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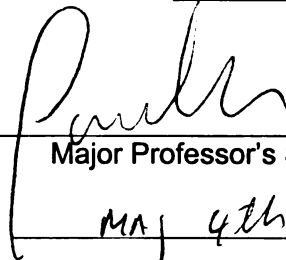
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**DIFFERENTIAL GENE EXPRESSION IN THE FRONTAL CORTEX AND  
HIPPOCAMPUS OF PIGLETS WEANED AT DIFFERENT AGES**

**By**

**Rosangela Poletto**

**A THESIS**

**Submitted to  
Michigan State University  
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for the degree of**

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## **ABSTRACT**

### **DIFFERENTIAL GENE EXPRESSION IN THE FRONTAL CORTEX AND HIPPOCAMPUS OF PIGLETS WEANED AT DIFFERENT AGES**

By

Rosangela Poletto

Early-weaned piglets show abnormal behaviors, aggression, and cognitive deficits. Therefore, it was hypothesized that early-weaned piglets experience aberrant expression of stress response genes in the frontal cortex (FC) and hippocampus (HP), brain areas involved with cognitive function and social behavior. The objective was to examine the effects of early and conventional weaning on gene expression in the FC and HP of piglets either socially isolated or kept with their littermates. Early (EW;  $n = 6$ ) and conventionally-weaned (CW;  $n = 6$ ) piglets were weaned at 10 and 21 days after birth, respectively. Non-weaned piglets of both age groups, 12 (NW;  $n = 6$ ) and 23 (NW;  $n = 6$ ) days, remained with their dams. Half of CW, EW, and NW animals were socially isolated for 15 minutes at 12 (EW) and 23 (CW) days of age, immediately before euthanasia. Brain areas were collected and RNA extracted. A porcine brain library cDNA microarray and quantitative real-time RT-PCR were used to measure the expression of stress-responsive genes. Social isolation suppressed gene expression in the frontal cortex of piglets at 12 and 23 days of age, while early weaning suppressed hippocampal gene expression. These results may help to elucidate some of the biological basis for cognitive deficits and behavioral changes previously reported in early-weaned piglets.

With love and care, I dedicate this achievement to my family, who have always believed in my dreams and supported my work with love, understanding, and patience.

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## TABLE OF CONTENTS

List of Tables .....	vi
List of Figures .....	vii
Keys to Symbols or Abbreviations .....	ix
Chapter One – Introduction .....	01
Chapter Two – Effects of early weaning and social isolation on the expression of glucocorticoid and mineralocorticoid receptor and 11 $\beta$ -hydroxysteroid dehydrogenase 1 and 2 mRNAs in the frontal cortex and hippocampus of piglets.....	08
Chapter Three – Investigation of changes in global gene expression in the frontal cortex of early-weaned and socially isolated piglets using microarray and quantitative real-time RT-PCR.....	25
Chapter Four – Discussion and Future Research Directions .....	46
Compiled References .....	57

## **LIST OF TABLES**

Chapter 2; Table 1: Primer sequences used for Q-RT-PCR to analyze gene expression in the hippocampus and frontal cortex of piglets.....	14
Chapter 2; Table 2: Average change in relative expression of stress-responsive genes in the frontal cortex and hippocampus of weaned compared with non-weaned piglets .....	17
Chapter 2; Table 3: Main effect of social isolation on the relative mRNA abundance for tested genes in the brain areas examined .....	18
Chapter 3; Table 1: Primers used for Q-RT-PCR analysis of gene expression in the frontal cortex of piglets.....	35
Chapter 3; Table 2: Genes identified by BLAST analysis of differentially expressed ESTs on the PBL cDNA microarray .....	36

## LIST OF FIGURES

Chapter 2; Figure 1: Relative levels of gene expression in the frontal cortex of 12 day old compared with 23 day old piglets. Positive values indicate higher mRNA levels in 12 day old compared with 23 day old piglets. The error bars represent the standard errors of the mean (SEM). ** $P < 0.01$ .....	19
Chapter 2; Figure 2: Relative levels of gene expression in the hippocampus of 12 day old compared with 23 day old piglets. Positive and negative values indicate higher or lower mRNA levels, respectively in 12 day old compared with 23 day old piglets. The error bars represent the standard errors of the mean (SEM). * $P < 0.05$ , *** $P < 0.001$ .....	19
Chapter 3; Figure 1: Loop design applied to the cDNA microarray experiment (representing samples from one litter). Three litters were used for this experiment ( $n = 3$ ). The arrows indicate the labeling order (dyes Cy3/Cy5) on each array. EWC = early-weaned control, EWI = early-weaned and socially isolated, NWC = non-weaned control, NWI = non-weaned and socially isolated .....	31
Chapter 3; Figure 2: Relative expression of stress-responsive genes in the frontal cortex of piglets subjected to early weaning and/or social isolation. (a) actin related protein 2/3 complex (ARP2/3), (b) diazepam binding inhibitor (DBI), (c) tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein (14-3-3 protein), (d) phosphoprotein enriched in astrocytes 15kDa (PEA-15), (e) ornithine decarboxylase antienzyme 2 (OAZ2), (f) carboxypeptidase E (CPE). The ratio represents the first treatment group compared to the second in each contrast. Negative values indicate smaller expression of the first group relative to the second. Positive values indicate greater expression of the first group compared with the second. Each bar represents the mean ( $\pm$ SEM) change in gene expression for each treatment comparison. * $P < 0.05$ , ** $P < 0.01$ . EWC = early-weaned control, EWI = early-weaned and socially isolated, NWI = non-weaned and socially isolated, NWC = non-weaned control. Note different scales on the y axes of the plots.....	40
Chapter 4; Figure 1: Diagram illustrating the potential effects of early weaning (EW) and social isolation (SI) on the hypothalamic-pituitary-adrenal axis and consequent changes in gene expression in the hippocampus and frontal cortex of piglets. Paraventricular nucleus (PVN); Corticotrophin release hormone (CRH); Adrenocorticotropin hormone (ACTH).....	47
Chapter 4; Figure 2: Power to detect 1.5 and 2-fold change in expression of genes in the frontal cortex of piglets as a function of sample size considering a median standard deviation = 0.84 .....	49

Chapter 4; Figure 3: Power to detect 1.5 and 2-fold change in expression of genes in the hippocampus of piglets as a function of sample size considering a median standard deviation = 0.67 .....	50
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## **KEYS TO SYMBOLS OR ABBREVIATIONS**

$\mu\text{g}$  – Microgram

$\mu\text{M}$  – Micromole

$\mu\text{l}$  – Microliter

11 $\beta$ -HSD1 – 11Beta-Hydroxysteroid Dehydrogenase 1

11 $\beta$ -HSD2 – 11Beta-Hydroxysteroid Dehydrogenase 2

14-3-3 protein – Tyrosine 3-monooxygenase / Tryptophan 5-monooxygenase Activation Protein

3' – 3' Primer End

5' – 5' Primer End

5-HT – Serotonin

ARP2/3 – Actin Related Protein 2/3 Complex

BLAST – Basic Local Alignment Search Tool

cDNA – Complementary Deoxyribonucleic Acid

CPE – Carboxypeptidase E

CWC – Conventionally-Weaned Control

CWI – Conventionally-Weaned Socially Isolated

DBI – Diazepam Binding Inhibitor

dT<sub>(18)</sub> – Deoxythymine (18 nucleic acid bases)

dUTP – Deoxyuridine Triphosphate

EST – Expressed Sequence Tag

EWC – Early-Weaned Control



EWI – Early-Weaned Socially Isolated

GC – Glucocorticoid

GR – Glucocorticoid Receptor

HPA – Hypothalamic-Pituitary-Adrenal

kDa – Kilo Dalton

LOESS – Locally Weighted Regression and Smoothing Scatter plots

mg – Milligram

MR – Mineralocorticoid Receptor

mRNA – Messenger Ribonucleic Acid

ng – Nanogram

NWC – Non-Weaned Control

NWI – Non-Weaned Socially Isolated

OAZ2 – Ornithine Decarboxylase Antienzyme 2

ODC – Ornithine Decarboxylase

PA – Polyamines

PBL – Porcine Brain Library

PEA-15 – Phosphoprotein Enriched in Astrocytes 15kDa

Q-RT-PCR – Quantitative Real Time Reverse Transcriptase Polymerase Chain Reaction

RNA – Ribonucleic Acid

SEM – Standard Error of the Mean

## **CHAPTER ONE**

### **Introduction**

Domestic pigs (*Sus scrofa*) raised in a free range environment are naturally weaned at approximately 17 weeks of age (Jensen and Recen, 1989). Better understandings of the nutritional needs of young pigs, and constraints dictated by the intensification of swine production systems have caused dramatic changes to the weaning age. For disease management purposes, the swine industry in the United States (US) has adopted a segregated early weaning system, which consists of weaning the animals at ages younger than 21 days and moving the animals to facilities physically separated from the breeding and farrowing units. Recent data indicate that in the US, 15% of piglets are weaned at less than 16 days of age, and approximately 64% of the animals are weaned younger than 20 days of age (NAHMS, 2001).

From a production perspective, there are important advantages of practicing early weaning of pigs. Early disease control is one of the major reasons supporting early weaning, since the animals are moved to a totally “clean” environment post-weaning (segregated early weaning) at the peak of their passive immunity (Hunter, 1986; Orgeur et al., 2001). Improvements in nutritional managements have also favored increasing weight gain and growth rates of early-weaned piglets (Kim et al., 2001; Patience et al., 2000). However, several studies indicate that early weaning may be deleterious to pig behavior and welfare (Gardner et al., 2001; Hay et al., 2001; Hohenshell et al., 2000; Weary et al., 1999; Worobec et al., 1999; Yuan et al., 2004).

Early-weaned piglets perform abnormal behaviors, such as belly nosing (Gardner et al., 2001) and bar chewing (Worobec et al., 1999). These animals also vocalize more (Weary et al., 1999) and exhibit increased levels of aggression (Hohenshell et al, 2000; Yuan et al., 2004) when compared to piglets weaned on later ages. Moreover, early weaning is a stressful event which increases plasma and urinary cortisol levels (Hay et al., 2001; Hohenshell et al., 2000) in addition to causing a transitory reduction in weight gain and growth (Hay et al., 2001). Hunger and nutritional deficits (Carroll et al., 1998; Worobec et al., 1999) may contribute to an impairment of neuronal mechanisms as a consequence of, for instance, deficiency of important amino acids responsible for neurotransmitter biosynthesis (e.g. Fernstrom, 2000; Kaufman et al., 2000). The occurrence of abnormal behaviors (Gardner et al., 2001; Worobec et al., 1999), increased aggression (Hohenshell et al, 2000; Yuan et al., 2004) and cognitive deficits (Laughlin & Zanella, 2003; Souza and Zanella, 2003) suggest that stress of early weaning, which is an adverse experience for the animals, alters the development and function of both the neuroendocrine and autonomic systems (Kaufman et al., 2000; Plotsky et al., 2001). For instance, corticotrophin release hormone, which is produced in response to stress, in addition to trigger release of cortisol from adrenal glands through activation of the hypothalamic-pituitary-adrenal (HPA) axis, also increases the release of norepinephrine in the brain (Kaufman et al., 2000).

A large body of scientific evidence indicates an age-dependent sensitivity of brain pathways to stress hormones (Kanitz et al., 1998; Kaufman et al., 2000; Plotsky et al., 2001). In pigs the first three weeks of age are critical “windows” of brain plasticity to alter behavior and brain development (Hemsworth et al., 1986; Weaver et al., 2000). For

instance, piglets neonatally handled showed permanent alteration of HPA axis function with increased plasma corticosteroid binding globulin binding capacity, decreased basal cortisol concentrations and increased adenocorticotropin hormone concentrations at the time of death (7 months of age). Additionally, handled animals showed greater locomotion during open field test and reduced body weight compared to non-handled piglets (Weaver et al., 2000)

Brain areas such as the hippocampus, which plays an important role in memory processes, and the frontal cortex, which facilitates behavioral organization and cognition, are targets of stress hormones, such as corticosteroids. Both hippocampus and frontal cortex have abundant levels of corticosteroid receptor binding sites (De Kloet, 2004; Diorio et al., 1993). Therefore, hippocampus and frontal cortex functions of piglets may be disrupted by stressful events (e.g. weaning, social isolation, and handling) primarily during the sensitive period of brain development (Hemsworth et al., 1986; Weaver et al., 2000). In a study performed with rats, Ordyan and colleagues (2001) examined corticosterone binding in the hippocampus and frontal cortex of animals that received glucocorticoid (GC) treatment at three weeks of age compared to one week old animals. Only animals treated at the third week showed prolonged corticosterone secretion at 30 days of age, and lower cerebral corticosteroid binding at 90 days of age, suggesting greater sensitivity to elevated levels of GC at early brain developmental phase. The presence of high levels of corticosteroids in these brain areas, induced by stress stimuli, has been credited with causing behavioral and cognitive deficits (Cook and Wellman, 2004; Mizoguchi et al., 2004). For instance, acute stress impairs learning acquisition of new information as well as memory of rats exposed to a hippocampal-dependent task

(Diamond et al., 1999). Moreover, acutely stressed rats show notable inhibition of long-term potentiation in the frontal cortex and hippocampus, as indicated by deficits in the acquisition and processing of information (Rocher et al., 2004). Changes in the frontal cortex caused by chronic stress affect spatial learning and memory in rats (Abidin et al., 2004; Radley et al., 2004). Additionally, the intensification of aggressive behavior is also mediated by stress hormones through altered neuronal morphology and function of frontal cortex (Blair, 2004) and hippocampus (Wood et al., 2003).

Stressful events trigger the hypothalamic production of corticotrophin-releasing hormone, which stimulates the pituitary gland to produce adrenocorticotrophin hormone (ACTH). This hormone stimulates the adrenal glands to synthesize corticosteroids (e.g. cortisol) and release them into the bloodstream. This physiological pathway is named the HPA axis (de Kloet, 2004). Cortisol crosses the blood brain barrier and affects the hypothalamus, hippocampus and frontal cortex, among other areas of the brain, by binding to glucocorticoid receptors (GR) and mineralocorticoid receptors (MR). Cortisol has higher affinity for MR, and when binding to MR, the stress response is buffered as corticosteroids are prevented from binding to GR (Perreau et al., 1999). One of the primary outcomes of central GC action is to mediate a negative feedback system which suppresses HPA axis activity when GC levels are elevated. The disruption of the HPA axis system is characterized by attenuated GC negative feedback, which is characterized by decreased expression of GR and MR (Mizoguchi et al., 2003). The enzymes 11 $\beta$ -hydroxysteroid dehydrogenase type 1 (11 $\beta$ -HSD1) and type 2 (11 $\beta$ -HSD2) are important pathways for GC metabolism (Holmes et al., 2003), and play a role in protecting the brain from deleterious effects of high concentrations of GC (Seckl, 1997). As dehydrogenases,

both enzymes inactivate GC by converting it on inactive 11-keto derivative cortisone. The 11 $\beta$ -HSD2 exclusively functions as a dehydrogenase (Seckl, 1997). However, 11 $\beta$ -HSD1 can also function as a reductase, regenerating active GC by transforming circulating cortisone.

The presence of GC in the brain is necessary for a wide range of normal physiological, behavioral and cognitive functions. Central levels of GC can be elevated in situations that may or may not be stressful, such as maternal care, changes in mood, fear and anxiety, attention, learning and memory (Erickson et al., 2003). In stressful circumstances, high levels of cortisol bind to GR activating a series of cellular events which regulate the expression of several neuronal genes (Herman, 1993). Taken together, available literature supports the hypothesis that early environmental manipulations, mainly during the first weeks of age, can result in permanent changes in the HPA axis function and behavior of piglets (Hemsworth et al., 1986; Weaver et al., 2000), given that early exposure to high levels of GC causes neuronal death (Lee et al., 2002) and alters organization of stress sensitive pathways (Mirescu et al., 2004).

The negative outcomes of stress on neuronal function in the frontal cortex and hippocampus can be intensified when individuals endure an additional stressful stimulus (Silva-Gomez et al., 2003). For instance, socially isolated early-weaned piglets show cognitive deficits compared to non-socially isolated animals (Laughlin & Zanella, 2002, Souza & Zanella, 2004). As a stressor, social isolation also elicits the negative feedback response controlled by the HPA axis, raising cortisol levels in pigs (Kanitz et al., 2004) and in rats (Weiss et al., 2004). Social isolation also impairs learning and memory in rhesus monkeys (Washburn & Rumbaugh, 1991), and rats (Rudy et al., 1999) and

induces fear in rats (Molina-Hernandez et al., 2001) and anxiety in pigs (Kanitz et al., 2004) and rats (Weiss et al., 2004).

Cerebral changes caused by stress, at the cellular level, can be studied in detail with the help of state of the art molecular biology techniques. Gene expression microarray can be used to characterize change in global gene expression in various tissues (Xiang & Chen, 2000), following exposure to stress. A porcine brain library cDNA microarray (Nobis et al., 2003) is currently available for screening changes in gene expression in 866 genes within the brain of pigs. Also, quantitative real time reverse transcriptase polymerase chain reaction (Q-RT-PCR) is extensively used to examine expression of specific genes. Q-RT-PCR has high sensitivity and accuracy in detecting low-abundance mRNA in various tissues. Microarray hybridization and Q-RT-PCR are viable approaches for examining underlying neuronal changes that may affect animal behavior and welfare in piglets.

We previously demonstrated that early-weaned piglets when socially isolated for 15 minutes showed reduced capacity to learn a spatial task (Laughlin & Zanella, 2002), and had an impaired ability to recognize familiar animals (Souza & Zanella, 2004). These changes indicate that some aspects of cognition may be affected by the inability of piglets to cope with stress when weaned at this stage of brain development. Connecting changes in gene expression in the brain to behavioral alterations in response to stressors will facilitate a better understanding of the mechanisms underlying neuronal and behavioral effects of stress in early-weaned piglets. Thus, our overall objective is to understand how stressful events, such as early weaning and social isolation, differently affect brains of early-weaned (10 days old) and conventionally-weaned piglets (21 days old). Our

specific objective is to study changes in expression of stress-responsive genes in the frontal cortex and hippocampus of early- and conventionally-weaned piglets that were either subjected to 15 minutes of social isolation or kept with littermates. Hence, we hypothesize that early-weaned piglets experience aberrant expression of stress-responsive genes in the frontal cortex and hippocampus.



## **CHAPTER TWO**

### **Effects of early weaning and social isolation on the expression of glucocorticoid and mineralocorticoid receptor and 11 $\beta$ -hydroxysteroid dehydrogenase 1 and 2 mRNAs in the frontal cortex and hippocampus of piglets**

#### **Abstract**

Pigs weaned younger than 21 days of age show behavioral abnormalities, aggressive behavior, impaired learning and memory, and social recognition deficits. Our aim in this experiment was to investigate whether age, weaning and (or) social isolation impacts the expression of genes regulating glucocorticoid response [glucocorticoid receptor (GR), mineralocorticoid receptor (MR), 11 $\beta$ -hydroxysteroid dehydrogenases 1 and 2 (11 $\beta$ -HSD1 and 11 $\beta$ -HSD2)] in the frontal cortex and hippocampus, brain areas involved in behavior organization and memory. Early- (EW;  $n = 6$ ) and conventionally-weaned (CW;  $n = 6$ ) piglets were weaned 10 and 21 days after birth, respectively. Non-weaned (NW;  $n = 6$ /group) piglets of both age groups remained with their dams. Two days after weaning, immediately before euthanasia and tissue collection, half of CW, EW, and NW animals were socially isolated for 15 minutes at 12 (EW) and 23 (CW) days of age. Frontal cortex and hippocampus were collected and RNA extracted. Differences in amounts of 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, GR and MR mRNAs in both brain areas were determined by quantitative real time RT-PCR and data subjected to multivariate linear mixed models analysis and effects of age, weaning status and social isolation were tested. When compared with non-weaned pigs at 12 days of age, the

hippocampi of early-weaned piglets showed a decrease in expression of the four genes ( $P < 0.01$ ), but no differences in expression were observed in CW compared to NW animals at age 23 ( $P > 0.1$ ). Social isolation decreased the expression of 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, GR and MR mRNAs ( $P < 0.05$ ) in the frontal cortex of both 12 and 23 days old pigs. As an age effect, 12 day old piglets showed higher MR mRNA in the frontal cortex ( $P < 0.01$ ) and lower 11 $\beta$ -HSD2 ( $P < 0.05$ ) and GR ( $P < 0.001$ ) mRNA in the hippocampus compared to 23 days old animals. The results indicate that early weaning affected the hippocampus of piglets at 12 days of age, and social isolation affected frontal cortex of piglets regardless of age. These results may be correlated with behavioral and cognitive changes reported in early-weaned piglets.

## **1. Introduction**

Early maternal separation has been extensively studied and shown to cause long term psycho-physiological effects on brain and behavior of humans and animals (Kuhn and Schanberg, 1998; Sanchez et al., 2001). Maternal separation interferes with the proper development of both psychobiological and neuroendocrine regulatory mechanisms in the developing brain (Kanitz et al., 2004; Kaufman et al., 2000; Plotsky et al., 2001). Moreover, maternal separation affects the individual's behavior by eliminating the predictability and controllability provided by the mother-infant interaction (Plotsky et al., 2001). The early weaning of piglets can provide a useful model for studying early maternal separation effects on behavior and neuroendocrine mechanisms. Previous studies revealed that piglets weaned younger than 21 days of age show abnormal behaviors (Gardner et al., 2001; Orgeur et al., 2001) and intensified aggression

(Hohenshell et al., 2000; Yuan et al., 2004) later in life. Early-weaned piglets, when exposed to fifteen minutes of social isolation, show cognitive deficits compared to non-socially isolated animals (Laughlin & Zanella, 2002; Souza & Zanella, 2004). The behavioral outcomes and cognitive deficits reported may result from modifications in responsiveness of neuronal mechanisms during a sensitive period of brain development (Plotsky et al., 2001; Tuchscherer et al., 2004). An age-dependent sensitivity of the brain to stress hormones, such as corticosteroids, has been reported to occur in piglets during the first three weeks after birth (Hemsworth et al., 1986; Hemsworth and Barnett, 1992; Weaver et al., 2000).

Hippocampus and frontal cortex functions include cognition and behavioral organization (e.g. Cao et al., 2004; Kesner et al., 1996, 2004; Ongur & Price, 2000). Basal concentrations of endogenous corticosteroid hormones like glucocorticoids (GC) are essential for maintaining these functions (Erickson et al., 2003). However, hippocampus and frontal cortex can be affected by stressful events since both areas contain high density binding sites for corticosteroids. Thus, high concentrations of corticosteroids in the hippocampus during brain development cause behavioral and cognitive deficits that may not be reversible (McEwen, 1997), as well as cognitive deficits in the frontal cortex by altering neuronal morphology and function (Cook and Wellman, 2004; Mizoguchi et al., 2004).

Stressful challenges, such as early weaning and social isolation, are responsible for activation of the stress axis resulting in increased GC levels (Hay et al., 2001; Hohenshell et al., 2000, Kanitz et al., 2004). One of the primary outcomes of increased central GC action is to trigger a negative feedback system which suppresses further

activation of the HPA axis, preventing serious neuronal damage directly caused by GC (Lee et al., 2002). Therefore, at early brain developmental stages, the disruption of the GC negative feedback system, which is characterized by decreased GR expression in the hippocampus and frontal cortex, may be responsible for brain dysfunction (Mizoguchi et al., 2003, 2004). The GC action is mediated by cytoplasmic mineralocorticoid (MR) and glucocorticoid receptors (GR) which bind GCs with different affinities in the brain (Erickson et al., 2003). Mineralocorticoid receptors, when activated, buffer the activation of the stress response by preventing GC from binding to GR (Perreau, 1999), which once heavily bound mediates various neuronal changes (Herman, 1993, Meaney et al., 1996). Therefore, during early stages of development, the disruption of the HPA axis may compromise the developing brain and be accountable for some aspects of cognitive impairment and abnormal behaviors (Mizoguchi et al., 2003, 2004). Glucocorticoids indirectly regulate the activity of the enzymes 11 $\beta$ -hydroxysteroid dehydrogenase type 1 (11 $\beta$ -HSD1) and type 2 (11 $\beta$ -HSD2), which modulate GC action (Holmes et al., 2003). When acting as dehydrogenases, both enzymes protect the brain from the deleterious effects of excessive GC by rendering them inactive (Seckl, 1997).

Therefore, our research focus is to understand the molecular events associated with the cognitive deficits reported previously in early-weaned piglets subjected to social isolation, a short-term stressor (Laughlin & Zanella, 2002; Souza & Zanella, 2004). We hypothesize that spatial and social cognitive impairments experienced by early-weaned piglets are preceded by aberrant expression of stress sensitive genes in the frontal cortex and hippocampus. Our aim was to investigate the effects of weaning at two ages, 10 and 21 days, on 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, GR and MR mRNA abundance in the frontal cortex

and hippocampus of piglets, when the animals were either socially isolated or kept with their littermates.

## **2. Materials and Methods**

### *2.1 Animals*

Twenty-four Large White female piglets from six litters were used in this experiment. Females were used as the experimental animals instead of males because male piglets are subjected to castration on the first days after birth, which is an adverse experience that may interfere with later stress response. The animals were housed at the Swine Teaching and Research Center, Michigan State University. Housing and feeding routines followed standard swine production practices. All animal housing and experimental procedures were approved by the Michigan State University All-University Committee on Animal Use and Care.

Four littermates from each litter were randomly assigned to one of four treatment groups belonging either to early or conventional weaning model. The early weaning model consisted of early-weaned control (EWC;  $n = 3$ ), early-weaned socially isolated (EWI;  $n = 3$ ), non-weaned control (NWC;  $n = 3$ ) and non-weaned socially isolated (NWI;  $n = 3$ ) treatments. The conventional weaning model consisted of conventionally-weaned control (CWC;  $n = 3$ ), conventionally-weaned socially isolated (CWI;  $n = 3$ ), non-weaned control (NWC;  $n = 3$ ) and non-weaned socially isolated (NWI;  $n = 3$ ) treatments. Early-weaned piglets (EW) were weaned 10 days after birth and the littermates were kept together until day 12 after birth. Conventionally-weaned piglets (CW) were weaned 21 days after birth and weaned littermates were kept together until day 23 after birth. Non-

weaned animals were left with their dams until days 12 or 23. On days 12 or 23 after birth, piglets assigned to EWI and CWI, respectively, and NWI groups, were socially isolated for 15 minutes and immediately euthanized. Social isolation was performed in a pen located in the same room as the dams and littermates but with no visual contact. Control animals (EWC, CWC and NWC) were then taken from their pens and immediately euthanized. Euthanasia was preceded by induction of general anesthesia with 5% isoflurane using a Moduflex Coaxial anesthesia machine (Dispomed, Quebec, Canada). Immediately after reaching a profound general anesthesia state, euthanasia was performed using an intracardiac injection of Sodium Pentobarbital (86mg/kg; Fatal Plus®, Vortech Pharmaceuticals, USA).

## *2.2 Tissue preparation and RNA extraction*

Brains were removed from all animals within 10 minutes of euthanasia. Frontal cortices and hippocampi from all animals were dissected out of both brain hemispheres and placed in RNAlater™ (Ambion, Austin, TX) to protect RNA integrity, and then snap frozen in liquid nitrogen. Samples were then stored at –80°C. The RNAlater™ was removed from the samples according to manufacturer's guidelines. Total RNA from individual frontal cortex and hippocampus samples was isolated using Ribo Pure Kit (Ambion) following the manufacturer's instructions. Quantity and purity of isolated RNA samples were analyzed using an RNA 6000 Nano Chip on an Agilent 2100 Bioanalyzer (Agilent Technologies, Wilmington, DE).

### 2.3 Quantitative Real-Time RT-PCR

Quantitative real-time reverse transcriptase polymerase chain reaction (Q-RT-PCR) was performed to examine the relative abundance of 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, GR and MR mRNA in the frontal cortex and hippocampus of piglets. Q-RT-PCR was performed as described previously (Gibson et al., 1996; Heid et al., 1996). A total of 2  $\mu$ g of total RNA from each sample was reverse transcribed with oligo (dT)<sub>18</sub> and SuperScript II reverse transcriptase (Invitrogen Life Technologies Corp., Carlsbad, CA). A ND-1000 spectrophotometer (NanoDrop Technologies, Inc., Rockland, DE) was used to determine quality and quantity of the resulting complementary DNA. Primer sequences for Q-RT-PCR were designed using Primer Express 2.0 Software (Applied Biosystems) and synthesized by Qiagen (Valencia, CA). Primer sequences for tested and control genes are shown in Table 1.

Table 1. Primer sequences used for Q-RT-PCR to analyze gene expression in the hippocampus and frontal cortex of piglets.

Gene name	GenBank Accession no.	Forward primer (5' → 3' end)	Reverse primer (5' → 3' end)
11 $\beta$ - HSD1	AF414124	GCAGCTTTGCGCCAAGAG	GATTTCCCAGCAGGAGAGAAGTC
11 $\beta$ - HSD2	AF414125	GCGAAAGCTTCCCACTGAAC	AGGGTCTGTTTGGGCTCATG
GR	AF141371	GATCATGACCGCACTCAACATG	TTGCCTTTGCCCATTTTAC
MR	U88893	GCGCAATCTGGAAGGTTCTTC	CGGGAGCGTGTTTTTAAGC
Beta actin	AF054837	CTCCTTCCTGGGCATGGA	CGCACTTCATGATCGAGTTGA
18S	AY265350	GGCTCATTAATCAGTTATGGTTCCT	AGCTCTAGAATTACCACAGTTATCCAAG

A total of 30ng of template cDNA and 12.5μl of SYBR Green (Applied Biosystems, Foster City, CA) were employed in each real-time reaction. Primer mix (forward and reverse) was used in a concentration of 5μM. *Sus scrofa* 18S ribosomal RNA and beta actin were selected as control genes for frontal cortex and hippocampus samples, respectively and used for normalization purposes. All Q-RT-PCR reactions were performed in triplicate using template from individual animals in each reaction. A relative standard curve was used as the Q-RT-PCR quantification method (Livak, 1997; Johnson et al., 2000). The standard curve was constructed using the following amounts of cDNA (in duplicate): 95ng, 40ng, 10ng, 0.1ng and 0.01ng. A single control sample was chosen to be used as template for the standard curve, which was constant for each tissue and for each group of samples (12 or 23 days). Standard curves for the control genes and genes of interest were incorporated into every run. Q-RT-PCR was performed and analyzed on an ABI Prism 7000 Sequence Detection System (Applied Biosystems).

#### *2.4 Q-RT-PCR data analysis*

The relative standard curve quantification software yielded 3 expression values for the tested and reference genes in each sample. These three technical replicates were averaged and the result for each tested gene was divided by the corresponding value of the control to obtain the normalized gene expression in each biological sample. For further analysis, the log-transformation of the normalized quantity for each sample was considered as the response variable. The expression of the four genes was analyzed simultaneously using a multivariate linear mixed model (Littell et al., 1996). Social isolation, age (12 and 23 days), weaning (weaned and non-weaned), gene (11β-HSD1,



11 $\beta$ -HSD2, GR and MR) and all possible interactions were set as fixed effects. Litter was considered as a random effect. All the (co)variances were estimated and the model assumptions (e.g. normality) were assessed. The main or simple effect contrasts were computed depending on the significance of the higher order interactions. The main effects are represented by the average difference in expression of two conditions. For instance, the difference of all socially isolated versus non-socially isolated individuals averaged across genes, weaning and age. The simple effects are represented by the differences between two groups within two levels of another factor. For instance, the simple effect of age within gene is the difference between the expression at two ages within each gene averaged across social isolation and weaning. Fold changes (ratios) were obtained by back transforming the linear estimates. The back transformation of the SEM was obtained by taking the anti-log of the mean plus or minus the standard error of the mean (SEM). For presentation of the results in which the gene expression was lower in the first treatment compared to the second, the ratio ( $< 1$ ) was divided into -1 to give a negative relative expression value ( $-1/\text{ratio}$ ). Fold changes showing with  $P < 0.05$  were considered statistically significant. Fold change values are presented as the means with the corresponding SEM.

### **3. Results**

The piglets studied in this experiment were weaned at two ages. Early-weaned animals were weaned at 10 days of age and samples collected at 12 days of age. Conventionally-weaned animals were weaned at 21 days after birth, and frontal cortex and hippocampus collected at 23 days of age. When examining mRNA levels for 11 $\beta$ -

HSD1, 11 $\beta$ -HSD2, GR and MR using real-time RT-PCR, a significant effect of weaning on gene expression was observed only in the hippocampus of early-weaned animals (interaction of age by weaning;  $P = 0.004$ ). Early-weaned piglets showed suppressed expression of the four tested genes in the hippocampus by an average fold of -2.52 ( $P = 0.004$ ), when compared with non-weaned piglets at 12 days of age (Table 2). Conversely, no significant changes in expression of the four genes were detected in the hippocampus of conventionally-weaned piglets when compared with non-weaned piglets at 23 days of age (Table 2). Interestingly, when examining the mRNA abundance for 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, GR and MR in the frontal cortex, there were no evidences of significant differences in mRNA levels in either early-weaned compared with non-weaned piglets at age 12, or in conventionally-weaned compared with non-weaned piglets at age 23 (Table 2). The interaction of age by weaning was not significant for this brain area ( $P > 0.1$ ).

Table 2. Average change in relative expression of stress-responsive genes in the frontal cortex and hippocampus of weaned compared with non-weaned piglets.

Tissue	Weaning status	Fold change	SEM	P-value
Frontal cortex	EW	1.35	[0.913, 1.914]	NS
	CW	-1.48	[-2.196, -0.808]	NS
Hippocampus	EW	-2.52	[-3.337, -1.244]	< 0.01
	CW	1.50	[1.1299, 1.904]	NS

Note. Positive and negative values indicate higher or lower gene expression, respectively, in weaned compared with non-weaned piglets at 12 and 23 days of age. SEM = standard error of the mean. NS = not significant.

At 12 or 23 days of age, a group of either weaned (EWI and CWI) or non-weaned (NWI) piglets were exposed to 15 minutes of social isolation. Social isolation significantly suppressed 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, GR, and MR mRNA by a mean fold of -1.94 ( $P < 0.05$ ) in the frontal cortex of both 12 and 23 days old piglets, regardless of whether the animals were weaned or non-weaned (Table 3). The interaction of gene with social isolation was not significant ( $P = 0.32$ ). Intriguingly, for all four genes tested in the hippocampus, no effects of social isolation were observed, and no significant interactions of social isolation with either age or weaning were detected ( $P > 0.1$ ) (Table 3).

Table 3. Main effect of social isolation on the relative mRNA abundance for tested genes in the brain areas examined.

Tissue	Average Fold change	SEM	P-value
Frontal cortex	-1.94	[-2.553, -1.092]	< 0.05
Hippocampus	1.15	[0.942, 1.438]	NS

Note. Negative values indicate lower gene expression in socially isolated compared with non-socially isolated animals regardless to the weaning status. SEM = standard error of the mean. NS = not significant.

Exclusively looking at age effects, 12 day old piglets showed significantly higher levels of MR mRNA ( $P = 0.007$ ) in the frontal cortex when compared to 23 day old piglets (Figure 1). Additionally, simple effect comparisons of age within gene indicated that 12 day old piglets had lower expression of 11 $\beta$ -HSD2 ( $P = 0.03$ ) and GR ( $P =$

0.0009) in the hippocampus (Figure 2) when compared to 23 day old piglets (interaction of gene by age;  $P = 0.006$ ).

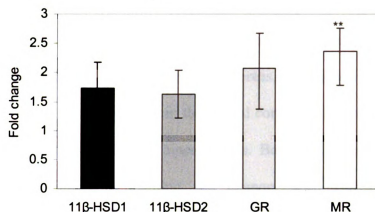


Figure 1. Relative levels of gene expression in the frontal cortex of 12 day old compared with 23 day old piglets. Positive values indicate higher mRNA levels in 12 day old compared with 23 day old piglets. The error bars represent the standard errors of the mean (SEM). \*\*  $P < 0.01$ .

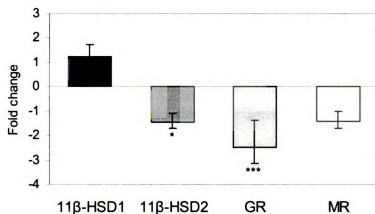


Figure 2. Relative levels of gene expression in the hippocampus of 12 day old compared with 23 day old piglets. Positive and negative values indicate higher or lower mRNA levels, respectively in 12 day old compared with 23 day old piglets. The error bars represent the standard errors of the mean (SEM). \* $P < 0.05$ , \*\*\* $P < 0.001$ .

#### **4. Discussion**

Our data illustrate distinct regulation of mRNA expression for 11 $\beta$ -HSD1 and 2, GR and MR in the frontal cortex and hippocampus of piglets. Interestingly, early weaning affected the studied genes in the hippocampus of piglets, but did not affect frontal cortex expression of the same genes. Whereas, 15 minutes of social isolation affected expression of genes examined in the frontal cortex of piglets, regardless of age, but did not affect expression in the hippocampus. Both brain areas are involved in cognitive function, control of learning and memory and behavioral organization processes (McEwen, 1997; Radley et al., 2004).

As described in other species, maternal separation also causes activation of the HPA axis in piglets as demonstrated by studies which reported that weaning increased cortisol levels in piglets when performed at different ages (Hay et al., 2001; Hohenshell et al., 2000; Kanitz et al., 2004). Our results showed that piglets weaned at 10 days of age (early-weaned) had consistently suppressed mRNA abundance for 11 $\beta$ -HSD1 and 2, GR and MR in the hippocampus at 48 hours post-weaning (12 days of age) compared to non-weaned piglets. However, there may be a confounding, and (or) additive effect of age with weaning. When exclusively considering age effects, 12 day old piglets were found to have lower levels of 11 $\beta$ -HSD2 and GR than 23 day old animals. The decreased expression of GR mRNA in this brain area may suggest that younger animals may experience difficulties in reacting to raised GC levels, and consequently may be less competent in activating the negative feedback to regulate HPA axis function. The disruption of the GC negative feedback system may be associated with decreased GR expression in hippocampus and may be associated with brain dysfunction (Mizoguchi et

al., 2003, 2004). Also, the decreased levels of  $11\beta$ -HSD2 mRNA may indicate greater vulnerability of younger piglets to high GC levels since this enzyme inactivates circulating GC (Holmes et al., 2003). Other studies showed that, during the early postnatal period,  $11\beta$ -HSD2 expression correlates with GR expression in brain regions where GCs strongly affect neuronal division, growth and maturation (Robson et al., 1998).

The suppression of GR expression found in the hippocampus of early-weaned piglets partially support the work of Kanitz and colleagues (1998) who found a decrease in GR binding in the hippocampus of piglets four days after weaning (at 35 days of age), compared to 2 hours before weaning. Decreased GR expression in the hippocampus suggests potential attenuation of negative feedback, which is responsible for suppressing further activation of HPA axis and GC synthesis (Mizoguchi et al., 2003). Our results are also in agreement with findings from a previous study in which rats exposed to 24 hours of maternal deprivation developed reduced MR and GR mRNA in the hippocampus (Vazquez et al., 1996). Moreover, we observed a suppression of the mRNA for dehydrogenases  $11\beta$ -HSD1 and 2 mRNA levels in the hippocampus of early-weaned piglets. It is important to mention that the regulation of mRNA for both enzymes in the brains of either weaned or socially isolated piglets has not being previously reported. Based on studies performed mostly with rodents, it is known that both enzymes play a role in GC metabolism, protecting the brain from the deleterious effects of excessive GC (Seckl, 1997). This indicates that the hippocampus of early-weaned piglets may be exposed to greater concentrations of active GC, which may be directly responsible for

negative effects on cognition, due mostly to hippocampal neuronal death (Antonawich et al., 1999; Lee et al., 2002).

Twelve day old piglets showed significantly higher MR mRNA levels in the frontal cortex when compared with 23 day old piglets. Unfortunately, limited information is known about the role of MR in the frontal cortex, but Diorio et al. (1993) reported GR and MR binding in the frontal cortex of rats and suggested that the frontal cortex mediates an inhibitory effect of GC on stress-induced HPA activity. Therefore, it is plausible to argue that the function of MR in the frontal cortex may be similar to that found in other brain areas in mediating GC negative feedback (de Kloet, et al., 1993; Diorio et al., 1993). In the hippocampus, the beneficial effects of GC in neuronal transmission and integrity are mediated by MR binding (de Kloet et al., 1993). No differences in expression of either GR or the dehydrogenases were detected in the frontal cortex of 12 compared to 23 day old animals.

In addition to early weaning, the impact of 15 minutes of social isolation, a short-term stressor, was tested in this experiment. We limited social isolation to only 15 minutes because our goal was to minimize nutritional deprivation and repeat the same protocol used in a previous study which reported cognitive deficits in early-weaned piglets (Laughlin & Zanella, 2002; Souza & Zanella, 2004). Fifteen minutes of social isolation significantly suppressed expression of 11 $\beta$ -HSD1 and 2, GR and MR mRNAs in the frontal cortex while no effect was observed in the hippocampus. In this case, we could speculate that social isolation, primarily a psychological stress, encompasses social separation from littermates and dam and exposure to a novel environment (Hennessy et al., 2004). Previous research using longer periods of social isolation showed different

patterns of gene expression in both frontal cortex and hippocampus of piglets. For instance, Kanitz et al. (2004) reported that 2 hours of daily social isolation from 3 to 11 days of age in piglets caused changes in behavioral, neuroendocrine and immune regulation and produced long-term effects on HPA axis activity. Also, according to Lapiz and colleagues (2003), social isolation, when applied as an early adverse event for long periods, causes long-term effects on the behavior and neurobiology involving hippocampus and frontal cortex functions. Short-term periods of social isolation may not be enough to cause changes in the hippocampal mRNA abundance for genes examined. Previous studies performed in piglets showed that repeated social isolation significantly altered GR binding in the hippocampus (Kanitz et al., 2004; Tuchscherer et al., 2004).

When comparing the differential responses to weaning versus social isolation observed, one should consider that the weaning period consisted of 48 hours of “stress”, while 15 minutes of social isolation could be characterized as an acute stressor. Therefore, the intensity and duration of the stress stimuli may be accountable for the differences in regulation of gene expression in the frontal cortex versus the hippocampus. However, the reasons for observed differences between frontal cortex and hippocampus, in regards to regulation of expression of 11 $\beta$ -HSD1 and 2, GR and MR, in response to distinct stressors (SI and EW) are unclear. Both brain areas are targets of GC and are intrinsically involved in stress response regulation (Meaney et al., 1996). However, it is intriguing that the negative feedback effects of GC on HPA axis activity in the frontal cortex of rats vary according to the nature of the stress (Diorio et al., 1993).

In summary, our results indicate that early weaning affected hippocampal expression of 11 $\beta$ -HSD1 and 2, GR and MR in piglets at 12 days of age while no effects



were observed in conventionally-weaned piglets. Thus, piglets at 10 days of age may be more vulnerable to weaning stress than 21 day old animals. Furthermore, fifteen minutes of social isolation suppressed the expression of all four tested genes examined in the frontal cortex, but not hippocampus, regardless of whether the piglets were 12 or 23 day old. These changes may be correlated to some behavioral and cognitive deficits previously reported in early-weaned piglets. Thus, early maternal separation in piglets may have the same long-term negative effects as observed in other species (Sanchez et al., 2001), but further studies should address if changes in mRNA abundance would also be confirmed at the level of receptor binding and enzyme activity.

## **CHAPTER THREE**

### **Investigation of changes in global gene expression in the frontal cortex of early-weaned and socially isolated piglets using microarray and quantitative real-time RT-PCR**

#### **Abstract**

We hypothesize that early-weaned piglets experience aberrant expression of stress-responsive genes in the frontal cortex (FC), a key brain area involved in cognitive function and behavior organization. To test this hypothesis early-weaned piglets (EW;  $n = 6$ ) were weaned 10 days after birth, while non-weaned (NW;  $n = 6$ ) piglets were left with their dams. Half of EW and NW animals were socially isolated (SI) for 15 minutes at 12 days of age when euthanasia and frontal cortex collection were performed. The effects of SI and EW were examined by gene expression profiling using cDNA microarray hybridizations, generated from a porcine brain cDNA library. A total of 108 genes were differentially expressed ( $P < 0.05$ , fold change  $> 1.25$ ) among the four comparisons. Forty-two genes had known functions, and 24 of these have important brain-related functions. Quantitative real-time polymerase chain reaction (Q-RT-PCR) was used to confirm regulation of expression of a subset of 6 genes, with important brain function selected from the microarray outcomes. In non-weaned animals a significant suppression of mRNA abundance for carboxypeptidase E, 14-3-3 protein and phosphoprotein enriched in astrocytes 15kD was observed in response to SI. Also, in early-weaned animals, diazepam binding inhibitor and actin related protein 2/3 complex

mRNA levels were suppressed in response to SI. Results suggest that social isolation of non- and early-weaned piglets may impact the expression of genes involved in regulation of neuronal function, development and protection in the frontal cortex of young pigs.

## **1. Introduction**

Weaning is a stressful event that may psychologically and physiologically challenge several animal species. In particular, weaning stress in piglets causes increases in plasma (Hohenshell et al., 2000) and urinary cortisol levels as well as temporary reductions in weight gain and growth (Hay et al., 2001). In addition, several studies have reported that early-weaned piglets perform abnormal behaviors (Gardner et al., 2001; Orgeur et al., 2001; Worobec et al., 1999), show more vocalization (Weary et al., 1999) and escape behaviors (Worobec et al., 1999) in addition to increased levels of aggression (Hohenshell et al., 2000; Orgeur et al., 2001; Yuan et al., 2004) relative to animals weaned later. Some of these behaviors suggest correlations between early weaning stress and increased stress hormone levels, which may negatively impact development of the central nervous system.

A large body of scientific evidence indicates an age-dependent sensitivity of brain pathways to stress hormones such as cortisol (Kanitz et al., 1998; Kaufman et al., 2000; Plotsky et al., 2001). In support of this hypothesis, early adverse experiences, such as maternal separation, may have long-term affects on brain function and behavior (Hay et al., 2001; Plotsky et al., 2001). Maternal separation interferes with proper development of both the autonomic and neuroendocrine systems (Kanitz et al., 2004; Kaufman et al., 2000; Plotsky et al., 2001) and affects behavior as a consequence of eliminating the

predictability and controllability provided by the mother-infant interaction (Plotsky et al., 2001).

Previous studies reported that early-weaned piglets when socially isolated for 15 minutes at 2 days post-weaning showed impaired spatial learning and memory (Laughlin & Zanella, 2002) and social recognition deficits (Souza & Zanella, 2004) compared to non-isolated animals. Moreover, impaired learning and memory are consequences of social isolation in rhesus monkeys (Washburn & Rumbaugh, 1991) and rats (Rudy et al., 1999). Social isolation pre- and post-weaning also activates the hypothalamic-pituitary-adrenal (HPA) axis, characterized by an increase in cortisol levels in pigs (Kanitz et al., 2004) and corticosterone in rats (Weiss et al., 2004), which may produce long-term neuroendocrine and behavioral effects (Hellemans et al., 2004; Tuchscherer et al., 2004). Social isolation of rats induces fear-like behavior (Molina-Hernandez et al., 2001), as well as anxiety when the animals were tested in the elevated plus maze (Weiss et al., 2004). Also, piglets socially isolated for 2 hours/day from day 3 to day 11 of age show behavioral, neuroendocrine and immunological changes, which may be indicative of depressed and anxious states (Kanitz et al., 2004). Altered behavioral responsiveness to opiates and psycho-stimulants has also been described as consequence of social isolation in rats (Kosten et al., 2000). These outcomes may result from modification of neuronal mechanisms in response to environmental challenges during a period of sensitive postnatal brain development (Tuchscherer et al., 2004).

The frontal cortex in humans, monkeys and rats is responsible for regulation of executive function, cognition and learning and memory, among other functions (Ongur & Price, 2000). A study performed by Rocher and colleagues (2004) demonstrated that

acutely stressed rats show notable inhibition of long-term potentiation in the frontal cortex, as indicated by deficits in the acquisition and processing of information. Moreover, changes in the frontal cortex caused by chronic stress affect spatial learning and memory in rats (Abidin et al., 2004). Kesner et al. (1996) described significantly impaired spatial learning during task performance in rats with lesions in the frontal cortex areas. These changes were also responsible for modifying social behaviors (Seguin, 2004), including aggression (Blair, 2004). Moreover, Lyons & Schatzberg (2003) showed that maternal availability alters the development of frontal cortex regions involved in reward-related memory in squirrel monkeys.

Currently, information on the impact of stress on development of the brain in young pigs is limited (Hay et al., 2001; Kanitz et al., 1998, 2004; Tuchscherer et al., 2004). Associating changes in brain gene expression to behavioral changes in response to stressors would allow for a better understanding of potential mechanisms disrupted by stress. In a previous experiment, we found that the expression of stress-response genes in the frontal cortex was affected by fifteen minutes of social isolation but not by weaning age (Chapter 2). Therefore, to further investigate potential mechanisms correlated with early weaning and social isolation stress in the frontal cortex, a novel and unique porcine brain cDNA microarray (Nobis et al., 2003) was utilized to determine effects of weaning and social isolation on gene expression profiles in the frontal cortex of piglets. In addition, quantitative real-time reverse transcriptase polymerase chain reaction (Q-RT-PCR) was employed to more precisely measure expression of a set of genes selected according to their function, from the microarray outcome. We hypothesize that early-

weaned piglets experience aberrant expression of stress-sensitive genes in the frontal cortex.

## **2. Material and Methods**

### *2.1 Animals and housing*

Twelve Large White female piglets, from three litters were used in this experiment. Only females were used as the experimental animals instead of males because male piglets are subjected to castration on the first days after birth, which is an adverse experience that may interfere with later stress responses. The animals were housed at the Swine Teaching and Research Center at Michigan State University. Housing and feeding routines followed standard swine production practices. Animal housing and experimental procedures were approved by the Michigan State University All-University Committee on Animal Use and Care and were in compliance with United States Department of Agriculture standards. Four female littermates from each of the three litters were randomly assigned to one of four treatment groups: non-weaned control (NWC;  $n = 3$ ), non-weaned and socially isolated (NWI;  $n = 3$ ), early-weaned control (EWC;  $n = 3$ ), and early-weaned and socially isolated (EWI;  $n = 3$ ). Early-weaned piglets were weaned 10 days after birth and the animals from each litter were kept together until 12 days of age. Non-weaned animals were left with their dams until day 12 after birth. On day 12, piglets assigned to EWI and NWI groups were visually and individually socially isolated from other pigs for 15 minutes, then immediately euthanized. Control animals, EWC and NWC, were taken from the pens with littermates or dams respectively and immediately euthanized. General anesthesia was induced with 5% isoflurane using a

Moduflex Coaxial anesthesia machine (Dispomed, Quebec, Canada). Immediately after reaching deep general anesthesia state, euthanasia was performed using an intracardiac injection of sodium pentobarbital (86mg/kg; Fatal Plus®, Vortech Pharmaceuticals, USA).

## *2.2 Tissue preparation and RNA extraction*

Brains were removed from all animals within 10 minutes of euthanasia. Frontal cortices were dissected out and placed in RNAlater™ (Ambion, Austin, TX), to protect RNA integrity, and snap frozen in liquid nitrogen. Samples were moved from liquid nitrogen and stored at –80°C. Prior to isolating mRNA, the RNAlater™ was removed from the samples according to the manufacturer’s guidelines. Total RNA from frontal cortex samples was isolated using Ribo Pure Kit (Ambion) following the manufacturer’s instructions. Quantity and purity of RNA samples were analyzed using an RNA 6000 Nano Chip Kit on an Agilent 2100 Bioanalyzer (Agilent Technologies, Wilmington, DE).

## *2.3 Microarray Loop Design*

The samples were arranged in three loops (Kerr & Churchill, 2001) representing three biological replicates per treatment. Each loop accommodated samples from littermates (Figure 1). The decision was made *a priori* to compare: *a*) EWC vs. EWI, *b*) EWI vs. NWI, *c*) NWI vs. NWC, and *d*) NWC vs. EWC. Comparison *a* directly addressed the effect of social isolation in early weaned animals. The effect of social isolation in non-weaned animals was directly tested using comparison *c*. Finally,

comparisons *b* and *d* were designed to directly examine the effect of early weaning in socially isolated and control animals respectively.

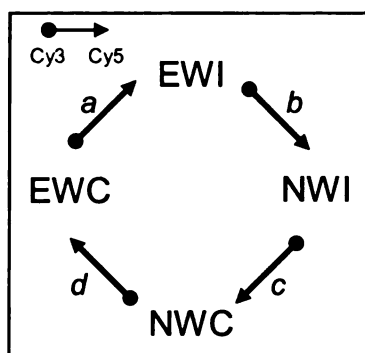


Figure 1. Loop design applied to the cDNA microarray experiment (representing samples from one litter). Three litters were used for this experiment. The arrows indicate the labeling order (dyes Cy3/Cy5) on each array. EWC = early-weaned control, EWI = early-weaned and socially isolated, NWI = non-weaned and socially isolated, NWC = non-weaned control.

## 2.4 cDNA Microarrays

A porcine brain library (PBL) cDNA microarray containing 866 expressed sequence tags (EST) was used for gene expression profiling. The PBL microarray is described in Nobis et al. (2003). During the data analysis for this experiment we found 858 unique porcine brain ESTs spotted in triplicate and another 8 ESTs spotted six times, resulting in a total of 866 instead of 877 unique features as previously reported (Nobis et al., 2003).

For this study, 12 cDNA microarray hybridizations were performed according to Figure 1. Microarray hybridizations were performed essentially as described (Nobis et al.,



2003). Briefly, 8 µg of total RNA from each frontal cortex sample was used as a template. The cDNA was produced using a reverse transcription reaction incorporating a modified dUTP into the cDNA (BD Atlas PowerScript Fluorescent labeling kit; BD Biosciences, Alameda, CA). Oligo(dT)<sub>18</sub> was used as a primer, and 0.6 ng of synthetic lambda Q-gene RNA was added to each reaction as a positive control for cDNA synthesis and hybridization. First-strand cDNA was labeled with Cy3 and Cy5 dyes (Amersham Biosciences, Piscataway, NJ) according to instructions for the BD Atlas PowerScript Fluorescent labeling kit (BD Biosciences). Dye-labeled products were purified using QIAquick spin columns (Qiagen, Valencia, CA), recombined and concentrated to 10 µl using Microcon 30 spin concentrators (Millipore, Bedford, MA). SlideHyb solution (Ambion) was added to the probe to reach a final volume of 110 µl. Microarray hybridizations were performed using GeneTAC HybStation (Genomic Solutions, Ann Arbor, MI). Final microarrays were scanned using a GeneTAC LS IV microarray scanner (Genomic Solutions). Images were processed and final intensity reports created using GeneTAC Integrator 4.0 software (Genomic Solutions).

Log intensities were background subtracted and LOESS (Yang et al., 2002) normalized for each array. A moderated t-test (Smyth, 2004) was used to assess significant differences in gene expression between treatment comparisons. Genes differentially expressed in at least one comparison at  $P < 0.05$  and exhibiting fold change greater than or equal to 1.25 (Nobis et al., 2003) were submitted to basic local alignment search tool (BLAST; Altschul et al., 1990) analysis on our database (<http://nbfgc.msu.edu>) under PBL, to disclose identities. For the BLAST analysis, the expectation values (E value) were set at a minimum of  $10^{-14}$  for gene homology. The biological functions of

these genes were determined based on PubMed literature (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi>) and AmiGO search (<http://www.godatabase.org/cgi-bin/amigo/go.cgi>). Genes differentially expressed were clustered in ontogeny groups according to functions of proteins encoded (e.g. structure, development and protection).

### *2.5 Quantitative Real-Time RT-PCR*

Six genes encoding proteins with known relevant brain-related functions, which were differentially expressed in the cDNA microarray hybridization, were selected for further investigation using Q-RT-PCR procedures. The selection criteria consisted of differential expression at  $P < 0.05$  and a 1.25 minimum fold change based on microarray outcome and functions related to neuronal function, structure and protection, mechanisms potentially affected by stress. The selected genes were differentially expressed in at least one of the four comparisons. Four of the six genes chosen were differentially expressed in two of the four comparisons.

Q-RT-PCR was performed as described previously (Gibson et al., 1996; Heid et al., 1996). Briefly, a total of 2  $\mu$ g of total RNA from each sample was reverse transcribed using oligo (dT)<sub>18</sub> and SuperScript II reverse transcriptase (Invitrogen Life Technologies Corp., Carlsbad, CA). Reverse transcribed cDNA was quantified using ND-1000 spectrophotometer (NanoDrop Technologies Inc., Rocklnd, DE). A total of 30 ng of cDNA was employed in each real-time reaction. Forward and reverse primer sequences were designed with Primer Express 2.0 Software (Applied Biosystems, Foster City, CA) and synthesized by Qiagen. The oligonucleotide sequences of the primers are summarized in Table 1. To confirm that primer dimer products were not influencing final

Ct values, control reactions without template but with each set of primers were performed, with the anticipated result that no product was amplified. Q-RT-PCR was performed and analyzed on an ABI Prism 7000 Sequence Detection System (Applied Biosystems). *Sus scrofa* 18S ribosomal RNA was selected as the control gene to be used for normalization purposes based on preliminary test reactions, as expression of this control gene did not change relative to treatments. All reactions were performed using template from individual animals in triplicate. Relative quantification methods were determined based on the primer amplification efficiency tests (Livak, 1997; Livak & Schmittgen, 2001). Control primer 18S ribosomal RNA amplification efficiency was equal to 1. Relative gene expression quantification using  $2^{-\Delta\Delta Ct}$  method (Livak & Schmittgen, 2001) was applied to measure mRNA abundance for actin related protein 2/3 complex (ARP2/3), diazepam binding inhibitor (DBI), phosphoprotein enriched in astrocytes 15kDa (PEA-15) and tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein (14-3-3 protein) (GenBank accession nos. NM\_005719, AJ301366, NM\_003768, and NM\_145690 respectively; Table 1), which showed amplification efficiencies equal to 1. A relative standard curve method (Livak, 1997) was applied to examine expression of carboxypeptidase E (CPE) and ornithine decarboxylase antienzyme 2 (OAZ2) mRNAs (GenBank accession nos. NM\_001873 and NM\_002537 respectively; Table 1), which showed amplification efficiencies different from 1. The four treatment comparisons used in the cDNA microarray experiment were also considered for Q-RT-PCR data analysis (Figure 1). Hence, for this study, changes in gene expression result from the comparison of the first treatment group relative to the second for each contrast. For presentation of results in which gene expression was lower in the

first treatment compared to the second, the ratio ( $< 1$ ) was divided into -1 to give a negative relative expression value ( $-1/\text{ratio}$ ). Values are presented as the mean  $\pm$  standard error of the mean (SEM). Statistical significance of relative changes in gene expression was assessed using paired t-tests. Genes with  $P < 0.05$  were considered differentially expressed.

Table 1. Primers used for Q-RT-PCR analysis of gene expression in the frontal cortex of piglets.

GenBank accession no.	Forward primer (5' – 3' end)	Reverse primer (5' – 3' end)
NM_005719	ATGGACCCCGACACCAAAC	GTCCCTTGAACTGACTCCTGATAGG
AJ301366	GGAAGTTAAGAACCTTAAGACCAAACC	TCGCTTGTTTGTAGTGGCTGTAG
NM_003768	TGTTGCACTGATCCCCAGTTC	CCAAGGTGCCAGGATATTGAG
NM_145690	ACATCGGATACCCAAGGAGATG	TTGGAAGGCCGGTTAATTTTC
NM_001873	GCTGAGCTACGGTGGAAGCTC	AAATCATCCAATAAACCTCCTAAAG
NM_002537	CCTTCAGCTTCTTGGGCTTT	TCTGGCCGAGAGGGAACAC

### 3. Results

#### 3.1 cDNA Microarray

The BLAST analysis of the results from the cDNA microarray hybridizations revealed 103 unique ESTs differentially expressed ( $P < 0.05$  and at least 1.25 fold change) among the four comparisons. Only 67 of the unique sequences display significant similarity with known genes in the GenBank database (Table 2). Forty-two of these genes had known function from which five were identified as ribosomal proteins. Twenty-five EST sequences matched only genomic or EST sequences in the database were classified as genes with unknown function. Six of 42 genes were identified as

playing known roles in neuronal function, structure and protection, functions relevant to our model, and had their relative expression further examined by Q-RT-PCR.

Table 2. Genes with identified by BLAST analysis of differentially expressed ESTs on the PBL cDNA microarray.

GenBank Accession no.	Gene Name	Gene Function
AJ301366 NM_001873	Sus scrofa partial mRNA for diazepam binding inhibitor (DBI) Homo sapiens carboxypeptidase E (CPE)	Neurosteroidogenesis Biosynthesis of neuropeptides
NM_145690/ BC000179 NM_002537	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein Homo sapiens ornithine decarboxylase antizyme 2 (OAZ2)	Biosynthesis of neurotransmitters Biosynthesis of polyamines
AF162445 NM_005938	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) Homo sapiens myeloid/lymphoid or mixed-lineage leukemia 7 (MLLT7)	Cell function and metabolism Cell protection
AB079894 AJ251914 AJ251829 NM_003768	Sus scrofa gene for T-cell receptor beta-chain Sus scrofa MHC class I SLA genes, haplotype H01 Sus scrofa MHC class I SLA genomic region, haplotype H01 Homo sapiens phosphoprotein enriched in astrocytes 15 (PEA15)	Cell protection Cell protection Cell protection Cell
NM_006406 BC032148 NM_000089	Homo sapiens peroxiredoxin 4 (PRDX4) Homo sapiens, troponin I Homo sapiens collagen, type I, alpha 2 (COL1A2)	protection/apoptosis Cell protection/catalysis Cell structure Cell
J04204 X59048 Bc016812	Bos taurus 32 kd accessory protein Bovine mRNA heart mitochondrial oxidoreductase Homo sapiens ATP synthase, H <sup>+</sup> transporting, mitochondrial F1 complex	structure/component Energy metabolism Energy metabolism Energy metabolism
NM_005690 NM_006876	Homo sapiens dynamin 1-like (DNM1L) Homo sapiens UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (B3GNT6)	Energy metabolism Energy metabolism
AJ504726 X86791 AF304202 L11869 NM_015286 BC030589	Sus scrofa mut gene for methylmalonyl-CoA mutase Sus scrofa beta-globin gene Sus scrofa breed Landrace mitochondrion Porcine growth hormone-releasing hormone receptor Homo sapiens desmuslin (DMN) Homo sapiens aldehyde dehydrogenase 1 family, member A2,	Energy metabolism Energy metabolism Energy metabolism Growth Membrane protein Metabolism of neurotransmitters
K00800 NM_005719 XM_114617 NM_004522 BC015149 Z99716 NM_145330 NM_000982 NM_001030 X03342	Bos taurus fibronectin mRNA Homo sapiens actin related protein 2/3 complex (ARP3/3) Homo sapiens beta 5-tubulin (OK/SW-cl.56) Homo sapiens kinesin family member 5C (KIF5C) Homo sapiens, similar to microtubule-associated protein 4 Human DNA similar to neuronal-specific septin 3 Homo sapiens mitochondrial ribosomal protein L33 (MRPL33) Homo sapiens ribosomal protein L21 Homo sapiens ribosomal protein S27 Human mRNA for ribosomal protein L32	Neuronal development Neuronal development Neuronal development Neuronal development Neuronal development Ribosomal protein Ribosomal protein Ribosomal protein Ribosomal protein

Table 2 (cont'd).

AK002787	Mus musculus adult male kidney cDNA ribosomal protein L13	Ribosomal protein
NM_016545	Homo sapiens immediate early response 5 (IER5), mRNA	Transcription
BC036013	Homo sapiens mitogen-activated protein kinase (MAPK)	Transcription
NM_032188	Homo sapiens MYST histone acetyltransferase 1 (MYST1)	Transcription
AF087481	Homo sapiens retinoblastoma binding protein 2 homolog 1 (RBBP2H1)	Transcription
NM_004264	Homo sapiens SRB7 suppressor of RNA polymerase B homolog (yeast) (SURB7)	Transcription
BC014269	Homo sapiens, similar to eukaryotic translation termination factor	Translation
AC090976	Bos taurus clone RP42-400M23, complete sequence	Unknown
Y17923	Bos taurus mRNA for lyncein	Unknown
AC023050	Homo sapiens 12 BAC RP11-428G5	Unknown
AC019171	Homo sapiens BAC clone RP11-173C1 from 2	Unknown
BC033863	Homo sapiens BAC clone RP11-455J15 from 7	Unknown
AC013449	Homo sapiens BAC clone RP11-558C24 from 2	Unknown
AF038540	Homo sapiens brain NSP-like 1 (NSPL1) (neuroendocrine-specific protein)	Unknown
AK057557	Homo sapiens cDNA FLJ32995 fis, clone THYMU1000136	Unknown
AC022392	Homo sapiens chromosome 10 clone RP11-150D20	Unknown
AC008378	Homo sapiens chromosome 5 clone CTC-209H22	Unknown
BC027921	Homo sapiens CXYorf1-related protein	Unknown
AL021408	Homo sapiens DNA sequence from PAC 523C21 on chromosome 6q23.1-23.3.	Unknown
AP001201	Homo sapiens genomic DNA, chromosome 11	Unknown
XM_114482	Homo sapiens heat shock 70kD protein 4 (HSPA4)	Unknown
BC024023	Homo sapiens LOC317671, mRNA	Unknown
AB020681	Homo sapiens mRNA for KIAA0874 protein	Unknown
AL359597	Homo sapiens mRNA; cDNA DKFZp547B146	Unknown
BC024316	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone KFZp564H1916)	Unknown
BC011583	Homo sapiens, clone IMAGE:3834272	Unknown
BC034275	Homo sapiens, clone IMAGE:4179671	Unknown
BC019624	Homo sapiens, Similar to hypothetical protein	Unknown
AL732326	Human DNA sequence from clone RP11-723P2 on chromosome X, complete sequence	Unknown
AL139255	Human DNA sequence from clone RP4-753C8 on chromosome 1p31.3-32.3.	Unknown
M29512	Pig unidentified hepatic protein mRNA	Unknown
AC097230	Sus scrofa clone RP44-254G1	Unknown

### 3.2 *Q-RT-PCR*

From the cDNA microarray experiment, six differentially expressed genes presenting relevant brain-related function were selected to carry out further studies using Q-RT-PCR. This method was chosen to allow more precise quantification of changes in expression of the selected genes. The genes selected for Q-RT-PCR examination were DBI, OAZ2, tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein (14-3-3 protein), CPE, PEA-15 and ARP2/3 (Table 2).

#### 3.2.1 *Effect of social isolation*

The contrast between NWI and NWC allowed us to examine the effect of 15 minutes of social isolation on 12 day old non-weaned piglets. Interestingly, social isolation significantly suppressed mRNA levels of 14-3-3 protein and CPE in the frontal cortex of NWI versus NWC animals ( $P < 0.05$ ). In addition, a significant decrease in PEA-15 mRNA abundance was detected in NWI animals ( $P < 0.01$ ) compared to controls, as shown in Figure 2.

#### 3.2.2 *Effect of early weaning*

Examining the contrast between EWC and NWC allowed investigating the effects of weaning (48 hours post-weaning). Our findings indicated that there is no evidence of effects caused by weaning in the expression of the tested genes in the frontal cortex of early-weaned compared to non-weaned control piglets.

### *3.2.3 Effect of social isolation in the presence of early weaning*

The comparison EWI versus EWC highlighted the effect of social isolation in early-weaned piglets. The DBI mRNA expression was remarkably suppressed in EWI animals compared to early-weaned control animals ( $P < 0.05$ ), and the levels of ARP2/3 mRNA were also significantly suppressed in EWI when compared to the non-socially isolated control group ( $P < 0.05$ ; Figure 2). Based on the Q-RT-PCR results, there was no major effect of weaning or social isolation on gene expression in the frontal cortex when early-weaned piglets were compared to non-weaned animals exposed to fifteen minutes of social isolation (EWI versus NWI).



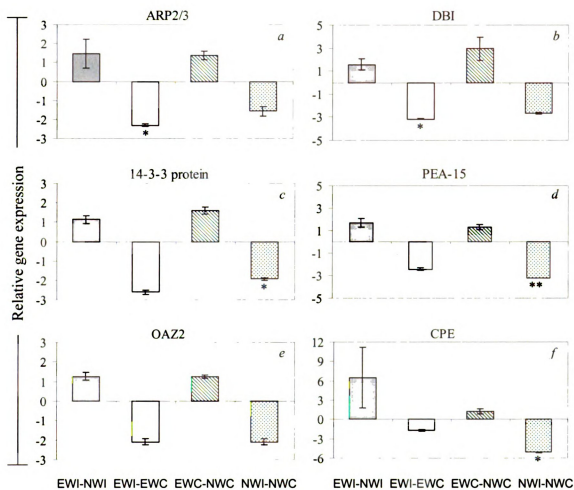


Figure 2.

Figure 2. Relative expression of stress-responsive genes in the frontal cortex of piglets subjected to early weaning and/or social isolation. (a) actin related protein 2/3 complex (ARP2/3), (b) diazepam binding inhibitor (DBI), (c) 14-3-3 protein, (d) phosphoprotein enriched in astrocytes 15kDa (PEA-15), (e) ornithine decarboxylase antienzyme 2 (OAZ2), (f) carboxypeptidase E (CPE). The ratio represents the first treatment group compared to the second in each contrast. Negative values indicate smaller expression of the first group relative to the second. Positive values indicate greater expression of the first group compared with the second. Each bar represents the mean ( $\pm$  SEM) change in gene expression for each treatment comparison. \*  $P < 0.05$ ; \*\*  $P < 0.01$ . EWC = early-weaned control, EWI = early-weaned and socially isolated, NWI = non-weaned and socially isolated, NWC = non-weaned control. Note different scales on the y axes of the plots.

#### **4. Discussion**

Our results show that expression of five of the six genes examined by Q-RT-PCR, associated with neuronal function, structure and protection, was significantly suppressed by 15 minutes of social isolation in either non-weaned or early-weaned piglets. Interestingly, this study partially agrees with a prior study in which the effects of weaning at two ages, and social isolation were investigated. We consistently found that the expression of the stress-responsive genes 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, GR and MR mRNAs was reduced following 15 minutes of social isolation but not affected by weaning age (Chapter 2). In this experiment, however, some of the changes found as a result of social isolation may be confounded with the effects of 48 hours post-weaning. Potentially distinct effects on gene expression may be observed following longer periods of social isolation. It is also possible that the transitory nutritional deficits that early-weaned animals experience, at least for 2 days post weaning (Carroll et al., 1998), may have influenced some of our findings. Previous studies reported that early weaning stress experienced by piglets is associated with the occurrence of abnormal behaviors, intensified aggression and related neuroendocrine changes (Hay et al., 2001; Kanitz et al., 2004; Yuan et al., 2004). Additionally, social isolation pre- and post-weaning has also been reported to activate the stress axis, causing long-term neuroendocrine and behavioral effects (Hellemans et al., 2004; Tuchscherer et al., 2004).

Twelve day old non-weaned piglets, when exposed to fifteen minutes of social isolation, showed suppressed mRNA abundance of 14-3-3 protein in the frontal cortex, a brain area in which this protein is highly expressed (Takahashi, 2003). In the brain, 14-3-3 protein activates tyrosine and tryptophan hydroxylases, stabilizing the phosphorylation

state of these enzymes (Ichimura et al, 1988) and indirectly regulates the biosynthesis of neurotransmitters, such as serotonin (5-HT) and catecholamines (Ichimura et al., 1987). Albeit we did not measure 5-HT or catecholamine levels in the experimental animals, our results suggest that socially isolated animals may experience deficits in neurotransmitter biosynthesis. Changes in 5-HT and catecholamine levels in the prefrontal cortex can impair attentional control and reward-based learning (Rogers et al., 1999). For instance, acute reduction in 5-HT in the frontal cortex induces impaired decision-making and spatial working memory in primates (Clarke et al., 2004). Interestingly, previous studies showed that early-weaned piglets exposed to 15 minutes of social isolation 2 days after weaning showed cognitive deficits (Laughlin & Zanella, 2002; Souza & Zanella, 2004).

Effects of early weaning and social isolation on CPE mRNA also were examined in the frontal cortex. Carboxypeptidase E is a key enzyme in the biosynthesis of neuropeptides (Fricker et al., 1986) and directs neuropeptide precursors, such as pro-opiomelanocortin, proenkephalin and prodynorphin to the proper secretory pathways in neuroendocrine cells (Loh et al., 2002, 2004). In this study, a significant decrease in CPE mRNA levels was observed as an effect of social isolation in non-weaned animals compared to controls (NWI vs. NWC). This may suggest that social isolation interfered with neuroendocrine peptide metabolism in the frontal cortex mainly in non-weaned piglets. Abnormal behaviors in pigs are correlated with opioid receptor density in the brain (Zanella et al., 1996). Also, differences in stress response among pigs are influenced by neuroendogenous opioid systems (Loijens et al., 2002). Interestingly, CPE knockout mice show diminished reactivity to stimuli, impaired coordination and visual placing, in addition to other dysfunctions (Cawley et al., 2004). Further studies measuring

levels of neuropeptides in the frontal cortex of socially isolated piglets would help to confirm the biological significance of our findings.

Non-weaned piglets when subjected to social isolation also showed decreased PEA-15 mRNA in the frontal cortex, compared to non-socially isolated piglets. This gene is abundantly expressed in astrocytes and plays a role in controlling cell proliferation and apoptosis (Danziger et al., 1995; Renault et al., 2003). It either inhibits or enhances apoptosis depending on the pathway activated (Estelles et al., 1999). Interestingly, Kitsberg et al. (1999) demonstrated that astrocytes lacking PEA-15 rapidly showed signs of apoptosis when exposed to tumor necrosis factor (TNF), but astrocyte protection and survival was reinstated once PEA-15 levels recovered. Non-weaned piglets when socially isolated may be experiencing reduced neuronal protection in the frontal cortex, however further studies are needed to elucidate the role of PEA-15 in this brain area.

We also observed more than 3 fold decrease in DBI mRNA in the frontal cortex of early-weaned piglets exposed to social isolation versus early-weaned control. Diazepam binding inhibitor plays a major role in regulation of neurosteroidogenesis in the brain by binding to benzodiazepine receptors associated with GABA receptors (Costa & Guidotti, 1991; Ferrarese et al., 1993). The decrease in DBI gene expression in early-weaned piglets, when socially isolated suggests that this acute stressor may be negatively affecting neurosteroidogenesis in the frontal cortex. Lack of steroids in the brain impairs myelination (Chan et al., 1998) and affects modulation of neurotransmitter systems impairing cognitive processes, in particular learning and memory (Schumacher et al., 2003; Vallee et al., 2001). A previous study demonstrated that piglets weaned at 12 days of age, when socially isolated, showed lower levels of steroids such as cortisol and

corticosterone, in the hippocampus compared to non-weaned animals (Zanella et al., 2004). No study has been performed previously in piglets examining the expression of DBI in the brain.

Social isolation of early-weaned piglets also reduced mRNA abundance for the protein complex ARP2/3, which is involved with neuronal development (Meyer & Feldman, 2002). Goldberg and colleagues (2000) demonstrated that neuronal growth factor stimulated actin polymerization by recruiting the ARP2/3 complex. Thus, social isolation may adversely affect the neuronal development process in the frontal cortex of early-weaned piglets since reduction of the ARP2/3 expression in frontal cortex may be associated with abnormal development of the brain (Weitzdoerfer et al., 2002).

In summary, our findings suggest that social isolation is associated with reduction in mRNAs encoding for factors involved in biosynthesis of neurotransmitters and neuropeptides, and neurosteroidogenesis pathway; therefore potentially affecting proper neuronal function in the frontal cortex of young piglets. Results reveal potential pathways associated with impaired learning and memory and social recognition deficits reported in early-weaned piglets when socially isolated.

## **CHAPTER FOUR**

### **Discussion and Future Research Directions**

#### **Discussion**

The impact of early weaning on occurrence of intensified aggression, abnormal behaviors, and neuroendocrine modifications in piglets has been previously documented (Gardner et al., 2001; Hay et al., 2001; Kanitz et al., 1998, 2004; Worobec et al., 1999; Yuan et al., 2004). The postnatal cerebral development of piglets is characterized by a period sensitive to stress, during which the brain may be more vulnerable to manipulations carried out at early ages, mainly during the first 3 weeks after birth (Hemsworth et al., 1986; Weaver et al., 2000). As described in Chapters Two and Three, early weaning suppressed expression of 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, MR and GR in the hippocampus of piglets, while social isolation suppressed the expression of genes encoding 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, MR and GR in the frontal cortex of piglets, regardless of age or weaning status. Fifteen minutes of social isolation also suppressed expression of 14-3-3 protein, PEA-15, CPE, DBI and ARP2/3 in the frontal cortex of either early- or non-weaned piglets. One effect of social isolation and early weaning is enhanced expression of glucocorticoids, particularly cortisol.

Glucocorticoids, such as cortisol, are potentially one class of indirect regulators of the changes in gene expression observed in the frontal cortex and hippocampus of piglets. The glucocorticoid receptors GR and MR are hormone-activated transcription factors that have the potential to influence gene expression in a wide variety of central nervous system neurons (e.g. Drouin et al., 1989; Herman, 1993; de Kloet et al., 1993; Shaaf et

al., 2000) interfering, for instance, with neuronal growth and viability (Diaz et al., 1998; Herman, 1993). Glucocorticoids are also important regulators of stress-induced immediate early gene expression in the brain (Senba & Ueyama, 1997). In this study, in addition to suppressed GR and MR gene expression, several other genes studied had lower mRNA levels in the frontal cortex and hippocampus in response to social isolation and early weaning (Figure 1).

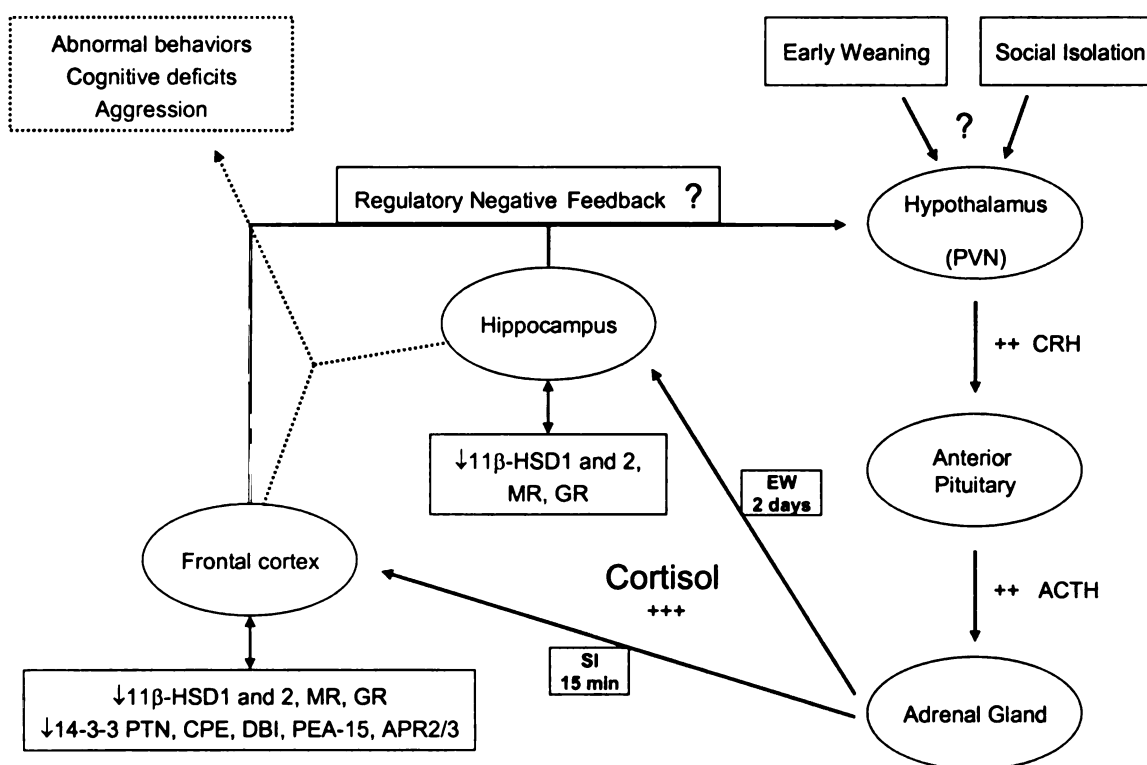


Figure 1. Diagram illustrating the potential effects of early weaning (EW) and social isolation (SI) on the hypothalamic-pituitary-adrenal axis and consequent changes in gene expression in the hippocampus and frontal cortex of piglets. Paraventricular nucleus (PVN); Corticotrophin release hormone (CRH); Adrenocorticotropin hormone (ACTH).



Despite progress in understanding the effects of increased cortisol on brain function and gene expression, biologists have yet to uncover the basic molecular processes leading to cognitive deficits. In this study, we employed techniques such as cDNA microarray hybridization and Q-RT-PCR to begin investigating changes in gene expression as a result of early weaning and social isolation. The porcine brain library cDNA microarray (Nobis et al., 2003) used in our work is a novel and powerful approach for screening gene expression profiles. Also, Q-RT-PCR is a sensitive and accurate technique that measures mRNA abundance in a small amount of sample (Bustin, 2000). One caveat to both of these techniques is that they measure only mRNA levels and therefore, interpretation of results presented on chapters 2 and 3 should be strictly limited to a discussion on mRNA levels for the genes encoding various proteins of interest and not directly used to infer changes in the proteins themselves.

A larger porcine cDNA brain library than the one used for this study (Nobis et al., 2003) would likely help to identify additional brain pathways affected by stress and may have implicated more pathways and mechanisms associated with behavioral and neuroendocrine changes resulting from weaning and social isolation stress. Also, a larger sample size would provide greater statistical power, and more effectively enable detection of differentially expressed genes. This would add significantly to the limited information available on potential genes involved with brain development and plasticity that are affected by early adverse experiences in piglets (Kanitz et al., 1998, 2004; Tuchscherer et al., 2004). To estimate sample sizes for future gene expression studies, power of tests were computed using the median standard deviation of gene expression for frontal cortex and hippocampus of piglets. For instance, as shown on Figure 2,

approximately 15 animals are needed to have an 80% probability of detecting a 2-fold change in gene expression in the frontal cortex of piglets. Also, as shown on Figure 3, approximately 8 animals are needed to have an 80% probability of detecting a 2-fold change in gene expression in the hippocampus of piglets.

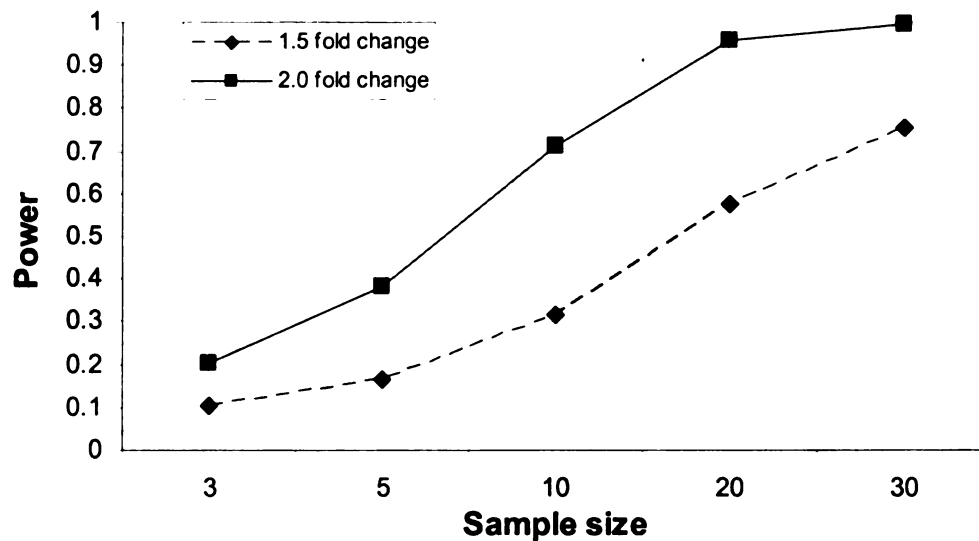


Figure 2. Power to detect 1.5 and 2-fold change in expression of genes in the frontal cortex of piglets as a function of sample size considering a median standard deviation equals to 0.84.

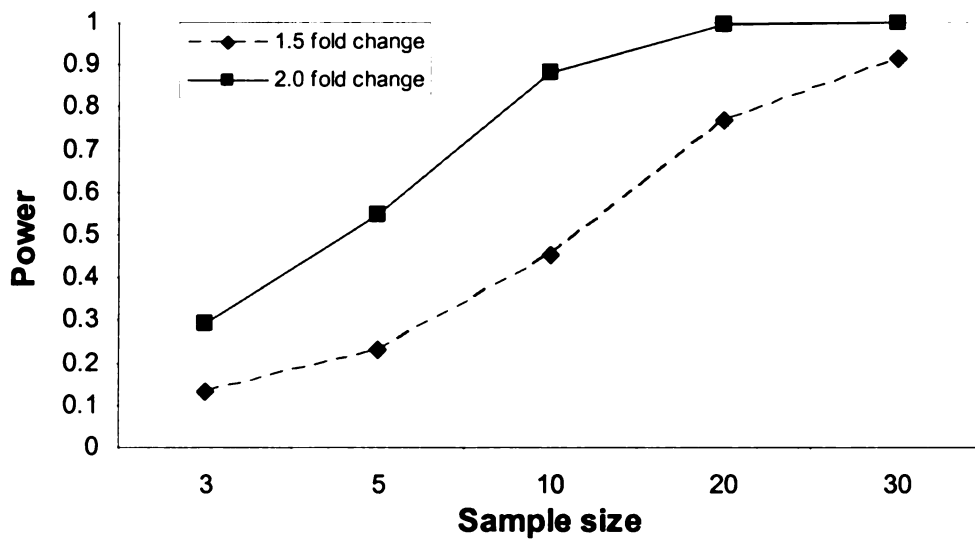


Figure 3. Power to detect 1.5 and 2-fold change in expression of genes in the hippocampus of piglets as a function of sample size considering a median standard deviation equals to 0.67.

In addition to neuroendocrine changes resulting from early adverse experiences (e.g. Kanitz et al., 1998, 2004; Tuchscherer et al., 2004), previous studies reported that when socially isolated for 15 minutes, early-weaned piglets showed impaired spatial learning and memory (Laughlin & Zanella, 2002) and social recognition deficits (Souza & Zanella, 2004) tested two days post-weaning. It was suggested that the stress of early weaning altered cellular and biochemical parameters in the frontal cortex and hippocampus of piglets during a sensitive period of brain development. Both, frontal cortex and hippocampus, play important roles in cognitive function, such as visual and spatial learning and memory (e.g. Abidin et al., 2004; Cao et al., 2004), and social behavior, including aggression (Kolb et al., 2004; Wood et al., 2003). Therefore, the

objective of this study was to directly investigate changes in expression of stress-response genes in the frontal cortex and hippocampus of early- and conventionally-weaned piglets subjected to additional stress through social isolation or when kept with littermates.

The age at which piglets were weaned affected expression of 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, MR and GR in the hippocampus, but did not influence frontal cortex gene expression. When comparing weaned versus non-weaned piglets at ages 10 and 21, it was demonstrated that early weaning suppressed expression of stress-response genes (i.e. 11 $\beta$ -HSD1, 11 $\beta$ -HSD2, MR and GR) in the hippocampus. Interestingly, no effect on expression of the tested genes was observed when piglets were weaned at 21 days of age. These results suggest that the hippocampus of piglets may be more vulnerable to weaning stress at 10 days than at 21 days. If, in fact, mRNA levels are related or result in reduced protein levels, then lower expression of GR in the hippocampi of early-weaned compared to conventionally-weaned piglets, suggests that early-weaned animals would be exposed to higher levels of active unbounded glucocorticoids, such as cortisol. This effect could be aggravated since early-weaned piglets also showed reduced mRNA levels of the dehydrogenases 11 $\beta$ -HSD1 and 11 $\beta$ -HSD2 in the hippocampus. However, transitory nutritional deficits potentially experienced by the piglets during the two days post-weaning (Carroll et al., 1998) could also have contributed to the cognitive deficits, since for instance amino acids such as tyrosine and tryptophan available on the diet, are essential for biosynthesis of neurotransmitters (Fernstrom, 2000).

Our results suggest that the negative effects of early weaning can be exacerbated when piglets are challenged by an additional short-term stressor, such as social isolation. In this study, the fifteen minutes of social isolation was used as a stressor to replicate the

protocol that, in previous studies, induced cognitive deficits (Laughlin & Zanella, 2002; Souza & Zanella, 2004), and to minimize nutritional deprivation, but to cause a biologically relevant stressful situation for the piglets. Previous studies showed that social isolation increases circulating glucocorticoid levels in response to activation of the hypothalamic-pituitary-adrenal axis (e.g. Laughlin & Zanella, 2002; Kanitz et al., 2004). In our study only the immediate effects of short-term social isolation on frontal cortex and hippocampal gene expression were analyzed, thus reducing contributions from potential nutritional deficits.

Based on our results, overall, social isolation reduced the mRNA abundance for several genes in the frontal cortex of piglets, independently of the weaning status. In the first experiment (Chapter 2), social isolation suppressed mRNA levels for genes encoding 11 $\beta$ -hydroxysteroid dehydrogenase 1 and 2 (11 $\beta$ -HSD1 and 11 $\beta$ -HSD2, respectively), enzymes mainly responsible for inactivation of cortisol, and the mRNA abundance for genes encoding mineralocorticoid and glucocorticoid receptors (MR and GR respectively), which are responsible for mediating the stress axis response by binding glucocorticoids, in the frontal cortex of both 12 and 23 days old piglets. In the second experiment (Chapter 3), when using the PBL cDNA microarray and Q-RT-PCR to analyze expression profiles of genes in the frontal cortex of 12 days old piglets, whether weaned or not, it was found that 15 minutes of social isolation significantly suppressed the expression of genes encoding 14-3-3 protein, PEA-15, CPE, DBI and ARP2/3. If mRNA levels translate to changes in protein abundance, then neuronal development, function and protection may be impaired in socially-isolated piglets. Thus, the psychological stress, which encompasses social separation and exposure to a novel

environment (Hennessy et al., 2004) encountered by the piglets may have influenced their responses to social isolation.

Overall, results from this study in association with previous research, indicate that the hippocampus of piglets weaned at 10 days of age may experience decreased mRNA expression of important genes encoding proteins that are mediators of the stress response, such as  $11\beta$ -HSD1 and 2, GR and MR. When examining gene expression in the frontal cortex, the mRNA expression of several genes encoding proteins involved in neuronal development, function, and protection, in addition to  $11\beta$ -HSD1 and 2, GR and MR, were found to be suppressed as a result of 15 minutes of social isolation. Therefore, our results demonstrated that social isolation affected the expression of genes examined in frontal cortex but not hippocampus, indicating that the effects of distinct stressors are additive in order to cause cognitive deficits in young piglets.

### **Future Research Directions**

Further studies should focus on the investigation of long-term effects of early weaning on swine behavioral and neuroendocrine development. Studies exploring the relationship of early weaning stress and cognitive deficits, and their association with aggression, should be encouraged. One hypothesis that I would like to explore is that early weaning stress increases aggressive behavior as a consequence of neuronal exposure to high glucocorticoid levels during a sensitive period of brain development. Therefore, to investigate at brain level the long-term effects of weaning, brain areas such as hippocampus and frontal cortex should be further studied. As discussed earlier, both

brain areas play important roles in cognitive functions and social behavior including aggression (Kolb et al., 2004; Wood et al., 2003).

To investigate potential correlations between glucocorticoid exposure in early-weaned piglets, and mechanisms that contribute to greater vulnerability of early-weaned animals to stressors such as social isolation, I would first measure the levels of proteins encoded by the most important genes reported in this study, such as 11 $\beta$ -HSD1 and 2, GR and MR, 14-3-3 protein, DBI and possibly CPE in the frontal cortex and hippocampus of early-weaned and socially isolated piglets.

Second, a controlled experiment to test the effects of peripheral glucocorticoid levels on gene expression in the hippocampus and frontal cortex of early-weaned piglets (weaned at 10 days of age) should be carried out. For this study, the following treatment groups would be used: early-weaned plus social isolation, early-weaned treated with exogenous glucocorticoid plus social isolation, non-weaned plus social isolation and non-weaning treated with exogenous glucocorticoid plus social isolation. The administration of cortisol, the exogenous glucocorticoid, to treated non-weaned and weaned animals should be performed at day 10 after birth, the same day that weaning is performed. This set up would replicate for non-weaned the state in which weaned animals are exposed to high cortisol level. One of the main objectives of this experiment would be to correlate the peripheral levels of cortisol with the levels of MR and GR binding, and also the enzymes 11 $\beta$ -HSD1 and 2 in the hippocampus and frontal cortex of early and non-weaned piglets.

To complement this experiment, behavioral observations should be taken, and spatial and cognitive tests, in addition to fear/anxiety tests performed as well. The

prediction would be that the cortisol treated early-weaned and non-weaned animals, when socially isolated, would show cognitive impairments as previously observed (Laughlin & Zanella, 2002; Souza & Zanella, 2004), and fear/anxious state (Kanitz et al., 2004; Molina-Hernandez et al., 2001; Weiss et al., 2004). Also, specific behavioral tests consisting of measuring specific brain area functions, such as frontal cortex and hippocampus would be useful to determine which brain area may be mediating the previously observed cognitive deficits (Laughlin & Zanella, 2002; Souza & Zanella, 2004).

A complementary tool for this last procedure would be the application of imaging techniques, such as photo-optic imaging (PET) scan or functional magnetic resonance imaging (fMRI) (Potchen, 2000), at different time points post-weaning, to provide information on the activated sites in the frontal cortex and hippocampus. However, currently, to apply these techniques for piglets, the animals would have to be anesthetized, and this procedure could influence the outcomes. Thus, to employ imaging tools, it may be valuable to train the animals to stand still while being tested.

Future studies should also control for the transitory nutritional deficits likely experienced by weaned piglets for at least two days post-weaning (Carroll et al., 1998). Amino acids, such as tyrosine and tryptophan, are essential for the biosynthesis of neurotransmitters, such as serotonin and catecholamines. Therefore, depletion of these neurotransmitters may lead to impaired neurosynaptic transmission, resulting in cognitive deficits (e.g. Clarke et al., 2005) and aggression (e.g. Chiavegatto and Nelson, 2003). Thus, the use of high performance liquid chromatography could be applied for monitoring brain catecholamines and serotonin and metabolites concentrations.



Further behavioral and neuroendocrine studies would certainly facilitate a better understanding of the stress physiology and its responsiveness to weaning, providing insights of the long-term consequences of the stress caused by early weaning. In summary, future studies should investigate the correlation of behavioral alterations and cerebral mechanisms, correlated to early weaning stress response, to improve swine welfare.

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