epithelial layer and antibody-producing B lymphocytes at the lamina propria. Immunoglobulin A (IgA) is produced by B lymphocytes (Lillehoj and Trout, 1996). Following *E. maxima* infection, intestinal IgA level and cytokine interferon-gamma (IFN-gamma) level were increased (Yun, et al., 2000b). Analysis of *E. acervulina*, *E. tenella* and *E. maxima* treated chicken macrophages showed common regulation of interleukins (IL) and chemokines. There was induced expression of IL-1 $\beta$ , IL-6, and IL-18 and repressed expression of IL-16. Expression of macrophage inflammatory protein (MIP)-1 $\beta$  (CCLi1), K203 (CCLi3), and ah221 (CCLi7) are commonly increased but CXCL chemokine K60 (CXCLi1) was found to be induced by macrophage exposure to *E. tenella* only (Dalloul, et al., 2007).

### **Liver-expressed antimicrobial peptide-2 (LEAP2)**

The chicken LEAP2 gene was first discovered by bioinformatics screening of the chicken genome (Lynn, et al., 2004). Based on the *in silico* sequence, LEAP2 expression was detected in a number of tissues including the small intestine, liver, lung and kidney (Townes, et al., 2004).

Birds orally challenged with *Salmonella enterica* showed upregulation of LEAP2 expression in both small intestine and liver. An *in vitro* assay showed that LEAP2 has antimicrobial activity against *Salmonella* (Townes, et al., 2004). Later, the same research group discovered that LEAP2 could interact with the outer membrane of the bacteria and change its permeability. LEAP2 also has broad-spectrum antimicrobial activity and plays an important role in the chicken innate host defense (Townes, et al., 2009). In contrast, in *E. maxima*-challenged chickens, LEAP2 showed up to 71-fold downregulation in the jejunum, and chickens with greater lesion scores showed greater downregulation of LEAP2. The mechanism behind this expression pattern is to be further investigated, but it is hypothesized that *E. maxima* causes a downregulation of LEAP2 in the intestinal epithelia (Casterlow, et al., 2011).

### **Expression of digestive enzymes and nutrient transporters in *E. maxima*- challenged chickens**

*Eimeria* infection reduces weight gain, which could be due to changes in expression of nutrient transporters. Analysis of the jejunum of *E. maxima*-challenged broilers showed decreased expression of the brush border membrane amino acid transporters EAAT3 and b<sup>0,+</sup>AT. Expression of the basolateral amino acid transporters LAT1 and ASCT1 was increased, whereas the zinc transporter was decreased (Paris and Wong, 2013). These results suggest that changes in expression of amino acid transporters may cause depletion of the energy source glutamate and some essential amino acids, which may be part of the host defense mechanism for eliminating infected cells and inhibition of pathogen replication.

### **Objectives**

Changes in expression of digestive enzymes and nutrient transporters in *Eimeria*-challenged chickens have been only studied in the jejunum of *E. maxima*-challenged broilers. In this thesis, the expression of digestive enzymes (APN and SI), a peptide transporter (Pept1), amino acid transporters (ASCT1, b<sup>0,+</sup>AT/rBAT, B<sup>0</sup>AT, CAT1, CAT2, EAAT3, LAT1, y<sup>+</sup>LAT1 and y<sup>+</sup>LAT2), sugar transporters (GLUT1, GLUT2, GLUT5 and SGLT1), a mineral transporter (ZNT1) and an immune factor (LEAP2) was examined in the duodenum, jejunum, ileum and ceca of *Eimeria*-challenged layers and broilers. The objective of the first experiment was to examine the effect of chicken breeds on gene expression following an *E. acervulina*-challenge. The objective of the second experiment was to compare *E. acervulina*-, *E. maxima*- and *E.*

*tenella*-challenged broilers to examine the effect of *Eimeria* species on digestive enzyme and nutrient transporter expression.

## **CHAPTER II. EXPRESSION OF DIGESTIVE ENZYMES AND NUTRIENT TRANSPORTERS IN *EIMERIA ACERVULINA*-CHALLENGED LAYERS AND BROILERS**

### **ABSTRACT**

Avian coccidiosis is caused by the intestinal protozoa *Eimeria*. Lesions in the intestinal mucosa cause reduced feed efficiency and body weight gain in *Eimeria*-challenged chickens. The growth reduction may be due to changes in expression of digestive enzymes and nutrient transporters in the intestine. The objective of this thesis was to examine the expression of digestive enzymes: APN and SI, peptide and amino acid transporters: Pept1, ASCT1, b<sup>0+</sup>AT/rBAT, B<sup>0</sup>AT, CAT1/2, EAAT3, LAT1 and y<sup>+</sup>LAT1/2, sugar transporters: GLUT1, GLUT2, GLUT5 and SGLT1, mineral transporter: ZNT1 and an immune factor: LEAP2 in the duodenum, jejunum and ileum of *E. acervulina*-challenged layers and broilers. Layers and broilers showed common downregulation of APN, b<sup>0+</sup>AT, B<sup>0</sup>AT, CAT2, EAAT3, GLUT2, rBAT, SI, ZNT1 and LEAP2 in the duodenum. In the jejunum and ileum there were no changes in expression of the genes examined in broilers but there were many changes in layers. These changes in intestinal digestive enzyme and nutrient transporter gene expression may result in a decrease in the efficiency of protein digestion, uptake of essential amino acids and the energy source (glutamate), and disruption of mineral balance. This may ultimately lead to cell death and may be part of the host defense mechanism for eliminating infected cells and inhibition of pathogen replication.

### **INTRODUCTION**

Avian coccidiosis is characterized by destruction of the mucosa and is caused by the intestinal protozoa *Eimeria* (Conway and McKenzie, 2007). Lesions in the intestinal mucosa reduce feed efficiency and body weight gain, and increase mortality in birds. Coccidiosis is responsible for the loss of billions of dollars in the poultry industry worldwide (Dalloul, et al., 2007). The parasite's site of infection in the small intestine is site specific and *Eimeria acervulina* mainly infects the duodenum (Lillehoj and Trout, 1996). In chicken, the small intestine is where the majority of nutrient absorption occurs (Leeson, et al., 2001). The final digestion of protein and polysaccharides is catalyzed by membrane bound peptidases and glucosidases, respectively. Short peptides, free amino acids and monosaccharides are absorbed by the enterocytes by specific transporters located at the brush border membrane and basolateral membrane (Leeson, et



al., 2001). The growth depression in *Eimeria*-challenged chickens may be due to changes in expression of digestive enzymes and nutrient transporters in the small intestine.

Layer and broiler chickens have been genetically selected for generations to increase egg production or rapid growth, respectively (Koenen, et al., 2002; Yuan, et al., 2009). As a consequence of the selection, these two types of chickens demonstrate striking differences in food intake, body weight gain, body composition and duration of life caused by genetic differences (Koenen, et al., 2002). In general, layers have lower food intake (Hocking, et al., 1997), protein intake (Shariatmadari and Forbes, 1993) and body weight gain (Swennen, et al., 2007) when compared to broilers. Layers and broilers also showed differences in their immunological response to the specific antigen TNP-KLH (trinitrophenyl-conjugated keyhole limpet hemocyanin) (Koenen, et al., 2002). These results demonstrated that broilers display a strong short-term humoral immune response and layers have a long-term humoral response in combination with a strong cellular response. The differences between layers and broilers in innate immune response need to be further analyzed. Upon *Eimeria* challenge, the changes in expression of digestive enzymes and nutrient transporters in the small intestine may also be different between layers and broilers. The objective of this study was to compare changes in nutrient transporter and digestive enzyme gene expression in different sections of the small intestine of layers and broilers following infection with *E. acervulina*.

## **MATERIALS AND METHODS**

### **Chicken and *Eimeria***

This study was approved by the Beltsville Research Center Animal Care and Use Committee and conducted at the Animal Parasitic Disease Laboratory (USDA Agricultural Research Service, Beltsville, MD). Chickens used in this study were Sexsall layer males, which are White rock females crossed with Rhode Island Red males from Moyers hatchery (Quakertown, PA), and Ross Heritage broiler males from Longeneckers Hatchery (Elizabethtown PA). Birds were housed in suspended wire cages (46cm x 30cm = 1380cm<sup>2</sup>) with 2-3 birds per cage. Birds were fed a standard poultry starter ration (crumbles, 24% protein) and had free access to water. *Eimeria acervulina* was USDA #12 isolate. 1 day old chicks were transported to the USDA-ARS facility (Beltsville, MD) and were orally gavaged with either 1mL *E. acervulina* oocysts at 200,000 oocysts/ bird or not gavaged (control) at 21 d of age.

### **Tissue sampling**

Seven days post challenge chickens were euthanized by cervical dislocation and intestinal segments were collected. Duodenum, jejunum and ileum samples were collected from Sexsal layers (n=5) and Ross Heritage broilers (n=6). The contents of the intestine were squeezed out and the tissue segments were immediately stored individually in RNAlater (Invitrogen, Grand Island, NY). The samples were stored at 4 °C for 24 hrs and then were frozen at -70 °C before being shipped to Virginia Tech. Upon arrival each intestinal segment was removed from RNAlater. After homogenizing, a 20-30 mg tissue aliquot was placed in a 2-mL microfuge tube for RNA extraction and the remaining homogenate was placed in a separate 2-mL microfuge tube. Both tubes were frozen on dry ice and stored at -80°C.

### **Total RNA extraction**

The 20-30mg of tissue was placed in 500µL Tri Reagent (Molecular Research Center Inc., Cincinnati, OH) and shaken twice at 25Hz/s for 2 min using a TissueLyser II (QIAGEN Inc., Valencia, CA) following the animal tissue protocol. After homogenization 100 µL of chloroform were added for phase separation. The RNA pellet was suspended in 0.1% DEPC (Diethylpyrocarbonate, Sigma-Aldrich, St. Louis, MO) treated water depending on the pellet size and incubated for 10 minutes at 56°C. RNA concentration was determined using a NanoDrop 1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE). Any sample that had a concentration greater than 2000ng/µL was further diluted and reassayed. RNA quality was assessed by agarose-formaldehyde gel electrophoresis. All extracted RNA samples were stored at -80°C.

### **Reverse Transcription**

Total RNA was diluted to 0.1 µg/µL in DEPC water. cDNA was synthesized using the high capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA). Each 20µL reverse transcription reaction contained 2 µL 10X reverse transcription buffer, 2 µL 10X random primers, 1 µL multiscribe reverse transcriptase (50 U/µL), 0.8 µL 25x dNTPs, 9.2 µL DEPC water, and 5 µL of 0.1 µg/µL diluted RNA sample. The RNA and master mix were combined in a 0.5-mL microfuge tube, which was then run in a thermocycler for 10 min at 25 °C followed by 120 min at 37 °C and 5 min at 85 °C. The cDNA was diluted 1:20 with DEPC water and stored at -20°C.

## Quantitative Real-Time PCR

Quantitative real-time PCR (qPCR) was performed using 96-well plates. Each reaction contained 5  $\mu$ L diluted cDNA, 20  $\mu$ L of PCR master mix which contained 12.5  $\mu$ L 2X SYBR Green Master Mix (Applied Biosystems), 0.5  $\mu$ L forward primer (5  $\mu$ M), 0.5  $\mu$ L reverse primer (5  $\mu$ M), and 6.5  $\mu$ L DEPC water. Each reaction was run in duplicate. The plate was sealed with a MicroAmp Optical Adhesive Film (Applied Biosystems) and spun down in a centrifuge to mix reagents and remove bubbles and loaded into an Applied Biosystems 7300 Real-Time PCR instrument (Applied Biosystems). The following real time PCR conditions were used: 95 °C for 10 min followed by 40 cycles of 95 °C for 15s and 60 °C for 1 min. Genes analyzed were APN, ASCT1, b<sup>o</sup>+AT, B<sup>0</sup>AT, CAT1, CAT2, EAAT3, GLUT1, GLUT2, GLUT5, LAT1, LEAP2, Pept1, rBAT, SGLT1, SI, y<sup>+</sup>LAT1, y<sup>+</sup>LAT2 and ZNT1 (Table I-1). The endogenous control was the *chicken beta-actin* gene. All forward and reverse primer sequences are shown in Table II- 1. Primers were designed using the Primer Express software (Applied Biosystems) and synthesized by Eurofins MWG Operon (Huntsville, AL).

Gene <sup>1</sup>	Forward Primer	Reverse Primer
Beta-actin	GTCCACCGCAAATGCTTCTAA	TGCGCATTTATGGGTTTTGTT
APN	AATACGCGCTCGAGAAAACC	AGCGGGTACGCCGTGTT
ASCT1	TTGGCCGGGAAGGAGAAG	AGACCATAGTTGCCTCATTGAATG
b <sup>0,+</sup> AT	CAGTAGTGAATTCTCTGAGTGTGAAGCT	GCAATGATTGCCACAACCTACCA
B <sup>0</sup> AT	GGGTTTTGTGTTGGCTTAGGAA	TCCATGGCTCTGGCAGAGAT
CAT1	CAAGAGGAAAACCTCCAGTAATTGCA	AAGTCGAAGAGGAAGGCCATAA
CAT2	TGCTCGCGTTCCCAAGA	GGCCACAGTTCACCAACAG
EAAT3	TGCTGCTTTGGATTCCAGTGT	AGCAATGACTGTAGTGCAGAAGTAATATATG
LAT1	GATTGCAACGGGTGATGTGA	CCCCACACCCACTTTTTGTTT
LEAP2 <sup>2</sup>	CTCAGCCAGGTGTACTGTGCTT	CGTCATCCGCTTCAGTCTCA
GLUT1	TCCTCCTGATCAACCGCAAT	TGTGCCCCGGAGCTTCT
GLUT2	CACACTATGGGCGCATGCT	ATTGTGCCTGGAGGTGTTGGT
GLUT5	TTGCTGGCTTTGGGTTGTG	GGAGGTTGAGGGCCAAAGTC
Pept1	CCCCTGAGGAGGATCACTGTT	CAAAAGAGCAGCAGCAACGA
rBAT	CCCGCCGTTCAACAAGAG	AATTAAATCCATCGACTCCTTTGC
SGLT1	ATACCCAAGGTCATAGTCCCAAAC	TGGGTCCCTGAACAAATGAAA
SI	CGCAAAAGCACAGGGACAGT	TCGATACGTGGTGTGCTCAGTT
y <sup>+</sup> LAT1	CAGAAAACCTCAGAGCTCCCTTT	TGAGTACAGAGCCAGCGCAAT
y <sup>+</sup> LAT2	GCCCTGTCAGTAAATCAGACAAGA	TTCAGTTGCATTGTGTTTTGGTT
ZNT1 <sup>3</sup>	TCCGGGAGTAATGGAAATCTTC	AATCAGGAACAAACCTATGGGAAA

**Table II-1. Forward and reverse primers of genes analyzed.**

<sup>1</sup>Primer sequence designed by Gilbert, et al., 2007, unless noted separately.

<sup>2</sup>Primer designed by Casterlow, et al., 2011.

<sup>3</sup>Primer designed by Paris and Wong, 2013.

## Quantitative Real-Time PCR Analysis

All plates were analyzed individually using the software provided with the 7300

Real-Time PCR instrument and raw Ct data was obtained. Average gene expression relative to the endogenous control for each sample was calculated using the  $2^{-\Delta\Delta Ct}$  method described by Livak and Schmittgen (2001). The average  $\Delta Ct$  of the control samples was used to calculate the  $\Delta\Delta Ct$  value, which was performed separately for each intestinal segment, *Eimeria* treatment and each gene are a group. Data points that exceed  $\pm 3$  standard deviations from the mean were discarded as outliers.

## Statistical Analysis.

All data were analyzed by one-way ANOVA using JMP<sup>®</sup> Statistical Discovery Software from SAS (SAS Institute, Cary, NC). Layers and broilers were analyzed separately. The model included the main effects of treatment, sorted by genes. Significance level was set at  $P < 0.05$  when compared to the control.

## RESULTS

### *E. acervulina*-challenged layers

Changes in expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in *E. acervulina*-challenged layers are shown in Table II-1. Expression of amino acid transporters  $b^{0,+}AT$ ,  $B^0AT$ , rBAT and EAAT3 was decreased to 35%, 19%, 27% and 18% of control, respectively, in the duodenum and to 50%, 46%, 48% and 38% of control, respectively, in the jejunum of *E. acervulina*-challenged layers. CAT2 was decreased to 54%, 61% and 73% of control in the duodenum, jejunum and ileum, respectively, and LAT1 was decreased to 63% of control in the ileum of *E. acervulina*-challenged layers.  $y+LAT1$  was decreased to 68%, 56% and 68% in the duodenum, jejunum and ileum, respectively, and  $y+LAT 2$  was decreased to 70% of control in the jejunum. Peptide transporter Pept1 was decreased to 65% and increased 2-fold in jejunum and ileum, respectively, in *E. acervulina*-challenged layers.

Expression of sugar transporters GLUT1 was decreased to 86% of control in the ileum; GLUT2 was decreased to 40% and 27% of control in the duodenum and jejunum, respectively; SGLT1 was upregulated 1.9 fold in the ileum of *E. acervulina*-challenged layers. Expression of digestive enzyme APN was decreased to 44% of control in the duodenum and increased 1.5-fold in the

ileum; Sucrase isomaltase (SI) was decreased to 55% and 61% of control in the duodenum and jejunum, respectively; zinc transporter (ZNT1) was decreased to 50% and 67% of control in the duodenum and jejunum, respectively, in *E. acervulina*-challenged layers. The antimicrobial peptide LEAP2 was reduced to 15% and 59% of control in the duodenum and jejunum, respectively, and increased 2.4-fold in the ileum of *E. acervulina*-challenged layers.

### ***E. acervulina*-challenged broilers**

Changes in expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in *E. acervulina*-challenged broilers are shown in Table II-2. Expression of APN, b<sup>0,+</sup>AT, B<sup>0</sup>AT, rBAT, CAT2 and EAAT3 was decreased to 46%, 24%, 31%, 25% 56% and 25% of control, respectively, in the duodenum. SI, GLUT2 and GLUT5 were decreased to 27%, 11% and 36% of control respectively, in the duodenum. ZNT1 was decreased to 43% and LEAP2 was decreased to 6% of control in the duodenum of *E. acervulina*- challenged broilers. No changes in gene expression were observed in the jejunum and ileum of *E. acervulina*- challenged broilers.

		Relative gene expression						
Tissue	Group	APN	ASCT1	b <sup>0,+</sup> AT	B <sup>0</sup> AT	CAT1	CAT2	EAAT3
DU	Cont	1.08±0.31	1.00±0.05	1.00±0.02	1.08±0.30	1.54±0.51	1.02±0.12	1.08±0.31
	<i>E.ace</i>	0.47±0.04	0.93±0.06	0.35±0.05	0.20±0.03	2.10±0.16	0.55±0.03	0.19±0.01
	P-val	0.04*	0.71	<.0001*	0.006*	0.27	0.004*	0.006*
JE	Cont	1.02±0.10	1.02±0.10	1.03±0.13	1.05±0.14	1.54±0.39	1.01±0.07	1.01±0.08
	<i>E.ace</i>	0.78±0.05	0.82±0.06	0.52±0.06	0.48±0.05	2.10±0.22	0.62±0.08	0.38±0.03
	P-val	0.06	0.11	0.007*	0.006*	0.25	0.006*	<.0001*
IL	Cont	1.07±0.17	1.02±0.12	1.17±0.29	1.14±0.26	1.48±0.36	1.01±0.08	1.25±0.33
	<i>E.ace</i>	1.62±0.05	0.80±0.07	1.42±0.20	1.84±0.27	1.81±0.10	0.74±0.03	1.44±0.14
	P-val	0.02*	0.14	0.50	0.10	0.41	0.01*	0.62

		Relative gene expression					
Tissue	Group	GLUT1	GLUT2	GLUT5	LAT1	LEAP2	PEPT1
DU	Cont	1.00±0.03	1.05±0.21	1.04±0.10	1.00±0.07	1.14±0.36	1.08±0.31
	<i>E.ace</i>	0.93±0.08	0.42±0.08	0.82±0.20	1.31±0.15	0.17±0.33	0.80±0.23
	P-val	0.31	0.007*	0.37	0.13	0.01*	0.39
JE	Cont	1.00±0.06	1.05±0.15	1.03±0.12	1.03±0.12	1.04±0.13	1.02±0.11
	<i>E.ace</i>	0.96±0.03	0.28±0.06	0.80±0.06	1.18±0.05	0.61±0.07	0.66±0.13
	P-val	0.46	0.001*	0.11	0.27	0.02*	0.07*
IL	Cont	1.00±0.03	1.05±0.21	1.04±0.10	1.03±0.13	1.19±0.30	1.12±0.25
	<i>E.ace</i>	0.93±0.08	0.42±0.08	0.82±0.20	0.65±0.02	2.87±0.29	2.22±0.29
	P-val	0.01*	0.35	0.66	0.02*	0.004*	0.02*

		Relative gene expression					
Tissue	Group	rBAT	SGLT1	SI	y <sup>+</sup> LAT1	y <sup>+</sup> LAT2	ZNT1
DU	Cont	1.03±0.17	1.05±0.18	1.02±0.11	1.00±0.06	1.50±0.48	1.03±0.17
	<i>E.ace</i>	0.28±0.04	1.16±0.16	0.56±0.16	0.68±0.04	1.07±0.07	0.51±0.07
	P-val	0.0006*	0.59	0.03*	0.001*	0.29	0.009*
JE	Cont	1.00±0.04	1.01±0.08	1.00±0.05	1.01±0.09	1.00±0.06	1.02±0.10
	<i>E.ace</i>	0.48±0.03	1.14±0.13	0.61±0.07	0.57±0.05	0.70±0.03	0.68±0.10
	P-val	<.0001*	0.42	0.001*	0.002*	0.002*	0.05*
IL	Cont	1.18±0.28	1.07±0.16	1.07±0.18	1.00±0.07	1.10±0.20	1.06±0.18
	<i>E.ace</i>	1.44±0.19	2.04±0.20	1.55±0.32	0.68±0.03	1.45±0.13	1.36±0.13
	P-val	0.46	0.006*	0.23	0.003*	0.18	0.23

**Table II-2. Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in *E. acervulina*-challenged layers.** DU=duodenum, JE=jejunum, IL=ileum, Cont=control chicks, *E.ace*=*E. acervulina*, P-val=P-value. Relative gene expression was determined using the 2<sup>-ΔΔCt</sup> method. APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT1 and CAT2= Cationic amino acid transporter-

1 and -2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to b<sup>0,+</sup>AT; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase; y<sup>+</sup>LAT1 and y<sup>+</sup>LAT2= y<sup>+</sup> L amino acid transporter-1 and -2, respectively; ZNT1= Zinc transporter-1. \* Indicates statistical significance from control at  $p<0.05$ .



		Relative gene expression						
Tissue	Group	APN	ASCT1	b <sup>0,+</sup> AT	B <sup>0</sup> AT	CAT1	CAT2	EAAT3
DU	Cont	1.08±0.16	1.04±0.12	1.10±0.20	1.18±0.25	2.89±1.67	1.11±0.16	1.13±0.23
	<i>E.ace</i>	0.50±0.09	1.28±0.23	0.26±0.03	0.37±0.04	11.45±3.37	0.62±0.06	0.28±0.05
	P-val	0.005*	0.83	0.0001*	0.01*	0.17	0.02*	0.002*
JE	Cont	1.14±0.23	1.05±0.16	1.30±0.46	1.47±0.64	3.39±1.93	1.03±0.11	1.31±0.41
	<i>E.ace</i>	0.89±0.16	1.07±0.10	0.87±0.26	0.88±0.26	10.50±2.90	1.39±0.44	0.74±0.11
	P-val	0.50	1.00	0.81	0.65	0.61	0.58	0.56
IL	Cont	1.04±0.13	1.05±0.14	1.11±0.23	1.07±0.19	3.99±2.73	1.09±0.20	1.10±0.22
	<i>E.ace</i>	0.88±0.06	1.14±0.13	0.87±0.13	1.10±0.19	9.58±2.70	1.11±0.17	1.11±0.17
	P-val	0.37	0.99	0.49	1.00	0.49	1.00	1.00

		Relative gene expression					
Tissue	Group	GLUT1	GLUT2	GLUT5	LAT1	LEAP2	Pept1
DU	Cont	1.03±0.11	1.19±0.25	1.10±0.21	1.04±0.12	1.20±0.24	1.19±0.26
	<i>E.ace</i>	1.58±0.26	0.13±0.03	0.40±0.14	1.40±0.21	0.07±0.02	0.82±0.20
	P-val	0.15	0.0004*	0.007*	0.78	0.002*	0.72
JE	Cont	1.02±0.09	1.11±0.18	1.12±0.20	1.06±0.19	1.14±0.18	1.12±0.25
	<i>E.ace</i>	1.16±0.09	0.39±0.12	1.23±0.39	1.37±0.18	0.94±0.24	0.90±0.21
	P-val	0.90	0.10	0.98	0.94	0.89	0.81
IL	Cont	1.03±0.10	4.06±3.14	1.04±0.14	1.08±0.18	6.03±4.57	1.10±0.22
	<i>E.ace</i>	1.00±0.08	1.35±0.50	0.97±0.23	1.14±0.21	2.64±0.68	1.18±0.34
	P-val	1.00	0.56	1.00	1.00	0.65	0.99

		Relative gene expression					
Tissue	Group	rBAT	SGLT1	SI	y <sup>+</sup> LAT1	y <sup>+</sup> LAT2	ZNT1
DU	Cont	1.12±0.22	1.05±0.15	1.13±0.21	1.08±0.17	1.04±0.12	1.10±0.20
	<i>E.ace</i>	0.28±0.06	0.72±0.07	0.30±0.10	0.74±0.17	0.78±0.09	0.47±0.06
	P-val	0.0004*	0.56	0.004*	0.24	0.22	0.008*
JE	Cont	1.13±0.24	1.02±0.09	1.02±0.09	1.04±0.12	1.03±0.10	1.04±0.13
	<i>E.ace</i>	0.93±0.16	1.05±0.11	0.99±0.10	1.39±0.73	0.98±0.10	0.95±0.13
	P-val	0.88	1.00	0.99	0.85	0.99	0.95
IL	Cont	1.03±0.11	1.04±0.13	1.15±0.28	1.04±0.12	1.01±0.05	1.16±0.30
	<i>E.ace</i>	0.89±0.11	0.83±0.11	1.38±0.14	0.83±0.14	0.96±0.08	1.04±0.12
	P-val	0.59	0.56	0.77	0.45	0.94	0.94

**Table II-3. Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in *E. acervulina*-challenged broilers.** DU=duodenum, JE=jejunum, IL=ileum, Cont=control chicks, *E.ace*=*E. acervulina*, P-val=P-value. Relative gene expression was determined using the 2<sup>-ΔΔCt</sup> method. APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT1 and CAT2= Cationic amino acid transporter-1 and -2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose

transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to  $b^{0,+}$ AT; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase;  $y^+$ LAT1 and  $y^+$ LAT2=  $y^+$  L amino acid transporter-1 and -2, respectively; ZNT1= Zinc transporter-1. \* Indicates statistical significance from control at  $p<0.05$ .

## DISCUSSION

In chicken, the duodenum is important for digestive enzyme secretion and some absorption of nutrients. Most nutrient absorption occurs in the jejunum and ileum (Leeson, et al., 2001). The difference in food intake and body weight gain between layers and broilers may be due to different expression profiles of digestive enzymes and nutrient transporters in jejunum and ileum. It is not surprising that layers and broilers shared many similarities in the duodenum in response to *E. acervulina*-challenge: down regulation of APN, b<sup>0,+</sup>AT/rBAT, B<sup>0</sup>AT, CAT2, EAAT3, GLUT2, LEAP2, SI and ZNT1 (Figure II-1) but no changes in gene expression was observed in the jejunum and ileum section in broilers (Figure II-2). This difference may result from the divergent selection of chickens. Layers were selected for egg laying and broilers were selected for rapid growth. At 21 day of age, a broiler chicken is about twice the body weight of a layer chicken. The difference in body weight gain in layers and broilers may result from physiological difference at the molecular level in the intestine. In this experiment, there were striking differences in changes of gene expression in the jejunum and ileum of *E. acervulina*-challenged layers and broilers.

Brush border membrane transporters like b<sup>0,+</sup>AT/rBAT, B<sup>0</sup>AT and EAAT3, which regulate free amino acid uptake from the intestinal lumen to the epithelial cells, are downregulated in the duodenum of *E. acervulina*-challenged layers and broilers. This would result in reduced influx of essential amino acids to infected cells. Especially decreased expression of EAAT3 would result in a depletion of the energy source (glutamate) to the intestinal cells. b<sup>0,+</sup>AT/rBAT and EAAT3 were also down regulated in *E. maxima*- challenged broilers (Paris and Wong, 2013), which may indicate a common mechanism of intestine cells responding to *Eimeria* challenge. Both ASCT1 and LAT1 were upregulated in the jejunum of *E. maxima*- challenged broilers (Paris and Wong, 2013), which indicated increased efflux of amino acid from the enterocyte. The upregulation of ASCT1 and LAT1 was not found in *E. acervulina*-challenged layers and broilers.

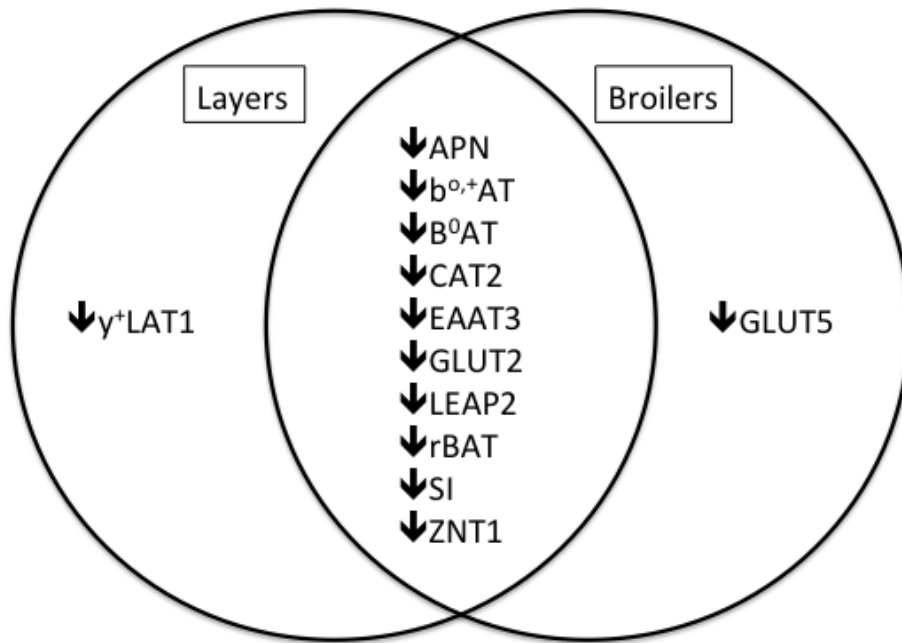
Brush border membrane cationic amino acid transporter b<sup>0,+</sup>AT/rBAT and basolateral membrane cationic amino acid transporter CAT2 were downregulated in the duodenum of *E. acervulina*-challenged layers and broilers. Decreased expression of b<sup>0,+</sup>AT/rBAT would lead to decreased cationic amino acid influx into the enterocyte. Downregulation of CAT2 may result from decreased substrate to this transporter.

Digestive enzyme SI at the brush border membrane hydrolyzes sucrose and isomaltose to monosaccharides. Decreased expression of SI can lead to less efficient digestion and absorption of polysaccharides. Downregulation of sugar transporter GLUT2 at the basolateral membrane may result from decreased expression of SI.

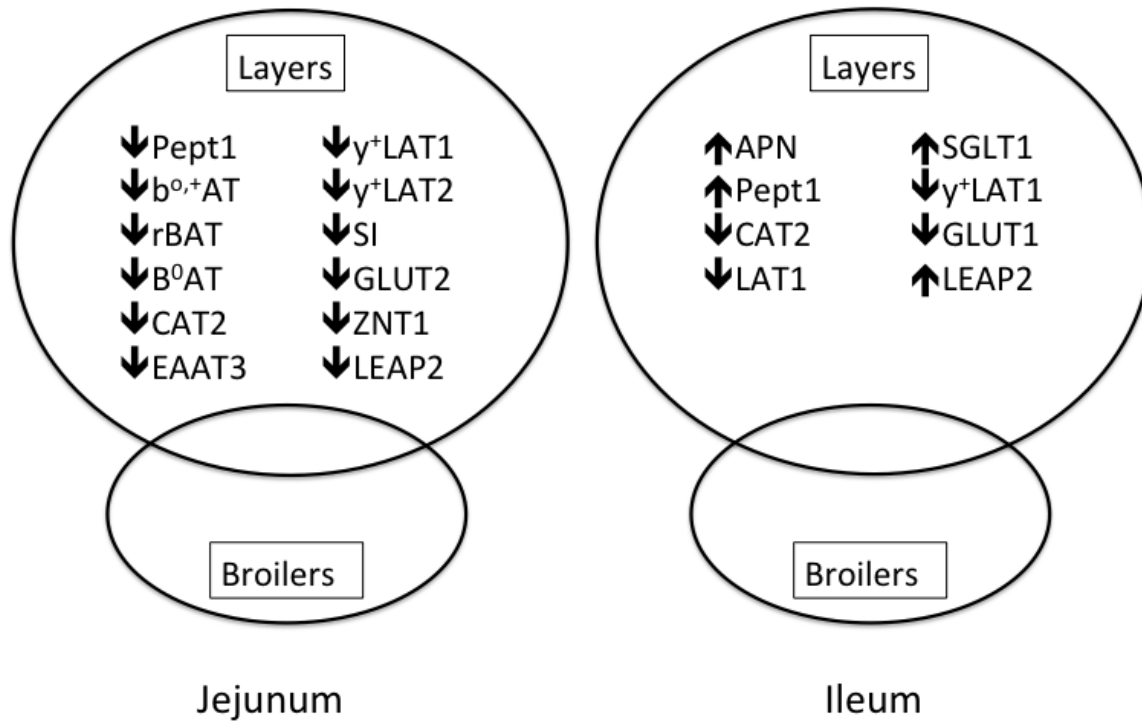
ZNT1 functions in efflux of  $Zn^{2+}$  at the basolateral membrane of enterocytes. Expression of ZNT1 is important to protect the cell against zinc toxicity (Nolte, et al., 2004). Zinc, as an antioxidant, can also protect the host against *E. acervulina*-induced oxidative damage (Georgieva, et al., 2011). Decreased expression of ZNT1 can either promote zinc toxicity and programmed cell death and/or reduce the damage caused by *Eimeria*.

LEAP-2 expression is proposed to be necessary for resistance to *E. maxima* infection and that upon entering cells, *E. maxima* leads to the downregulation of LEAP-2, resulting in more severe infection (Casterlow, et al., 2011). In both layers and broilers, LEAP-2 expression is decreased in the primary target site of *E. acervulina*: duodenum. Layers also showed downregulation of LEAP2 in the jejunum. There was an increase of LEAP-2 in the ileum in layers, which could be compensating for the low LEAP-2 level in the upper part of the intestine.

In summary, *E. acervulina*-challenged layers and broilers showed many similarities in downregulation of digestive enzymes and nutrient transporters in the duodenum, and no change in the jejunum and ileum in broilers compared to layers.



**Figure II-1. Summary of gene expression changes in duodenum of *Eimeria acervulina*-challenged layers and broilers.** APN= Aminopeptidase N;  $b^{0,+}AT$  and  $B^0AT$ =  $Na^+$ -independent and  $Na^+$ -dependent neutral amino acid transporter, respectively; CAT2= Cationic amino acid transporter-2; EAAT3= Excitatory amino acid transporter 3; GLUT2 and GLUT5= Glucose transporter-2 and -5, respectively; LEAP2= Liver-expressed antimicrobial peptide-2; rBAT= protein related to  $b^{0,+}AT$ ; SI= Sucrase isomaltase;  $\gamma^+LAT1$ =  $\gamma^+$  L amino acid transporter-1; ZNT1= Zinc transporter-1;  $\downarrow$ =downregulation.



**Figure II-2. Summary of gene expression changes in jejunum and ileum of *Eimeria acervulina*-challenged layers and broilers.** APN= Aminopeptidase N;  $b^{0,+}AT$  and  $B^{0}AT$ =  $Na^{+}$ -independent and  $Na^{+}$ -dependent neutral amino acid transporter, respectively; CAT2= Cationic amino acid transporter-2; EAAT3= Excitatory amino acid transporter 3; GLUT1 and GLUT2= Glucose transporter-1 and -2, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to  $b^{0,+}AT$ ; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase;  $y^{+}LAT1$  and  $y^{+}LAT2$ =  $y^{+}L$  amino acid transporter-1 and -2; ZNT1= Zinc transporter-1;  $\downarrow$ =downregulation;  $\uparrow$ =upregulation.

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## CHAPTER III. EXPRESSION OF DIGESTIVE ENZYMES AND NUTRIENT TRANSPORTERS IN *EIMERIA* CHALLENGED BROILERS

### ABSTRACT

Avian coccidiosis is caused by the intestinal protozoa *Eimeria*. The parasite's site of infection in the intestine is site specific. *Eimeria acervulina* infects the duodenum, *E. maxima* the jejunum, and *E. tenella* the ceca. Lesions in the intestinal mucosa cause reduced feed efficiency and body weight gain in *Eimeria*-challenged chickens. The growth reduction may be due to changes in expression of digestive enzymes and nutrient transporters in the intestine. The objective of this thesis was to examine the expression of digestive enzymes: APN and SI, peptide and amino acid transporters: Pept1, ASCT1, b<sup>0+</sup>AT/rBAT, B<sup>0</sup>AT, CAT1/2, EAAT3, LAT1 and y<sup>+</sup>LAT1/2, sugar transporters: GLUT1, GLUT2, GLUT5 and SGLT1, mineral transporter: ZNT1 and an immune factor: LEAP2 in the duodenum, jejunum, ileum and ceca of different *Eimeria*-challenged broilers. *E. acervulina*-challenged duodenum, *E. maxima*-challenged jejunum and *E. tenella*-challenged ceca samples showed common downregulation of APN, GLUT5 and ZNT1. In *E. acervulina*- and *E. maxima*-challenged chickens there was downregulation of LEAP2, but not in *E. tenella*-challenged chickens. CAT2, EAAT3, rBAT and SI were downregulated in *E. acervulina*- and *E. tenella*-challenged chickens, but not in *E. maxima*-challenged chickens. There was upregulation of LAT1 in *E. maxima*- and *E. tenella*-challenged chickens, but not in *E. acervulina*-challenged chickens. These results demonstrate that there are common and species-specific changes in intestinal gene expression in response to challenge by different *Eimeria* species in chicken. These changes in intestinal digestive enzyme, nutrient transporter gene expression may result in a decrease in the efficiency of protein digestion, uptake of essential amino acids and the energy source (glutamate), and disruption of mineral balance. This may ultimately lead to cell death and may be part of the host defense mechanism for eliminating infected cells and inhibition of pathogen replication.

### INTRODUCTION

Avian coccidiosis is a major disease of poultry caused by the intestinal protozoa *Eimeria* (Conway and McKenzie, 2007). Lesions in the intestinal mucosa reduce feed efficiency and body weight gain. A damaged intestinal barrier leads to bacterial infection, which can increase

mortality in birds. Coccidiosis is responsible for the loss of billions of dollars in the poultry industry worldwide (Dalloul, et al., 2007). In the U.S., the three species of *Eimeria* that most impact the poultry industry are *Eimeria acervulina*, *Eimeria maxima* and *Eimeria tenella*. *Eimeria* infection is site specific, *E. acervulina* infects the duodenum, *E. maxima* the jejunum, and *E. tenella* the ceca (Lillehoj and Trout, 1996). Analysis of immune factor expression in *E. acervulina*, *E. maxima*, and *E. tenella* oocysts challenged chicken macrophages showed common and different responses to *Eimeria* challenge. Many interleukins and chemokines were upregulated, but one chemokine K60 (CXCL1) was only found increased in *E. tenella* oocysts challenged macrophages (Dalloul et al., 2007). Liver-expressed antimicrobial peptide-2 (LEAP2) is an antimicrobial peptide that disrupts the membrane of bacteria, and is upregulated in *Salmonella*-challenged chickens (Townes, et al., 2004). In contrast, LEAP2 was found to be downregulated in the jejunum of *E. maxima*-challenged broilers (Casterlow, et al., 2011).

The small intestine is the primary site for nutrient absorption in chickens (Leeson, et al., 2001). The final digestion of proteins and polysaccharides is catalyzed by membrane bound peptidases and glucosidases, respectively. Short peptides, free amino acids and monosaccharides are transported by the intestinal enterocytes by specific transporters located at the brush border membrane and basolateral membrane (Leeson, et al., 2001). Because *Eimeria*-challenged chickens showed reduced feed efficiency and body weight gain, it is likely due to changes in expression of digestive enzymes and nutrient transporters in the intestine. Paris and Wong (2013) reported decreased expression of the brush border membrane amino acid transporters EAAT3 and b<sup>0,+</sup>AT, increased expression of the basolateral amino acid transporters LAT1 and ASCT1 and decreased expression of the zinc transporter ZNT1 in the jejunum of *E. maxima*-challenged broilers. The objective of this study was to compare changes in nutrient transporter and digestive enzyme gene expression in different sections of the small intestine following infection with *E. acervulina*, *E. maxima*, and *E. tenella*.

## MATERIALS AND METHODS

### Chicken and *Eimeria*

This study was approved by the Beltsville Research Center Animal Care and Use Committee and conducted at the Animal Parasitic Disease Laboratory (USDA Agricultural Research Service, Beltsville, MD). Chickens used in this study were Ross Heritage broiler males from

Longeneckers Hatchery (Elizabethtown PA). Birds were housed in suspended wire cages (46cm x 30cm = 1380cm<sup>2</sup>) with 2-3 birds per cage. Birds were fed a standard poultry starter ration (crumbles, 24% protein) and had free access to water.

*Eimeria* are all USDA strains: *E. acervulina* (USDA #12 isolate), *E. maxima* (Tysons isolate) and *E. tenella* (Wampler isolate). 1 day old chicks were transported to the USDA-ARS facility (Beltsville, MD) and were orally gavaged with either 1mL *Eimeria* oocysts or not gavaged at 21 d of age. The 4 treatments in this study are *E. acervulina* (200,000 oocysts/ bird), *E. maxima* (10,000 oocysts/bird), *E. tenella* (100,000 oocysts/bird) and control (not gavaged). Initial body weight of the chickens was obtained on 21d.

### **Tissue sampling**

Seven days post challenge chickens were weighted and euthanized by cervical dislocation and intestinal segments: duodenum, jejunum, ileum and ceca were collected (n=6). The contents of the intestine were squeezed out and the tissue segments were immediately stored individually in RNAlater (Invitrogen, Grand Island, NY). The samples were stored at 4 °C for 24 hrs and then were frozen at -70 °C before being shipped to Virginia Tech. Upon arrival each intestinal segment was removed from RNAlater. After homogenizing, a 20-30 mg tissue aliquot was placed in a 2-mL microfuge tube for RNA extraction and the remaining homogenate was placed in a separate 2-mL microfuge tube. Both tubes were frozen on dry ice and stored at -80°C.

### **Total RNA extraction**

The 20-30 mg of homogenized tissue was placed in 500µL Tri Reagent (Molecular Research Center Inc., Cincinnati, OH) and shaken twice at 25Hz/s for 2 min using a TissueLyser II (QIAGEN Inc., Valencia, CA) following the animal tissue protocol. After homogenization 100 µL of chloroform were added for phase separation. The RNA pellet was suspended in 0.1% DEPC (Diethylpyrocarbonate, Sigma-Aldrich, St. Louis, MO) treated water depending on the pellet size and incubated for 10 minutes at 56°C. RNA concentration was determined using a NanoDrop 1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE). Any sample that had a concentration greater than 2000ng/µL was further diluted and reassayed. RNA quality was assessed by agarose-formaldehyde gel electrophoresis. All extracted RNA samples were stored at -80°C.

## Reverse Transcription

Total RNA was diluted to 0.1 µg/µL in DEPC water. cDNA was synthesized using the high capacity cDNA reverse transcription kit (Applied Biosystems, Foster City, CA). Each 20µL reverse transcription reaction contained 2 µL 10X reverse transcription buffer, 2 µL 10X random primers, 1 µL multiscribe reverse transcriptase (50 U/µL), 0.8 µL 25x dNTPs, 9.2 µL DEPC water, and 5 µL of 0.1 µg/µL diluted RNA sample. The RNA and master mix were combined in a 0.5-mL microfuge tube, which was then run in a thermocycler for 10 min at 25 °C followed by 120 min at 37 °C and 5 min at 85 °C. The cDNA was diluted 1:20 with DEPC water and stored at -20°C.

## Quantitative Real-Time PCR

Quantitative real-time PCR (qPCR) was performed using 96-well plates. Each reaction contained 5 µL diluted cDNA, 20 µL of PCR master mix which contained 12.5 µL 2X SYBR Green Master Mix (Applied Biosystems), 0.5 µL forward primer (5 µM), 0.5 µL reverse primer (5 µM), and 6.5 µL DEPC water. Each reaction was run in duplicate. The plate was sealed with a MicroAmp Optical Adhesive Film (Applied Biosystems) and spun down in a centrifuge to mix reagents and remove bubbles and loaded into an Applied Biosystems 7300 Real-Time PCR instrument (Applied Biosystems). The following real time PCR conditions were used: 95 °C for 10 min followed by 40 cycles of 95 °C for 15s and 60 °C for 1 min. Genes analyzed were APN, ASCT1, b<sup>o+</sup>AT, B<sup>o</sup>AT, CAT1, CAT2, EAAT3, GLUT1, GLUT2, GLUT5, LAT1, LEAP2, Pept1, rBAT, SGLT1, SI, y<sup>+</sup>LAT1, y<sup>+</sup>LAT2 and ZNT1 (Table I-1). The endogenous control was the chicken beta-actin gene. All forward and reverse primer sequences are shown in Table II- 1. Primers were designed using the Primer Express software (Applied Biosystems) and synthesized by Eurofins MWG Operon (Huntsville, AL).

## Quantitative Real-Time PCR Analysis

All plates were analyzed individually using the software provided with the 7300

Real-Time PCR instrument and raw Ct data was obtained. Average gene expression relative to the endogenous control for each sample was calculated using the  $2^{-\Delta\Delta Ct}$  method described by Livak and Schmittgen (2001). For gene expression changes affected by different *Eimeria* challenge, the average  $\Delta Ct$  of the 6 control samples was used to calculate the  $\Delta\Delta Ct$  value, which

was performed separately for each intestinal segment, *Eimeria* treatment and each gene are a group. For comparison of gene expression in different segments of the intestine in the control group, the average  $\Delta\text{Ct}$  of the 6 duodenum samples was used to calculate the  $\Delta\Delta\text{Ct}$  value. Data points that exceed  $\pm 3$  standard deviations from the mean were discarded as outliers.

### **Statistical Analysis.**

All data were analyzed by ANOVA using JMP<sup>®</sup> Statistical Discovery Software from SAS (SAS Institute, Cary, NC). Tukey's test was used for pairwise comparisons of body weight gain between different treatment groups. For gene expression of each *Eimeria* challenge, the model included the main effects of treatment, sorted by genes. Significant effects ( $P < 0.05$ ) were further evaluated with Dunnett's test for comparisons with the control. For gene expression of each intestinal segment in control birds, the model included the main effects of intestinal segment, sorted by genes. Significant effects ( $P < 0.05$ ) were further evaluated with Tukey's test for pairwise comparisons.

## **RESULTS**

### **Body weight gain for *Eimeria* challenged broilers**

During the 7 d challenge, control chickens gained  $499 \pm 37$  g (mean  $\pm$  SE), whereas *E. acervulina*-challenged chickens gained  $291 \pm 95$  g, *E. maxima*-challenged chickens gained  $349 \pm 23$  g and *E. tenella*-challenged chickens gained  $460 \pm 31$  g. Body weight gain was numerically decreased in *E. acervulina*-, *E. maxima*- and *E. tenella*-challenged broilers by 42%, 30% and 8% of control, respectively, but not significantly different at  $P < 0.05$  (Table III-1).

Treatment group	Weight gain, g (mean±SE)	P-value	Weight gain depression (%)
Control	499±37 <sup>a</sup>		
<i>E. acervulina</i>	291±95 <sup>a</sup>	0.06 <sup>1</sup>	42
<i>E. maxima</i>	349±23 <sup>a</sup>	0.24	30
<i>E. tenella</i>	460±31 <sup>a</sup>	0.96	8

**Table III-1. Body weight gain for *Eimeria* challenged broilers.** <sup>a</sup>Means indicated with same superscript are not significantly different at P<0.05. <sup>1</sup>P-value listed in this table were from comparison with control.

Different species of *Eimeria* preferentially infect specific regions of the intestine. *Eimeria acervulina* infects the duodenum, *E. maxima* the jejunum, and *E. tenella* the ceca. Changes in expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in *E. acervulina*, *E. maxima*, and *E. tenella* challenged broilers are shown for duodenum (Table III-2), jejunum (Table III-3), ileum (Table III-4), and ceca (Table III-5).

#### ***E. acervulina*-challenged broilers**

Expression of the amino acid transporters APN, b<sup>0+</sup>AT, B<sup>0</sup>AT, rBAT, CAT2 and EAAT3 was decreased to 46%, 24%, 31%, 25% 56% and 25% of control, respectively, in the duodenum (Table III-2) and rBAT was decreased to 50% of control in the ceca (Table III-5) of *E. acervulina*- challenged broilers.

The glucose transporter GLUT2 was decreased to 11% and 39% of control in the duodenum (Table III-2) and ceca (Table III-5), respectively, and GLUT5 was decreased to 36% and 68% of control in the duodenum (Table III-2) and ceca (Table III-5), respectively, in *E. acervulina*-challenged broilers. Expression of SI and ZNT1 was decreased to 27% and 43% of control, respectively, in the duodenum (Table III-2). APN and ZNT1 was decreased to 33% and 32% of control, respectively, in the ceca (Table III-5). LEAP2 was decreased to 6% of control in the duodenum (Table III-2) of *E. acervulina*- challenged broilers. No change in gene expression was observed in the jejunum and ileum.

### ***E. maxima*-challenged broilers**

Changes in expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in *E. maxima*-challenged broilers are summarized in Tables III-2 to III-5. APN was decreased to 51% and 18% in jejunum (Table III-3) and ceca (Table III-5). ASCT1 was increased 2.4-, 3.2- and 2.5 fold in duodenum (Table III-2), jejunum (Table III-3) and ileum (Table III-4) of *E. maxima*-challenged broilers. Expression of b<sup>0+</sup>AT was decreased to 54%, 32% and 6% and in the duodenum (Table III-2), ileum (Table III-4) and ceca (Table III-5), respectively. B<sup>0</sup>AT was decreased to 0.2% of control and EAAT3 was decreased to 1.5% of control in ceca (Table III-5). CAT2 was decreased to 41% and 51% in duodenum (Table III-2) and ileum (Table III-4), and increased 1.8-fold in the ceca (Table III-5) in *E. maxima*-challenged broilers. rBAT was decreased to 48%, 45% and 0.9% of control in duodenum (Table III-2), ileum (Table III-4) and ceca (Table III-5), respectively. LAT1 was increased 3.2-, 5.3- and 4.2-fold in duodenum (Table III-2), jejunum (Table III-3) and ileum (Table III-4), respectively in *E. maxima*-challenged broilers. y<sup>+</sup>LAT1 was decreased to 60% of control in the ileum (Table III-4); Pept1 was decreased to 0.2% of control in the ceca (Table III-5) in *E. maxima*-challenged broilers.

SI was decreased to 1% of control in ceca (Table III-2). Sugar transporter GLUT1 was increased 1.9-, 2.1-, 1.5- and 1.6-fold in duodenum (Table III-2), jejunum (Table III-3), ileum (Table III-4) and ceca (Table III-5), respectively. GLUT2 was downregulated to 29% and 8% in duodenum (Table III-2) and ceca (Table III-5) in *E. maxima*-challenged broilers. GLUT5 was decreased to 50%, 24% and 5% of control in duodenum (Table III-2), jejunum (Table III-3) and ceca (Table III-5), respectively.

ZNT1 was decreased to 36% of control in jejunum (Table III-3) and increased to 1.7-fold in ceca (Table III-5). LEAP2 was decreased to 17%, 10% and 11% of control in duodenum (Table III-2), jejunum (Table III-3) and ceca (Table III-5) in *E. maxima*-challenged broilers.

### ***E. tenella*-challenged broilers**

Changes in expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in *E. tenella*-challenged broilers are summarized in Tables III-2 to III-5. In the ceca of *E. tenella*-challenged broilers, APN, Pept1, CAT2, EAAT3, rBAT, SI, GLUT5 and ZNT1 was downregulated to 9%, 31%, 18%, 29%, 33%, 17%, 40% and 13% of control (Table III-5). While LAT1 was up regulated 2.7-fold (Table III-5). LEAP2 was up regulated 2-fold in jejunum (Table

III-3) of *E. tenella*-challenged broilers. No gene expression changes were observed in the duodenum and ileum of *E. tenella*-challenged broilers.

Summaries of gene expression changes to different *Eimeria* species are shown for duodenum (Figure III-1), jejunum (Figure III-2), ileum (Figure III-3) and ceca (Figure III-4), which illustrate common and species-specific changes in response to *Eimeria* challenge. In the duodenum, there was downregulation of b<sup>0+</sup>AT, rBAT, CAT2, GLUT2 GLUT5 and LEAP2 in *E. acervulina*- and *E. maxima*-challenged broilers (Figure III-1). *E. acervulina*- challenged birds also showed decreased expression of APN, B<sup>0</sup>AT, EAAT3, SI and ZNT1. *E. maxima*-challenged broilers showed upregulation of ASCT1, GLUT1 and LAT1. No gene expression changes were observed in the *E. tenella*-challenged duodenum samples. In the jejunum, *E. maxima*-challenged broilers showed upregulation of ASCT1, GLUT1 and LAT1, and there were also downregulation of APN, GLUT5 LEAP2 and ZNT1 (Figure III-2). *E. tenella*-challenged jejunum samples had increased expression of LEAP2. No gene expression changes were observed in the *E. acervulina*-challenged jejunum samples. Only *E. maxima*-challenged broilers showed changes in gene expression in the ileum (Figure III-3). ASCT1, GLUT1 and LAT1 were upregulated and b<sup>0+</sup>AT/rBAT, CAT2 and y<sup>+</sup>LAT1 was downregulated. Upregulation of ASCT1, GLUT1 and LAT1 in *E. maxima*-challenged broilers was common for duodenum, jejunum and ileum. Since there was no change of gene expression on digestive enzyme and nutrient transporter in the small intestine of *E. tenella*-challenged birds, it is not surprising that *E. tenella*-challenged birds did not show body weight gain depression. Even though *E. tenella* only infects the ceca, there were many common and unique changes in different species of *Eimeria* challenged ceca samples (Figure III-4). APN, GLUT5, and rBAT were commonly downregulated in all three *Eimeria* species. *E. acervulina*- and *E. maxima*-challenged ceca samples showed common downregulation of GLUT2. *E. acervulina*- and *E. tenella*-challenged samples both had decreased expression of ZNT1. *E. maxima*- and *E. tenella*-challenged ceca samples showed down regulation of EAAT3, Pept1 and SI. *E. acervulina*- and *E. maxima* have specific infection sites in the small intestine, the changes in gene expression caused by *E. acervulina*- and *E. maxima* infection in the ceca may be due to the structural and functional difference between the small intestine and the ceca.



Group	Relative gene expression									
	APN	ASCT1	b <sup>0,+</sup> AT	B <sup>0</sup> AT	CAT1	CAT2	EAAT3	GLUT1	GLUT2	GLUT5
Cont	1.08±0.16	1.04±0.12	1.10±0.20	1.18±0.25	2.89±1.67	1.11±0.16	1.13±0.23	1.03±0.11	1.19±0.25	1.10±0.21
<i>E.ace</i>	0.50±0.09	1.28±0.23	0.26±0.03	0.37±0.04	11.45±3.37	0.62±0.06	0.28±0.05	1.58±0.26	0.13±0.03	0.40±0.14
P-val	0.005*	0.83	0.0001*	0.01*	0.17	0.02*	0.002*	0.15	0.0004*	0.007*
<i>E.max</i>	0.86±0.88	2.50±0.43	0.59±0.09	1.11±0.22	10.83±4.69	0.45±0.06	0.84±0.11	1.99±0.25	0.35±0.10	0.55±0.14
P-val	0.44	0.001*	0.01*	0.98	0.22	0.001*	0.37	0.008*	0.004*	0.04*
<i>E.ten</i>	1.05±0.10	0.94±0.06	1.05±0.08	1.24±0.16	4.89±2.08	0.92±0.09	1.13±1.47	1.21±0.12	1.16±0.17	0.89±0.06
P-val	1.00	0.98	0.98	0.99	0.94	0.66	1.00	0.86	1.00	0.59

Group	Relative gene expression								
	LAT1	LEAP2	Pept1	rBAT	SGLT1	SI	y <sup>+</sup> LAT1	y <sup>+</sup> LAT2	ZNT1
Cont	1.04±0.12	1.20±0.24	1.19±0.26	1.12±0.22	1.05±0.15	1.13±0.21	1.08±0.17	1.04±0.12	1.10±0.20
<i>E.ace</i>	1.40±0.21	0.07±0.02	0.82±0.20	0.28±0.06	0.72±0.07	0.30±0.10	0.74±0.17	0.78±0.09	0.47±0.06
P-val	0.78	0.002*	0.72	0.0004*	0.56	0.004*	0.24	0.22	0.008*
<i>E.max</i>	3.28±0.59	0.20±0.10	1.11±0.40	0.54±0.07	1.76±0.37	0.97±0.19	0.67±0.11	1.07±0.10	0.90±0.12
P-val	0.0003*	0.007*	1.00	0.01*	0.08	0.82	0.12	0.99	0.60
<i>E.ten</i>	1.06±0.11	1.45±0.32	0.76±0.30	1.03±0.10	0.85±0.15	1.11±0.11	0.95±0.08	1.07±0.10	1.03±0.11
P-val	1.00	0.73	0.62	0.93	0.84	1.00	0.86	0.99	0.96

**Table III-2. Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in duodenum of *Eimeria*-challenged broilers.** *E.ace*=*E.acervulina*; *E.max*= *E. maxima*; *E. ten*= *E. tenella*; Cont=control chicks; P-val=P-value. Relative gene expression was determined using the  $2^{-\Delta\Delta C_t}$  method. APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT1 and CAT2= Cationic amino acid transporter-1 and -2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to b<sup>0,+</sup>AT; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase; y<sup>+</sup>LAT1 and y<sup>+</sup>LAT2= y<sup>+</sup> L amino acid transporter-1 and -2, respectively; ZNT1= Zinc transporter-1. \* Indicates statistical significance from control at  $p<0.05$ .

Group	Relative gene expression									
	APN	ASCT1	b <sup>0,+</sup> AT	B <sup>0</sup> AT	CAT1	CAT2	EAAT3	GLUT1	GLUT2	GLUT5
Cont	1.14±0.23	1.05±0.16	1.30±0.46	1.47±0.64	3.39±1.93	1.03±0.11	1.31±0.41	1.02±0.09	1.11±0.18	1.12±0.20
<i>E.ace</i>	0.89±0.16	1.07±0.10	0.87±0.26	0.88±0.26	10.50±2.90	1.39±0.44	0.74±0.11	1.16±0.09	0.39±0.12	1.22±0.39
P-val	0.50	1.00	0.81	0.65	0.61	0.58	0.56	0.90	0.10	0.98
<i>E.max</i>	0.58±0.02	3.31±0.69	0.31±0.03	0.69±0.06	19.63±8.13	0.40±0.05	0.57±0.04	2.11±0.31	0.31±0.09	0.20±0.04
P-val	0.04*	0.002*	0.26	0.45	0.07	0.17	0.37	0.001*	0.06	0.04*
<i>E.ten</i>	1.04±0.12	1.13±0.38	1.51±0.67	1.26±0.50	6.99±4.02	0.84±0.14	1.50±0.60	0.91±0.13	1.50±0.40	1.02±0.22
P-val	0.93	0.94	0.97	0.97	0.92	0.89	0.97	0.95	0.50	0.98

Group	Relative gene expression								
	LAT1	LEAP2	Pept1	rBAT	SGLT1	SI	y <sup>+</sup> LAT1	y <sup>+</sup> LAT2	ZNT1
Cont	1.06±0.19	1.14±0.18	1.12±0.25	1.13±0.24	1.02±0.09	1.02±0.09	1.04±0.12	1.03±0.10	1.04±0.13
<i>E.ace</i>	1.37±0.18	0.94±0.24	0.90±0.21	0.93±0.16	1.05±0.11	0.99±0.10	1.39±0.73	0.98±0.10	0.95±0.13
P-val	0.94	0.89	0.81	0.88	1.00	0.99	0.85	0.99	0.95
<i>E.max</i>	5.57±0.92	0.11±0.03	0.61±0.16	0.32±0.03	1.05±0.19	0.72±0.08	0.71±0.10	0.68±0.05	0.37±0.05
P-val	<.001*	0.02*	0.25	0.06	1.00	0.14	0.87	0.38	0.02*
<i>E.ten</i>	1.02±0.20	2.30±0.39	0.55±0.23	1.33±0.37	1.25±0.48	1.11±0.14	0.96±0.13	1.25±0.31	1.07±0.24
P-val	1.00	0.01*	0.18	0.89	0.87	0.88	1.00	0.68	1.00

**Table III-3. Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in jejunum of *Eimeria*-challenged broilers.** *E.ace*=*E. acervulina*; *E.max*= *E. maxima*; *E. ten*= *E. tenella*; Cont=control chicks; P-val=P-value. Relative gene expression was determined using the 2<sup>-ΔΔCt</sup> method. APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT1 and CAT2= Cationic amino acid transporter-1 and -2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to b<sup>0,+</sup>AT; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase; y<sup>+</sup>LAT1 and y<sup>+</sup>LAT2= y<sup>+</sup> L amino acid transporter-1 and -2, respectively; ZNT1= Zinc transporter-1. \* Indicates statistical significance from control at p<0.05.

Group	Relative gene expression									
	APN	ASCT1	b <sup>0,+</sup> AT	B <sup>0</sup> AT	CAT1	CAT2	EAAT3	GLUT1	GLUT2	GLUT5
Cont	1.04±0.13	1.05±0.14	1.11±0.23	1.07±0.19	3.99±2.73	1.09±0.20	1.10±0.22	1.03±0.10	4.06±3.14	1.04±0.14
<i>E.ace</i>	0.88±0.06	1.14±0.13	0.87±0.13	1.10±0.19	9.58±2.70	1.11±0.17	1.11±0.17	1.00±0.08	1.35±0.50	0.97±0.23
P-val	0.37	0.99	0.49	1.00	0.49	1.00	1.00	1.00	0.56	1.00
<i>E.max</i>	0.77±0.08	2.61±0.11	0.36±0.01	0.89±0.004	12.70±2.80	0.55±0.42	0.76±0.002	1.51±0.21	1.74±0.01	0.87±0.01
P-val	0.07	0.002*	0.004*	0.74	0.18	0.05*	0.37	0.02*	0.67	0.95
<i>E.ten</i>	1.13±0.08	0.86±0.09	1.29±0.11	1.20±0.16	4.19±1.79	0.97±0.11	1.50±0.17	0.83±0.12	2.52±1.24	1.59±0.43
P-val	0.80	0.93	0.76	0.89	1.00	0.90	0.25	0.05	0.86	0.40

Group	Relative gene expression								
	LAT1	LEAP2	Pept1	rBAT	SGLT1	SI	y <sup>+</sup> LAT1	y <sup>+</sup> LAT2	ZNT1
Cont	1.08±0.18	6.03±4.57	1.10±0.22	1.03±0.11	1.04±0.13	1.15±0.28	1.04±0.12	1.01±0.05	1.16±0.30
<i>E.ace</i>	1.14±0.21	2.64±0.68	1.18±0.34	0.89±0.11	0.83±0.11	1.38±0.14	0.83±0.14	0.96±0.08	1.04±0.12
P-val	1.00	0.65	0.99	0.59	0.56	0.77	0.45	0.94	0.94
<i>E.max</i>	4.50±0.11	1.70±0.01	0.95±0.001	0.46±0.001	0.98±0.004	1.55±0.001	0.62±0.14	0.82±0.03	0.81±0.19
P-val	0.001*	0.47	0.97	0.001*	0.98	0.41	0.04*	0.23	0.61
<i>E.ten</i>	0.80±0.10	3.69±1.26	0.68±0.26	1.29±0.08	0.83±0.12	1.36±0.25	0.78±0.09	0.96±0.07	0.87±0.10
P-val	0.97	0.88	0.60	0.14	0.57	0.83	0.26	0.92	0.46

**Table III-4. Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in ileum of *Eimeria*-challenged broilers.** *E.ace*=*E. acervulina*; *E.max*= *E. maxima*; *E. ten*= *E. tenella*; Cont=control chicks; P-val=P-value. Relative gene expression was determined using the 2<sup>-ΔΔCt</sup> method. APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT1 and CAT2= Cationic amino acid transporter-1 and -2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to b<sup>0,+</sup>AT; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase; y<sup>+</sup>LAT1 and y<sup>+</sup>LAT2= y<sup>+</sup> L amino acid transporter-1 and -2, respectively; ZNT1= Zinc transporter-1.

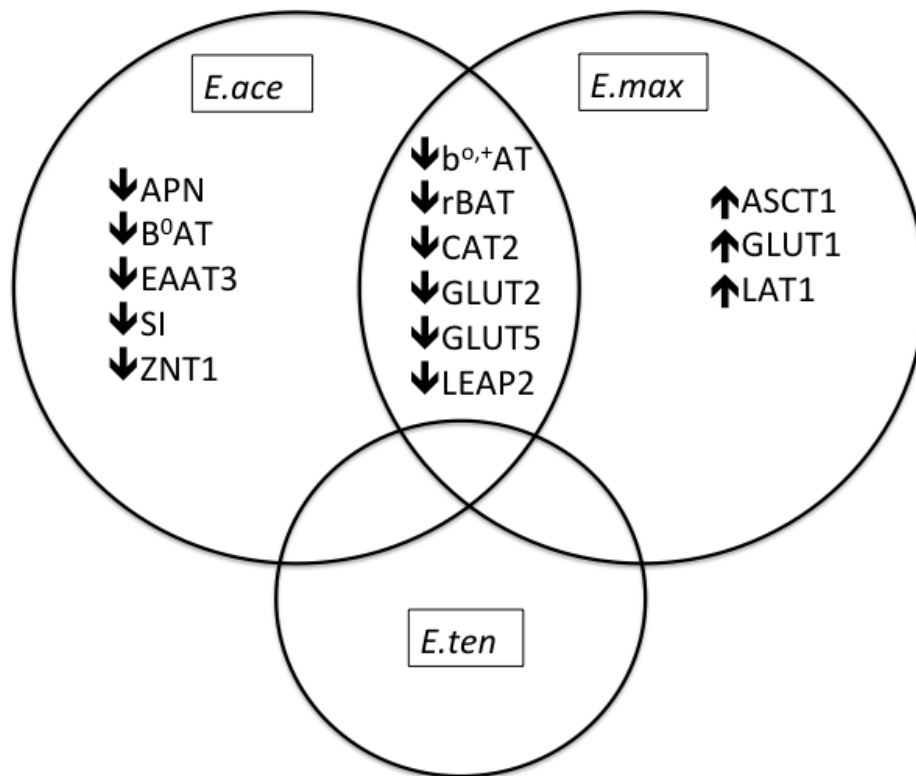
\* Indicates statistical significance from control at  $p < 0.05$ .

Group	Relative gene expression									
	APN	ASCT1	b <sup>0,+</sup> AT	B <sup>0</sup> AT	CAT1	CAT2	EAAT3	GLUT1	GLUT2	GLUT5
Cont	1.31±0.33	1.00±0.04	1.25±0.22	1.14±0.28	3.87±2.23	1.06±0.15	1.26±0.47	1.01±0.07	1.19±0.29	1.02±0.10
<i>E.ace</i>	0.43±0.20	0.91±0.15	1.76±0.26	1.46±0.31	8.67±3.58	0.74±0.10	0.55±0.08	0.62±0.09	0.46±0.08	0.69±0.10
P-val	0.01*	0.97	0.16	0.64	0.49	0.64	0.11	0.11	0.01*	0.01*
<i>E.max</i>	0.23±0.20	1.00±0.15	0.07±0.26	0.002±0.31	7.47±3.58	1.93±0.10	0.02±0.08	1.66±0.09	0.10±0.08	0.05±0.10
P-val	0.003*	1.00	0.0007*	0.006*	0.69	0.04*	0.004*	0.005*	0.001*	<.0001*
<i>E.ten</i>	0.12±0.02	1.21±0.28	1.57±0.16	0.86±0.19	5.31±2.41	0.19±0.06	0.37±0.05	0.90±0.09	0.80±0.14	0.41±0.05
P-val	0.001*	0.75	0.50	0.72	0.97	0.04*	0.04*	0.87	0.26	<.0001*

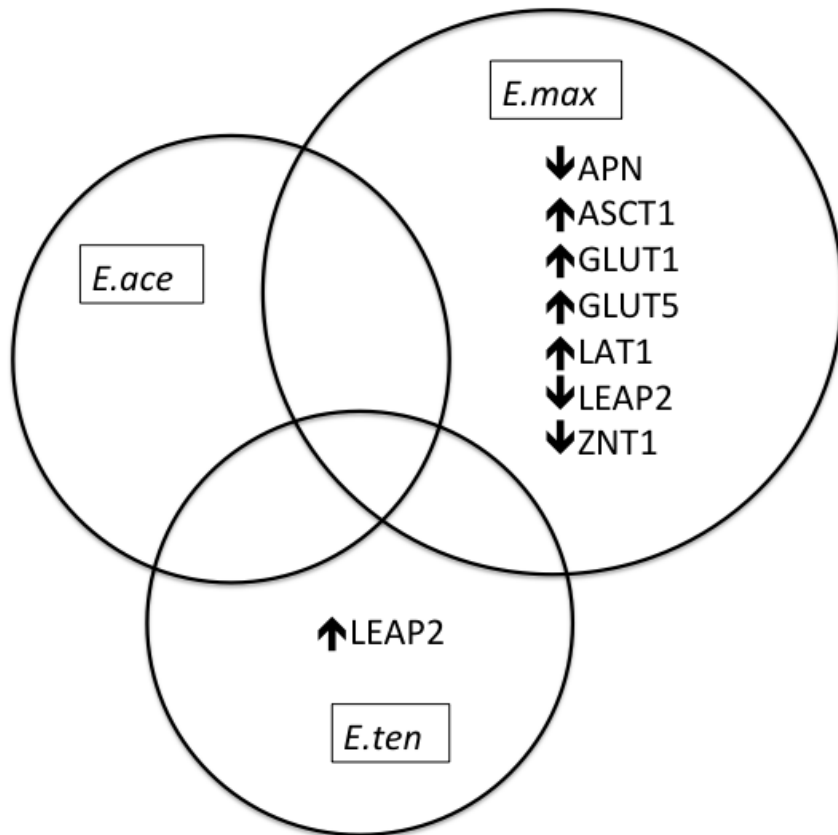
Group	Relative gene expression								
	LAT1	LEAP2	Pept1	rBAT	SGLT1	SI	y <sup>+</sup> LAT1	y <sup>+</sup> LAT2	ZNT1
Cont	1.01±0.07	2.45±0.98	1.43±0.48	1.17±0.23	1.09±0.21	1.09±0.19	1.03±0.11	1.01±0.08	1.04±0.14
<i>E.ace</i>	1.40±0.40	1.09±0.49	1.43±0.24	0.58±0.08	0.75±0.13	0.92±0.29	0.92±0.19	0.93±0.18	0.33±0.12
P-val	0.86	0.23	1.00	0.01*	0.94	0.83	0.92	1.00	0.004*
<i>E.max</i>	1.27±0.40	0.28±0.49	0.003±0.24	0.01±0.08	0.02±0.13	0.01±0.29	1.07±0.19	0.35±0.18	1.70±0.12
P-val	0.95	0.02*	0.004*	<.0001*	0.38	0.001*	0.99	0.34	0.006*
<i>E.ten</i>	2.77±0.74	0.54±0.15	0.44±0.13	0.39±0.11	2.77±1.05	0.19±0.06	0.51±0.15	1.60±0.61	0.13±0.05
P-val	0.02*	0.06	0.05*	0.001*	0.10	0.004*	0.06	0.44	0.0003*

**Table III-5. Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in ceca of *Eimeria*-challenged broilers.** *E.ace*=*E.acervulina*; *E.max*= *E. maxima*; *E. ten*= *E. tenella*; Cont=control chicks; P-val=P-value. Relative gene expression was determined using the  $2^{-\Delta\Delta Ct}$  method. APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT1 and CAT2= Cationic amino acid transporter-1 and -2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to b<sup>0,+</sup>AT; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase; y<sup>+</sup>LAT1 and y<sup>+</sup>LAT2= y<sup>+</sup>L amino acid transporter-1 and -2, respectively; ZNT1= Zinc transporter-1. \* Indicates statistical significance from control at  $p<0.05$ .

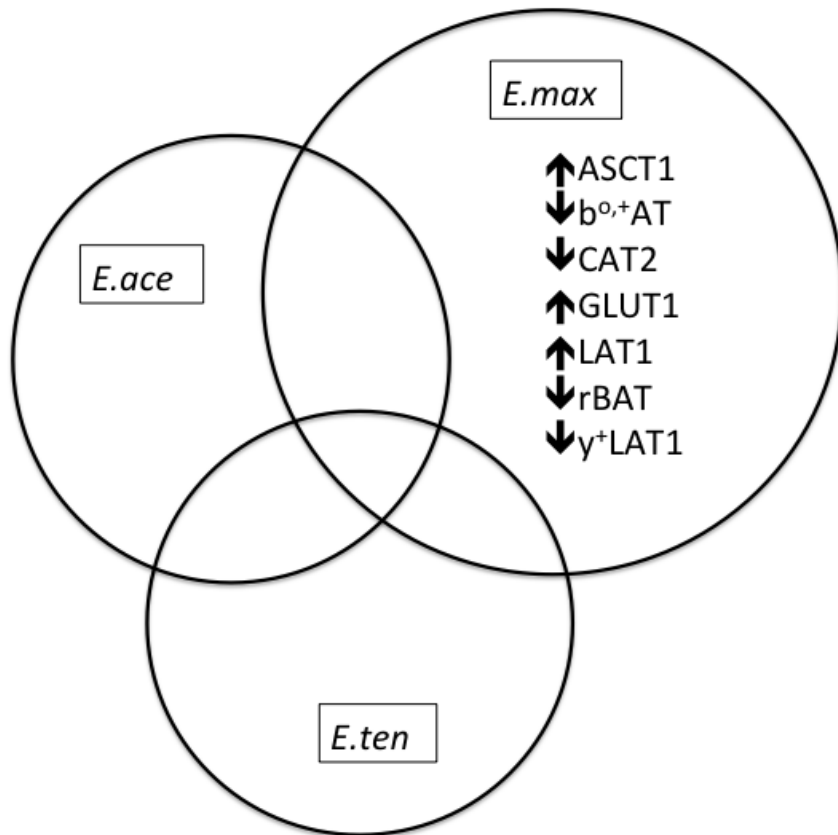


**Figure III-1. Summary of gene expression changes to different *Eimeria* in the duodenum.**

*E. ace*=*E. acervulina*; *E. max*= *E. maxima*; *E. ten*= *E. tenella*; APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT2= Cationic amino acid transporter-2; EAAT3= Excitatory amino acid transporter 3; GLUT2 and GLUT5= Glucose transporter-2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; rBAT= protein related to b<sup>0,+</sup>AT; SI= Sucrase isomaltase; ZNT1= Zinc transporter-1; ↓=downregulation; ↑=upregulation.

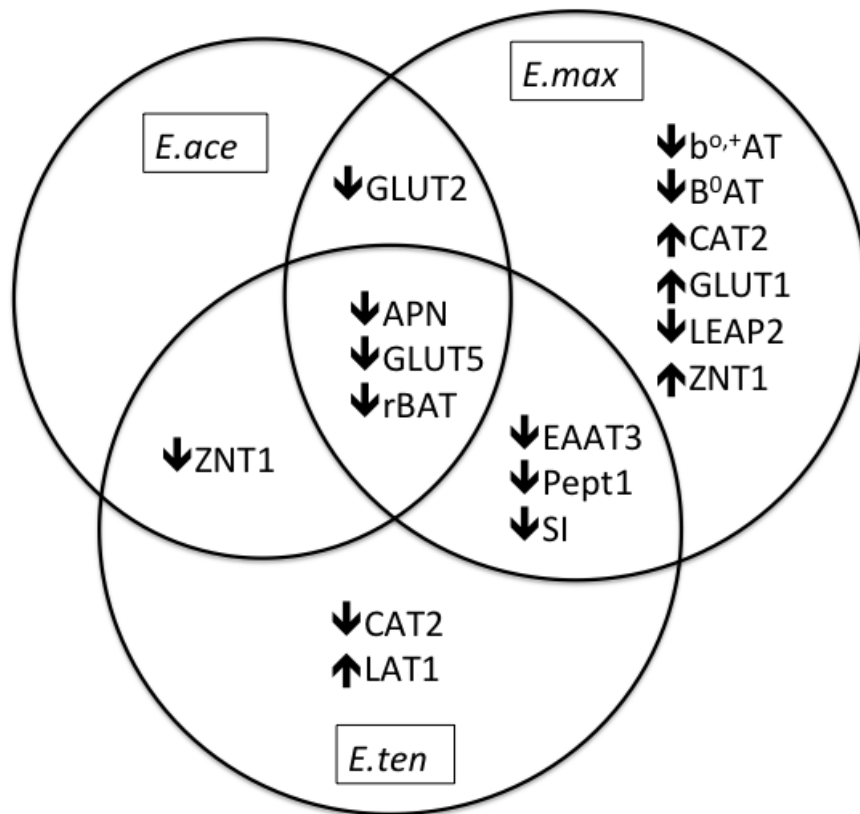


**Figure III-2. Summary of gene expression changes to different *Eimeria* in the jejunum.** *E.ace*=*E.acervulina*; *E.max*= *E. maxima*; *E. ten*= *E. tenella*; APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; GLUT1 and GLUT5= Glucose transporter-1 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; ZNT1= Zinc transporter-1; ↓=downregulation; ↑=upregulation.



**Figure III-3. Summary of gene expression changes to different *Eimeria* in the ileum.**

*E.ace*=*E.acervulina*; *E.max*= *E. maxima*; *E. ten*= *E. tenella*; ASCT1= Alanine, serine, cysteine and threonine transporter;  $b^{0,+}AT$  =  $Na^+$ -independent neutral amino acid transporter; GLUT1 = Glucose transporter-1; LAT1=L type amino acid transporter-1; rBAT= protein related to  $b^{0,+}AT$ ;  $y^+LAT1$ =  $y^+$  L amino acid transporter-1; ↓=downregulation; ↑=upregulation.



**Figure III-4. Summary of gene expression changes to different *Eimeria* in the ceca.**

*E.ace*=*E.acervulina*; *E.max*= *E. maxima*; *E. ten*= *E. tenella*; APN= Aminopeptidase N; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT2= Cationic amino acid transporter-2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to b<sup>0,+</sup>AT; SI= Sucrase isomaltase; ZNT1= Zinc transporter-1; ↓=downregulation; ↑=upregulation.



### **Relative gene expression in different intestinal segment**

Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in different intestinal segment in control birds is summarized in Table III-6. Relative expression level was standardized to duodenum samples. The main purpose of this part of the study is to examine the difference in gene expression between the small intestine and the ceca. Many genes were down regulated in the ceca when compared to the small intestinal samples. Expression level of B<sup>0</sup>AT, LEAP2, Pept1 and SI in the ceca was expressed at less than 1% of duodenum, jejunum and ileum samples. b<sup>0,+</sup>AT, EAAT3, GLUT2, GLUT5 rBAT and SGLT1 was expressed between 1 and 6% of the small intestinal samples. APN and y<sup>+</sup>LAT2 expression was expressed at about 40% in the ceca when compared to the small intestinal samples. There was an approximately 3-fold upregulation of CAT2 and GLUT1 in the ceca relative to the small intestine. Genes such as ASCT1, CAT1, LAT1, y<sup>+</sup>LAT1 and ZNT1 showed similar expression levels in duodenum, jejunum, ileum and ceca in the control group chickens.

Tissue	Relative gene expression						
	APN	ASCT1	b <sup>0,+</sup> AT	B <sup>0</sup> AT	CAT1	CAT2	EAAT3
DU	1.08±0.16 <sup>ab</sup>	1.04±0.12 <sup>a</sup>	1.10±0.20 <sup>a</sup>	1.18±0.25 <sup>ab</sup>	2.89±1.67 <sup>a</sup>	1.05±0.16 <sup>b</sup>	1.13±0.23 <sup>ab</sup>
JE	1.48±0.29 <sup>a</sup>	1.05±0.16 <sup>a</sup>	0.88±0.31 <sup>ab</sup>	1.60±0.70 <sup>a</sup>	2.38±1.36 <sup>a</sup>	0.86±0.09 <sup>b</sup>	2.44±0.77 <sup>a</sup>
IL	1.64±0.21 <sup>a</sup>	1.03±0.13 <sup>a</sup>	1.05±0.22 <sup>a</sup>	1.86±0.33 <sup>a</sup>	3.57±2.45 <sup>a</sup>	1.11±0.21 <sup>b</sup>	2.36±0.48 <sup>a</sup>
CE	0.47±0.12 <sup>b</sup>	1.02±0.04 <sup>a</sup>	0.04±0.01 <sup>b</sup>	0.002±0.0005 <sup>b</sup>	4.33±2.50 <sup>a</sup>	3.55±0.49 <sup>a</sup>	0.05±0.02 <sup>b</sup>

Tissue	Relative gene expression					
	GLUT1	GLUT2	GLUT5	LAT1	LEAP2	Pept1
DU	1.03±0.11 <sup>b</sup>	1.19±0.25 <sup>ab</sup>	1.10±0.21 <sup>a</sup>	1.04±0.12 <sup>a</sup>	1.20±0.24 <sup>a</sup>	1.19±0.26 <sup>a</sup>
JE	1.21±0.11 <sup>b</sup>	1.41±0.22 <sup>a</sup>	1.39±0.24 <sup>a</sup>	0.77±0.14 <sup>a</sup>	0.59±0.10 <sup>ab</sup>	0.84±0.18 <sup>a</sup>
IL	1.57±0.15 <sup>b</sup>	0.41±0.31 <sup>bc</sup>	0.96±0.13 <sup>a</sup>	0.82±0.14 <sup>a</sup>	0.43±0.33 <sup>ab</sup>	0.76±0.15 <sup>a</sup>
CE	3.18±0.23 <sup>a</sup>	0.02±0.005 <sup>c</sup>	0.06±0.01 <sup>b</sup>	1.12±0.08 <sup>a</sup>	0.003±0.001 <sup>b</sup>	0.003±0.001 <sup>b</sup>

Tissue	Relative gene expression					
	rBAT	SGLT1	SI	y <sup>+</sup> LAT1	y <sup>+</sup> LAT2	ZNT1
DU	1.12±0.22 <sup>a</sup>	1.05±0.15 <sup>b</sup>	1.13±0.21 <sup>b</sup>	1.08±0.17 <sup>a</sup>	1.04±0.12 <sup>a</sup>	1.10±0.20 <sup>a</sup>
JE	0.99±0.19 <sup>a</sup>	1.62±0.14 <sup>ab</sup>	1.97±0.16 <sup>a</sup>	1.08±0.57 <sup>a</sup>	0.98±0.10 <sup>a</sup>	0.69±0.09 <sup>a</sup>
IL	0.80±0.09 <sup>a</sup>	1.96±0.24 <sup>a</sup>	1.13±0.27 <sup>b</sup>	0.89±0.11 <sup>a</sup>	0.94±0.05 <sup>a</sup>	0.59±0.15 <sup>a</sup>
CE	0.02±0.003 <sup>b</sup>	0.03±0.01 <sup>c</sup>	0.005±0.001 <sup>c</sup>	1.30±0.13 <sup>a</sup>	0.36±0.03 <sup>b</sup>	0.87±0.11 <sup>a</sup>

**Table III-6. Expression of digestive enzymes, nutrient transporters and an antimicrobial peptide in different intestinal segments in control group chickens.** DU=duodenum; JE=jejunum; IL=ileum. Relative gene expression was determined using the 2<sup>-ΔΔCt</sup> method. APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter; b<sup>0,+</sup>AT and B<sup>0</sup>AT= Na<sup>+</sup>-independent and Na<sup>+</sup>-dependent neutral amino acid transporter, respectively; CAT1 and CAT2= Cationic amino acid transporter-1 and -2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to b<sup>0,+</sup>AT; SGLT1= Sodium glucose transporter-1; SI= Sucrase isomaltase; y<sup>+</sup>LAT1 and y<sup>+</sup>LAT2= y<sup>+</sup> L amino acid transporter-1 and -2, respectively; ZNT1= Zinc transporter-1. <sup>a,b,c</sup> Means not indicated with same superscript are significantly different at p<0.05.

## DISCUSSION

Although *Eimeria* challenged broilers did not show a significant difference in body weight gain when compared to the control birds, *E. acervulina*- and *E. maxima*-challenged broilers showed numerically 42% and 30% of weight gain depression, respectively. Since this study was designed to have about 20% of weight gain depression, it was very likely that the chickens did have true weight gain depression, but due to the biological variance, the depression was not statistically significant. From the result we see there was no significant difference in expression of digestive enzyme and nutrient transporter expression change in the small intestine of *E. tenella*-challenged chickens, this may explain why *E. tenella*-challenged birds did not show the expected body weight gain depression.

The expression level of digestive enzymes and nutrient transporters in different segments of the intestine indicated that most of the genes examined in this study have lower expression level in the ceca when compared to the small intestine. In the most extreme case: the expression of B<sup>0</sup>AT, the neutral amino acid transporter located at the brush border membrane, in the ceca was less than 0.2% of the amount in the small intestine. Most of the genes analyzed did not show a significant difference in expression level between different segments of the small intestine, but there were many differences between the small intestine and the ceca, this result indicates a functional difference between the small intestine and the ceca for nutrient digestion and absorption.

Changes in expression of digestive enzymes and nutrient transporters throughout development or in response to different diets have been extensively studied in chicken (Gilbert, et al., 2008a). The genes examined in *Eimeria*-challenged chickens are linked to immune factors expressed by the chicken or the *Eimeria* transcriptome. Recently, a microarray study reported the transcriptome for chicken cecal epithelial cells upon *E. tenella*-challenge (Guo, et al., 2013). These results indicated most upregulated genes are involved in the immune response, cell differentiation, apoptosis and signaling pathways. The downregulated genes are generally metabolic enzymes, membrane components, and some transporters. A specific study on transcription of digestive enzymes and nutrient transporters in *Eimeria*-challenged chickens is limited to jejunum sample of *E. maxima*-challenged broilers (Paris and Wong, 2013). This study

investigated the expression of digestive enzymes and nutrient transporters in the intestine of *E. acervulina*-, *E. maxima*- and *E. tenella*-challenged broilers.

Three genes (APN, GLUT5 and ZNT1) were down regulated in all three species of *Eimeria* at their respective target sites (Figure III-5). APN represents 8% of total protein at the brush border membrane (Semenza, 1986). GLUT5 and ZNT1 are also most abundantly expressed in the intestine compared to other tissues and organs (Davidson, et al., 1992; Yu, et al., 2007). APN is involved in the final digestion of protein where it releases free amino acids from the N-terminus of the peptide. Decreased expression of APN can result in reduced efficiency of amino acid absorption. GLUT5 is the high affinity fructose transporter in the small intestine, which is responsible for fructose uptake at the enterocytes. Reduced expression of APN and GLUT5 can contribute to the depression of nutrient supply for the enterocytes and further result in reduced body weight gain of the animal. ZNT1 functions in efflux of  $Zn^{2+}$  at the basolateral membrane of enterocytes. Expression of ZNT1 is important to protect the cell against zinc toxicity (Nolte, et al., 2004). Zinc, as an antioxidant, can also protect the host against *E. acervulina*-induced oxidative damage (Georgieva, et al., 2011). Decreased expression of ZNT1 can either promote zinc toxicity and cell death and/or reduce the damage caused by *Eimeria*. There is evidence that these three genes can be upregulated by increasing feeding of their respective substrates (Christel, et al., 2007; Monteiro, et al., 1999; Tako, et al., 2005). But the cause and effect between downregulation of these three genes and decrease in nutrient intake in *Eimeria*-challenged chickens are yet to be investigated.

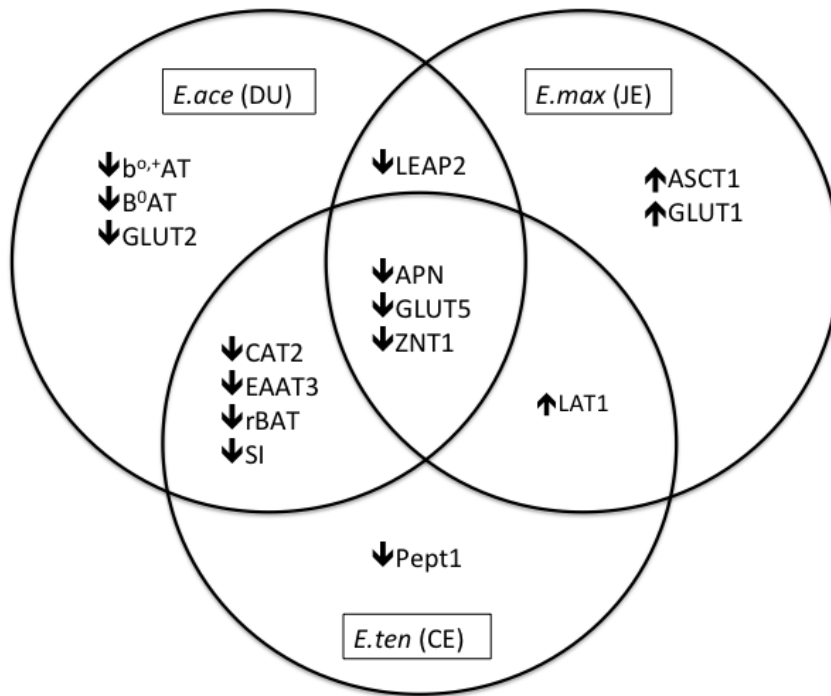
*E. acervulina*-challenged duodenum samples and *E. tenella*-challenged ceca samples showed the same common downregulation patterns for CAT2, EAAT3, rBAT and SI. Among those, EAAT3 plays an important role in enterocyte metabolism as it transports glutamate, the energy source of intestinal epithelial cells. Downregulation of EAAT3 also was observed by Paris and Wong (2013) in *E. maxima*-challenged jejunum samples but not in the jejunum samples in this study. This could be due to the difference in broilers used, Aviagen line A for Paris and Wong (2013) and Ross Heritage line for this study. Aviagen line A is a Ross line that was developed by feeding a corn-soy-based diet with lower relative amino acid concentrations (Gilbert, et al., 2007). The Ross Heritage line in this study was not been heavily selected. Decreased influx of glutamate can result in energy depletion, which can lead to accelerated programmed cell death. This may be part of the host defense mechanism for eliminating coccidial infection.

Downregulation of rBAT can result in reduced b<sup>0+</sup>AT presence at the brush border membrane, which may lead to reduced neutral amino acids transported into the cell. Decreased SI expression can affect the digestion of polysaccharides. Downregulation of CAT2 can lead to less cationic amino acid transport out of the cell, which may disrupt the electrical balance in the cell.

*E. maxima*-challenged jejunum samples and *E. tenella*-challenged ceca samples showed the same upregulation of LAT1. LAT1 transports large neutral amino acids like phenylalanine, which can be hydrolyzed into tyrosine (Ory and Lyman, 1955). Tyrosine is abundant in *E. maxima* oocysts walls (Belli, et al., 2009) and increased efflux of phenylalanine may cause a defect of oocyst wall formation. This may be a common mechanism for chickens to fight against *E. maxima* and *E. tenella* challenge. *E. maxima*-challenged chickens also showed increase expression of ASCT1. Even more robust increase of ASCT1 and LAT1 expression is observed in different strains of *E. maxima* infected broilers (Paris and Wong, 2013). Thus, increasing expression of basolateral amino acid transporters may be a common mechanism for *E. maxima* inhibition.

LEAP2 is an antimicrobial peptide that changes the permeability of parasite membranes. Intestinal LEAP2 level is upregulated in *Salmonella enterica*-infected chickens (Townes, et al., 2004). Both *E. acervulina*-challenged duodenum samples and *E. maxima*-challenged jejunum samples showed down regulation of LEAP2. The mechanism behind this downregulation is not yet clear, but it is proposed that upon entering the host cell *Eimeria* turns down the expression of LEAP2 (Casterlow, et al., 2011). In this study, in the jejunum of *E. tenella*-challenged broilers LEAP2 was up regulated and no significant change was observed in the ceca. In chickens challenged with 50,000 and 500,000 *Eimeria praecox* oocysts, LEAP2 is downregulated in both duodenum and jejunum at day 4 and day 5 after challenge (Sumners, et al., 2011). But at day 7 after challenge, no significant LEAP2 expression change is observed. In this study, there was no significant LEAP2 expression downregulation in the ceca of *E. tenella*-challenged broilers, LEAP2 change may be significant at a different time point.

In summary, many genes examined in this study showed common regulation in two or three species of *Eimeria* at their respective target site. Downregulation of APN, GLUT5 and ZNT1 may result in peptide and fructose depletion and zinc balance disruption in the infected cell. This may result in cell death and inhibits parasite replication.



**Figure III-5. Summary of gene expression changes to different *Eimeria* in their respective target tissue.** *E.ace*=*E.acervulina*, *E.max*= *E. maxima*, *E. ten*= *E. tenella*, DU=duodenum, JE=jejunum, CE=ceca, APN= Aminopeptidase N; ASCT1= Alanine, serine, cysteine and threonine transporter;  $b^{0,+}$ AT and  $B^0$ AT=  $Na^+$ -independent and  $Na^+$ -dependent neutral amino acid transporter, respectively; CAT2= Cationic amino acid transporter-2; EAAT3= Excitatory amino acid transporter 3; GLUT1, GLUT2 and GLUT5= Glucose transporter-1, -2 and -5, respectively; LAT1=L type amino acid transporter-1; LEAP2= Liver-expressed antimicrobial peptide-2; Pept1= Peptide transporter-1; rBAT= protein related to  $b^{0,+}$ AT; SI= Sucrase isomaltase; ZNT1= Zinc transporter-1; ↓=downregulation; ↑=upregulation.

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## CHAPTER IV. EPILOGUE

The results from these studies indicate that upon *Eimeria* challenge, many nutrient transporters in the enterocytes were downregulated. This may be the reason for the reduced feed efficacy in *Eimeria*-challenged chickens. *E. acervulina*-challenged layers and broilers showed many common downregulated genes in the duodenum. But the responses are very different in the jejunum and ileum, as broilers did not show any gene expression changes in these sections. The layers showed more changes compared to broilers, which may be due to the divergent selection for egg laying or rapid growth of the birds.

Many statistically significant changes in gene expression in this thesis did not exceed the range of 50% downregulation or 2-fold upregulation, these small changes in gene expression may be considered not biologically important. But when these small changes in digestive enzymes and nutrient transporters at the enterocyte are taken cumulatively, it can result in biologically significant changes. *E. acervulina*- and *E. maxima*-challenged broilers showed numerically 42% and 30% weight gain depression, respectively, when compared to the chickens in the control group. Although these changes were not statistically significant, a 30 to 40% weight gain depression of the birds would lead to a great economical impact in a commercial flock.

In the study of different species of *Eimeria* challenge on broilers, there are many changes in the ceca regardless of the specific target tissue of the *Eimeria* species. This may be due to the structural and functional differences of the ceca compared to the small intestine. *E. acervulina*, *E. maxima* and *E. tenella*-challenge resulted in common downregulation of APN, GLUT5 and ZNT1 at their respective target tissues. This indicates that there may be a common host response to *Eimeria* challenge.

LEAP2 is downregulated in the duodenum of *E. acervulina*-challenged layers and broilers, and in the jejunum of *E. maxima*-challenged broilers, but not in the ceca of *E. tenella*-challenged broilers. These results imply that downregulation of LEAP2 may be common in *Eimeria* which target the small intestine, but not for the ceca targeted *E. tenella*.

In this thesis, the effect of different species of *Eimeria* was compared in broilers but not in layers. It would be interesting to study how gene expression changes in layers following different *Eimeria* challenge. Also the comparison between layers and broilers can be investigated in both *E. maxima* and *E. tenella*-challenged birds.

In these studies, only the mRNA level of the genes was analyzed. It is important to note that mRNA levels sometimes do not reflect protein levels. Further research on protein level and distribution of the digestive enzymes and nutrient transporters can provide more information on gene expression in response to *Eimeria* challenge. All of the samples in the two studies were collected on day 7 after *Eimeria* challenge. As different genes may have expression changes at different times, it would be interesting to find out the time course for gene expressions changes after *Eimeria* challenge. Many genes did not show significant expression changes in these studies but may be significantly up or downregulated at different time points.

Genes analyzed in these two studies are limited to 16 nutrient transporters, 2 digestive enzymes and one antimicrobial peptide. The change in expression profiles of other nutrient transporters and digestive enzymes present in the intestine can be further studied.

This study provides an initial characterization of some of the changes in the intestinal gene expression profiles in *Eimeria*-challenged chickens and may help elucidate a novel molecular mechanism of host response to *Eimeria* challenge.

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