AN EXPLORATION INTO THE EPIGENETIC MECHANISMS RELATED TO PRENATAL FAMINE & LATER-LIFE HEALTH

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Abstract

Epigenetics is a fascinating field and one that researchers are continuously studying to learn more about and its effects over time. One group of individuals, in particular, has caught the eye of many, and it is those affected by what is commonly called today the Dutch hunger winter. This was a time when people in the Netherlands experienced extreme famine around the end of World War II. Those conceived during that time have grown up to have an increased rate of metabolic diseases, making this an interesting area of research for the developmental origins of health and disease hypothesis. Many researchers have found associations between in-utero exposures and variations in this cohort's epigenetic profile and mice studies. These include known epigenetically regulated loci such as IGF2 in humans and A^{vy} in mice. However, the molecular mechanisms are not completely understood yet for there to be distinct causality. Here I examine the history of the Dutch hunger winter, known epigenetic mechanisms, an in-depth look at what research has discovered, the logic behind the developmental origins of health and disease hypothesis, and ideas for future research.

The Dutch Hunger Winter

In the winter of 1944, those living in the Netherlands during the German occupation experienced extreme famine. Towards the end of World War II, the Germans prevented the import of food and coal from entering the Netherlands and the largest lake froze over [8]. Due to the lack of food and coal, many affected would burn old furniture, take wood from abandoned houses, and even illegally cut down trees (Figure 1) [8]. Additionally, the famine led to individuals eating toxic foods such as tulip bulbs or walking miles in the cold to buy from farmers using their jewelry and whatever remaining money they had [8]. This famine, while short in time, resulted in around 20,000 people dying [8].

Figure 1. A man and child removing wood from a house to use as firewood [8].

Unlike other natural cases of famine in history, the Dutch hunger winter was heavily documented, which included daily caloric intake, birth records, and a well-known timeline. The average caloric intake per day was around 400-800 calories for everyone, including those who were pregnant. To be considered as having experienced famine during gestation, the average amount of calories is less than 1000 calories a day for 13 weeks [1]. Individuals born anytime between January 7th of 1945 and December 8th of 1945 are a part of the cohort exposed to famine during prenatal development (Figure 2) [1]. Additionally, there were three distinct periods this cohort was divided into; late, mid, and early gestation. This unique birth cohort has provided a unique opportunity for researchers to assess the effects of prenatal undernutrition and its consequences. Almost 77 years have passed since this famine, but it has remained an interesting topic of research for the developmental origins of health and disease (DOHaD) hypothesis. This hypothesis tries to explain how exposure during critical points of development, periconceptional to infancy, could affect the function or structure of organ systems across post-natal development [2]. Individuals exposed to this famine during early gestation have shown in later life to have higher rates of obesity, manipulated lipid profiles, decreased glucose tolerance, and cardiovascular and metabolic diseases [9]. Additionally, this cohort has experienced poorer perceived general health and cognitive function at age 58 [1]. While it can be easy for researchers to notice this association, they do not fully understand the molecular mechanisms behind it. One of the hypothesized contributors is developmental programming, which includes epigenetic mechanisms [2].

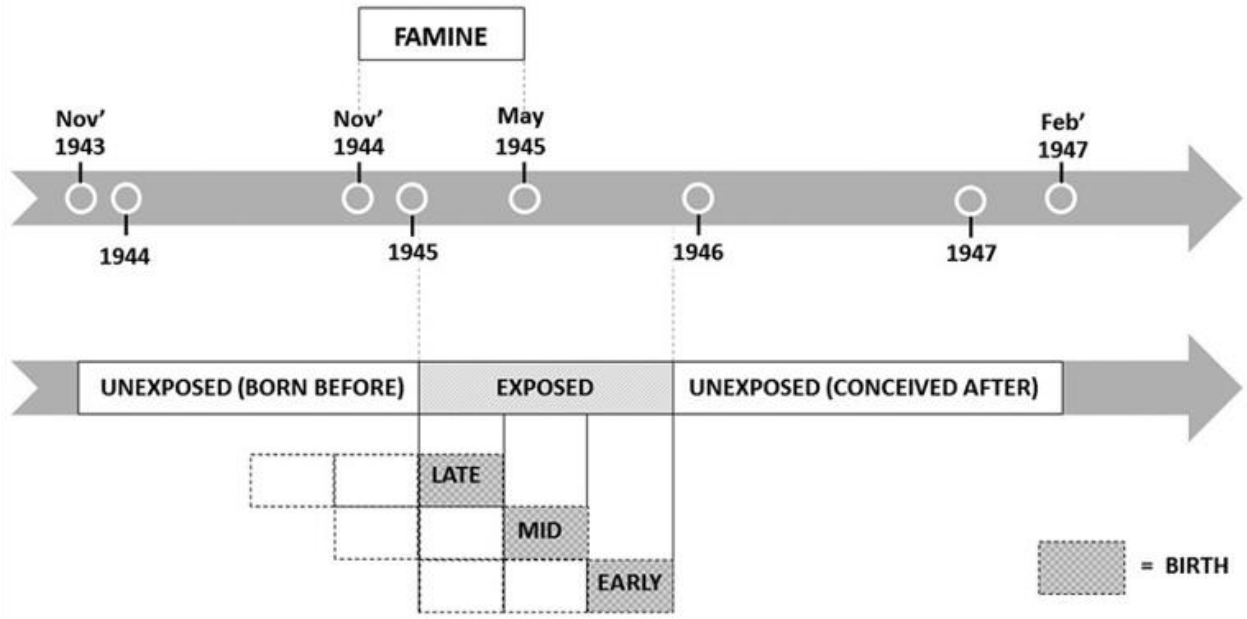

Figure 2. The timeline of those apart of the Dutch famine birth cohort and gestational famine exposure [11].

Epigenetic Mechanisms

DNA's primary function is to carry information regarding genes. DNA is divided and compacted into chromosomes so that they can then be passed down to future generations. If DNA was not tightly packaged, it would become uncontrollable. Every chromosome has proteins, known as histones and non-histone proteins, that help fold and pack its DNA into a more compact structure called chromatin. DNA wrapped around histones creates a nucleosome, which helps condense the chromatin. Certain chromatin structures can be inherited from a cell to its future generations. This is because the cell retains memory based on the structure of the chromatin instead of the DNA sequence. This is one example of an epigenetic mechanism.

There are two different types of chromatin. Heterochromatin is tightly condensed, typically at the centromeres and telomeres of chromosomes, and will prevent gene expression. These regions have little to no meiotic recombination and mainly contain satellite DNA and transposable elements [10]. However, there are several levels of compaction. This means that genes in heterochromatin regions are not all dead or turned off, but they are resistant to being expressed. Then there is euchromatin, which is less condensed and usually contains major genes, making it important for transcription. Heterochromatin regions usually encompass fewer genes than euchromatin regions. The level to which chromatin is packaged is due to numerous factors. Some include the linker histone H1, chromatin remodelers that use ATP hydrolysis, histone chaperones, and small chemical modifications to histones and DNA [11].

Interestingly, when euchromatin regions are converted or translocated to heterochromatin regions, due to chromosome breakage and rejoining, those genes get silenced in a stochastic pattern [12]. This is known as a position effect. It is also important to note that

heterochromatin formation heavily depends on the methylation of Histone H3 at lysine 9 and heterochromatin protein 1 [10]. These changes are then stable for the rest of the organism's life. Once it is established on a piece of chromatin, it tends to be inherited by all that cell's offspring. This is known as position effect variegation [12]. The most famous example of this is in Drosophila and their white gene. The phenotype of these flies' eyes was white with red patches instead of all red. The gene itself was not mutated, but it was silenced in some of the cells. The researchers found that there was an inversion in the heterochromatin and a break in the white gene [10]. Additionally, they also discovered that this silencing occurs in early embryogenesis and is inherited in somatic and germline lineages [10]. Another example is the inactivation of one of the X chromosomes in female mammals. This is a random process where there is a widespread of heterochromatin. This happens early in the embryo and the same X chromosome stays inactive for the cell's offspring. However, this inactivation is reversed for germ-cell formation.

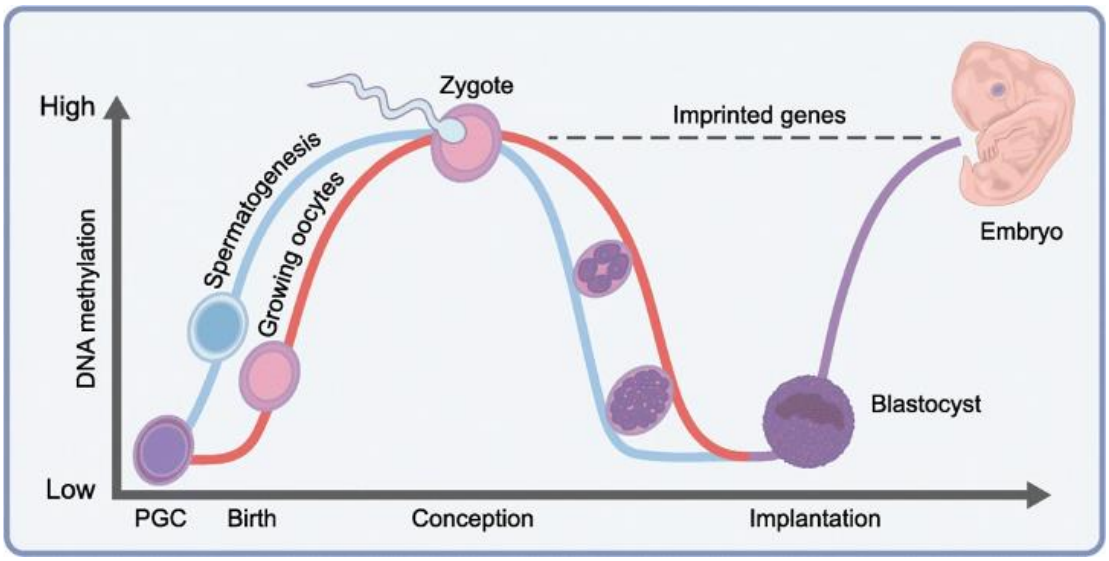

Figure 3. This graph shows the changes in DNA methylation across early development. The blue line (male) and the red line (female) display the different methylation patterns while the dashed lines display

On another note, there is also genomic imprinting. Genomic imprinting is the process where only one copy of a gene in an individual, either from their mother or their father, is expressed [12]. The other copy is suppressed through DNA methylation. DNA methylation is the covalent transfer of a methyl group to the carbon 5 position of the cytosine ring of DNA. This requires the appearance of a differentially methylated region (DMR) on one allele and not on the other. DMRs are areas in the DNA where the methylation status is different between two alleles at the same locus [13]. Additionally, early in the embryo, genes that go through imprinting are marked by methylation according to whether they came from a sperm or egg chromosome. While most methylation is removed during zygote formation and re-established in the embryo, imprinted genes are protected from demethylation after fertilization (Figure 3) [2]. This is what allows somatic cells to remember the origin of the two copies of the gene and regulate accordingly. Furthermore, there is the presence of CpG islands/sites. CpG islands are areas in

the DNA dense with guanines and cytosines [14]. These sites play an important role in transcriptional regulation, including gene silencing, imprinting, X chromosome inactivation, and even tumorigenesis, making them good gene markers [14].

Literature Review

Why might maternal famine exposure be critical during early development? Embryogenesis is when DNA methylation is actively changing [7]. One study wanted to explore the importance of DNA methylation during prenatal development by studying mice oocytes, sperm, and embryos. When these researchers analyzed the CpG methylation, they noticed that oocytes were globally hypomethylated and resembled early embryonic methylation levels when compared to sperm and post-implantation embryos [7]. Furthermore, when analyzing DNA methylation throughout development, there was significant demethylation at fertilization and significant re-methylation at the blastocyst stage (inner cell mass) (Figure 4a,b) [7]. Additionally,

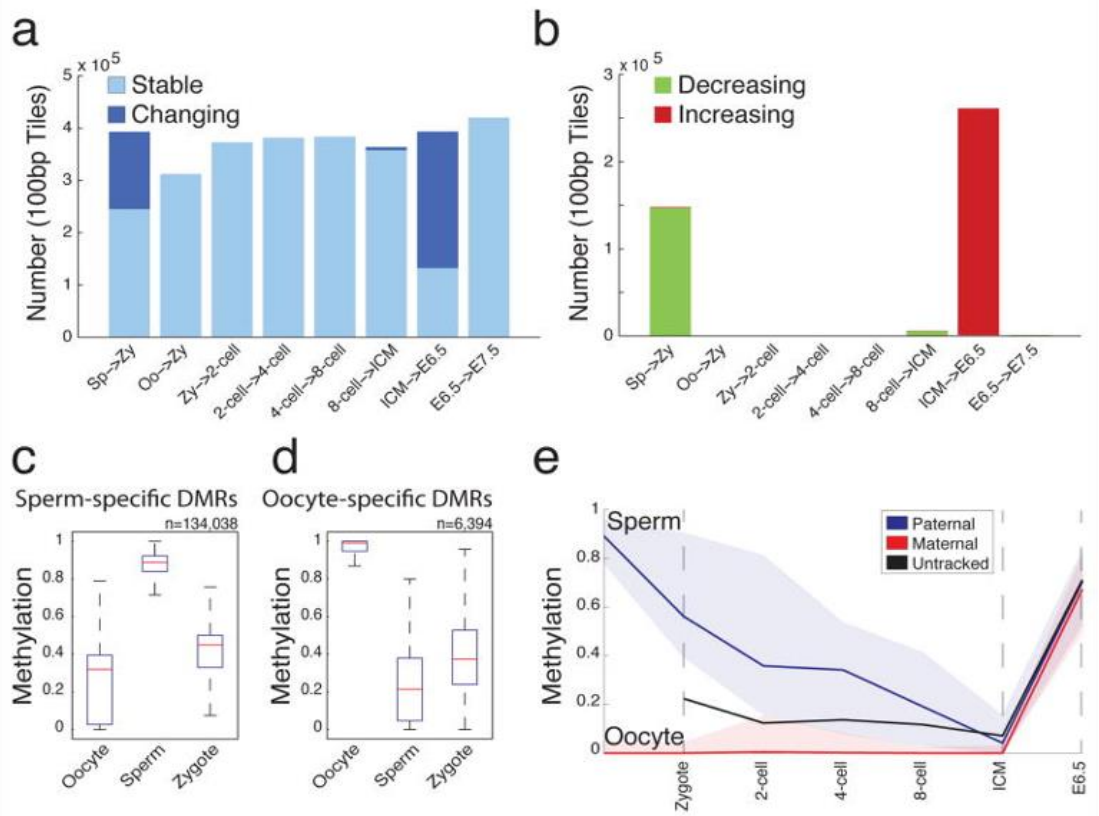

Figure 4. Graph (a) depicts the transitions in DNA methylation at the different stages in early embryonic development. Significant changes by > 0.2 are in dark blue labeled as changing while light blue shows stable methylation. E6.5 and E7.5 represent the embryonic day post implantation. Similarly, graph (b) shows significant increases of methylation in red and decreases in green. The boxplots (c) and (d) depict the methylation levels for sperm and oocyte specific DMRs, respectfully, and the red line representing the median. Graph (e) pictures CpG methylation at different embryonic development stages specific to either paternal (blue) or maternal (red) alleles. [7]

when analyzing significant methylation levels, they found 376 oocyte-contributed and 4,894 sperm-contributed differentially methylated regions (DMR) in the zygote [7].

Interestingly, the oocyte DMRs were mainly on CpG sites with promoters while the latter resided primarily in intergenic regions [7]. From this study, these researchers found that the methylation levels of the oocyte, which includes the hyper-methylated promoters in the CpG sites, can heavily influence those of the embryo [7].

Those exposed prenatally during the Dutch Hunger Winter allowed various researchers to evaluate the developmental origins hypothesis. More specifically, a handful of these studies have tried to see if there is an association between prenatal exposure to famine and diabetes later in life. Insulin-like growth factor II (IGF2) is a locus known to be epigenetically regulated and critical for human development. IGF2 is an imprinted locus regulated by the IGF2 differentially methylated region [6]. What makes the IGF2 loci special is that its methylation mark is steady even up to middle age in humans [6]. In one of these many studies, they looked at the methylation patterns of IGF2 in individuals with periconceptional (early conception) exposure and late gestational exposure during the famine (Figure 5).

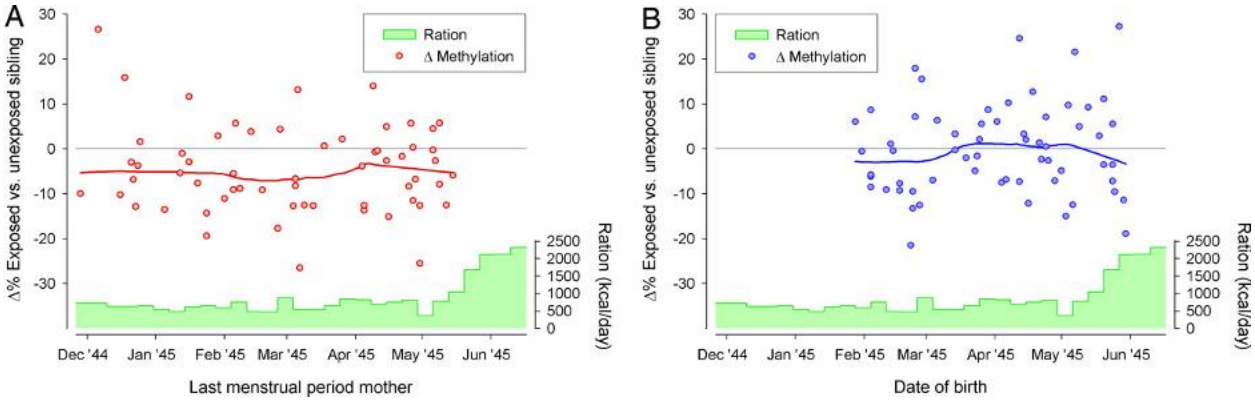

Figure 5. In green are the average calories distributed from December of 1944 to June of 1945 and the red and blue dots show the change in methylation of the IGF2 DMR. Graph (A) pictures the differing methylation in IGF2 DMR between the early prenatal exposure group and their siblings with the estimated time of conception of the individual exposed to the famine. Contrastingly, graph (B) pictures the differing methylation in IGF2 DMR between the late gestational exposure group and their siblings with the birth of the individual exposed to the famine. [6]

Looking at 60 people with periconceptional exposure and their unexposed same-sex siblings, they used quantitative mass spectrometry to examine the methylation of 5 CpG sites in the IGF2 DMR [6]. CpG sites are areas in DNA with a high amount of Cytosine and Guanine, which are typically located near or in promoter regions and can be good gene markers [2, 14]. When comparing the methylation fraction of IGF2 DMR, the early conception siblings were associated with 5.2% less methylation [6]. Interestingly, when looking at the IGF2 DMR methylation between those with late gestational exposure and their unexposed siblings, there was no statistically significant difference (P= 0.69) [6].

In this study, they found that exposure to famine during early pregnancy led to the hypomethylation of IGF2 almost 60 years later. One interpretation of these results was that the hypomethylation may be due to a lack of key methyl donors such as methionine because of the

famine and lack of nutrition. Another study, which implemented a low-protein diet during the preimplantation period with rats, discovered similar results and interpretations [15]. When analyzing the maternal serum at days 2 and 4 after mating, researchers found not only a significant reduction of insulin and the amino acid methionine when compared to their controls, but also isoleucine, leucine, proline, threonine, and valine [15]. What makes these findings interesting is the importance methionine has during early development. It is needed for protein synthesis and production of S-adenosylmethionine (SAM) which acts as a methyl donor [16].

Furthermore, another study also saw the downregulation of a gene due to a restricted maternal diet in early pregnancy. Transcription factor Hnf4a has been linked to type 2 diabetes and, from a study on rat islets epigenetically regulated by maternal diet [5]. Hnf4a, in both human and rat islets, plays an important role in pancreatic B-cell differentiation and glucose tolerance [5]. Additionally, many of the Hnf4a protein variants originated from mRNAs transcribed from the proximal promoter P1 and distal promoter P2 [5]. The P1 promoter is critical for the liver, kidney, and intestine and exhibits an interaction with an upstream enhancer,

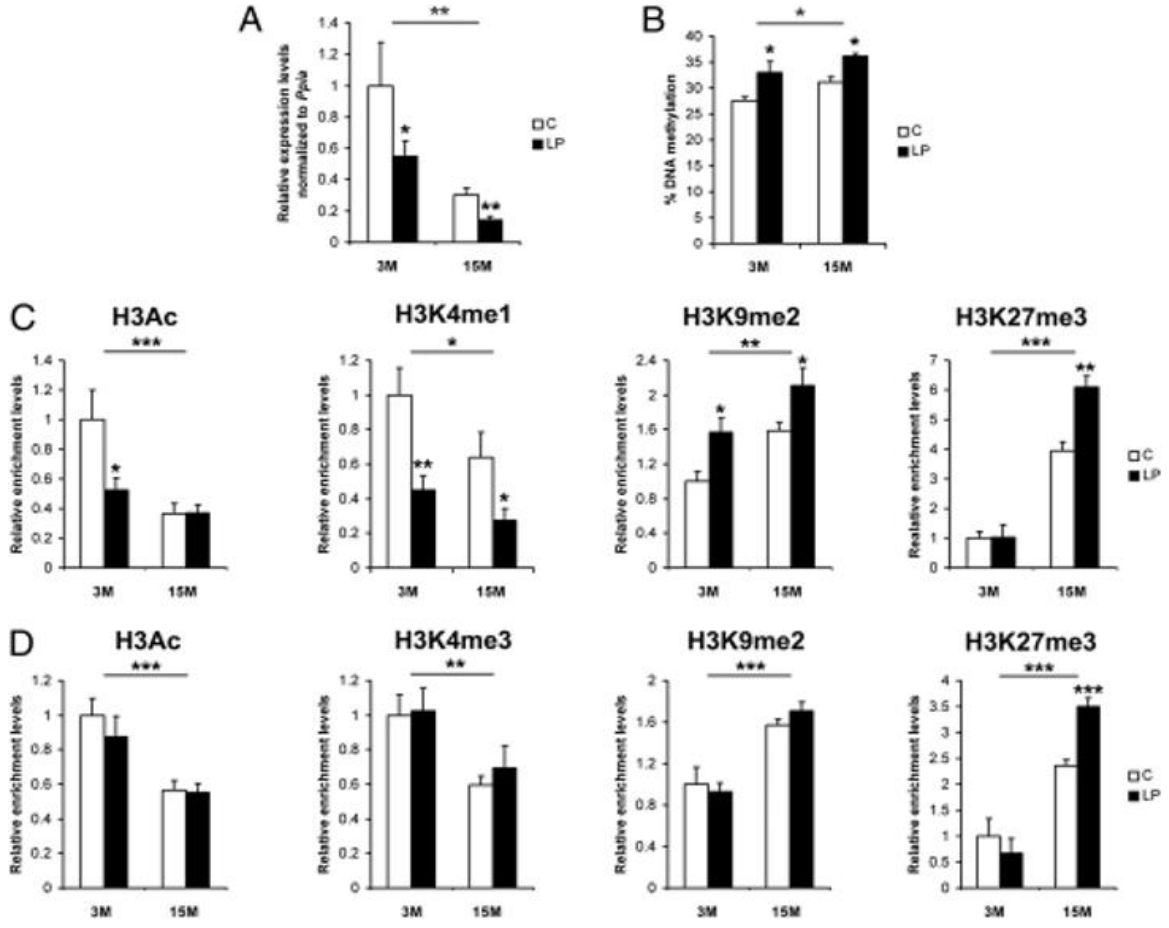

Figure 6. Each graph depicts the control diet (white bars) and the low-protein diet (black bars) for both age groups, 3-month-old and 15-month-old rat islet samples. Graph (A) pictures the mRNA analysis. Graph (B) pictures the DNA methylation at the P2 promoter. Graph (C) pictures the native ChIP analysis of histone marks at the enhancer. Graph (D) pictures the native ChIP analysis of histone marks at the P2 promoter. Error bars indicate SEM. *P < 0.05; **P < 0.01; ***P < 0.001. [5]

while P2 is important for early development [5]. Interestingly, promoter-specific quantitative RT-PCR revealed that high transcriptional activity of P2 was linked with low amounts of CpG methylation, but at P1, low transcriptional activity was associated with more CpG methylation [5]. Additionally, the P2 promoter was marked by H3 acetylation, and the active histone mark of H3K4me3 while not too far down from P2, the enhancer region was characterized by open chromatin [5]. To analyze this further, researchers examined the effects of alternating the levels of CpG methylation in insulin-secreting cell lines, like BRIN, on promoter activity [5]. Normally, BRIN cells have low levels of Hnf4a mRNA at the P2 promoter. However, when demethylated, it led to an increase in the expression of the P2 promoter and followed by even more demethylation [5].

When performing a qRT-PCR in islets from 3-month-old and 15-month-old rats who either were exposed to a low-protein or control diet in an early fetal diet, they discovered that Hnf4a mRNA levels were significantly lowered (60%) for the low-protein group than the control (Figure 6A) [5]. Similarly, using ChIP to examine the histone modification at the Hnf4a locus, they found in the enhancer region of the 3-month-old low-protein diet rats a significant reduction

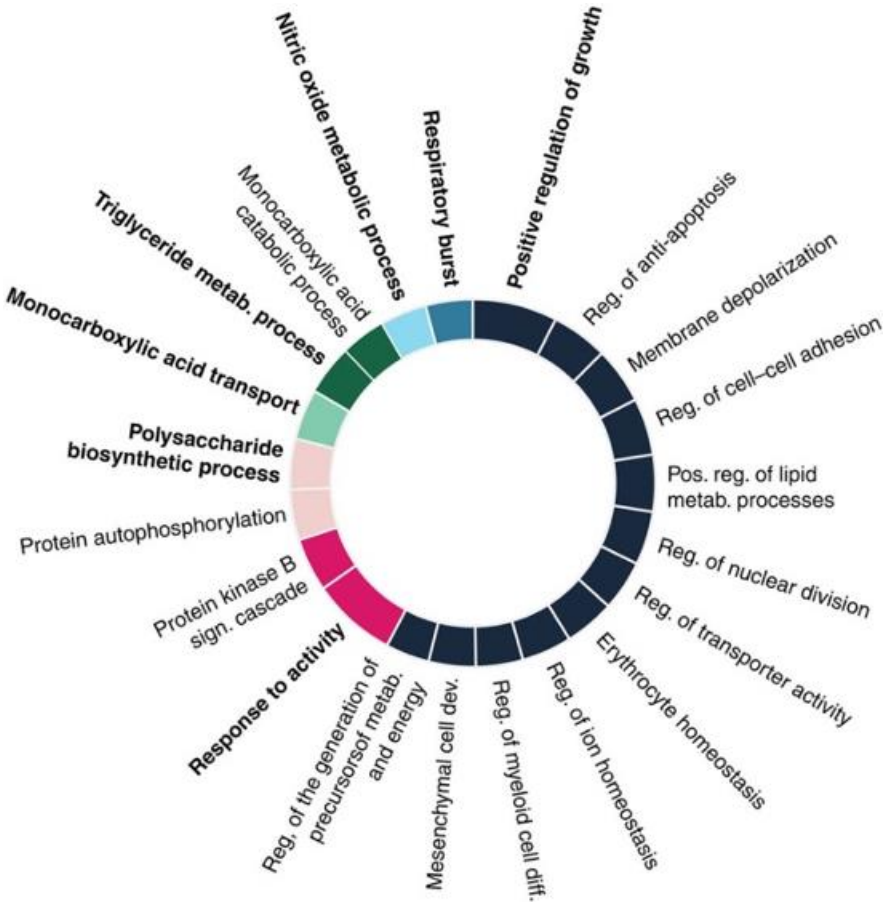

Figure 7. This graph displays 21 significant pathways linked to famine exposure using REVIGO analysis and gene ontology (GO) terms. The sizes of the boxes are proportional to the statistical ratio. The GO biological processes in bold are the are the dominant term of the clusters (based on color). [3]

in the active histone marks H3Ac ($P < 0.001$) and H3K4me1 ($P < 0.05$), but an increase of the repressive histone mark H3K9me2 ($P < .01$) when compared to their control group (Figure 6C) [5]. From these results, this study found that lower levels of Hnf4a expression are associated with hyper-methylation at the P2 promoter and reduced P2-enhancer interaction due to maternal diet and could increase the risk of type 2 diabetes [5].

In another study focusing on the individuals affected by the Dutch Hunger Winter during early development, they analyzed the methylation levels of CpG sites in comparison to their same-sex siblings [3]. After conducting a genome-scale analysis and then testing genomic annotations, they found 181 DMR regions possibly associated with famine during early development [3]. Additionally, in these regions, hyper-methylation was seen more in those exposed to famine during prenatal development than hypomethylation [3]. From the 181 DMRs, 6 loci appeared to play an important role in gestational timing [3]. Further genome-scale analysis of the DNA methylation around these loci found 21 significant gene ontology biological processes linked to famine exposure and were clustered based on relatedness (Figure 7) [3]. Many of these pathways also happened to be related to lipid and cholesterol metabolism [3]. Once the 6 loci were analyzed further, 2 significantly stood out, INSR and CPT1A [3]. Further analysis of these loci found that ISNR is involved in processes responsible for prenatal growth and insulin signaling, and CPT1A in cholesterol levels and lipid metabolism [3]. What made this data even more interesting was that those exposed to the famine in early development had a higher birth weight, BMI, modified glucose response, and increased low-density lipoprotein (LDL) and total cholesterol levels [3]. Additionally, both loci were associated with enhancer activity, but only CPT1A was downregulated by hyper-methylation [3]. From this study, these researchers were able to

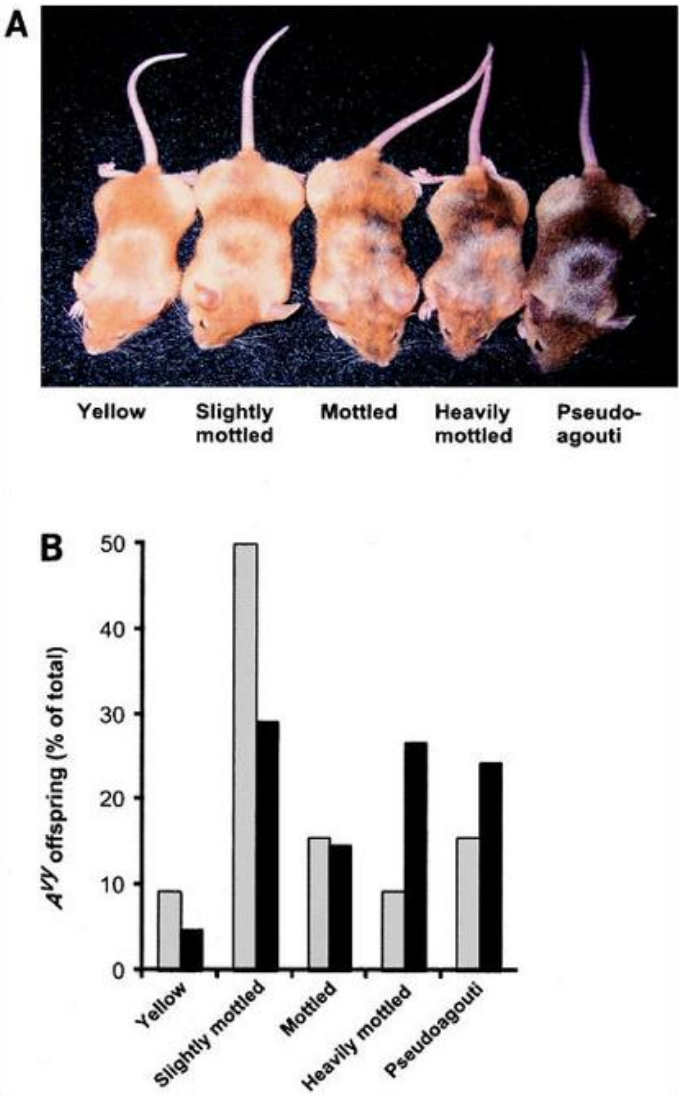

Figure 8. (A) Pictured are the 5 different coat colors of A^{vy} offspring. Mice with yellow coats are hypomethylated and mice with pseudoagouti (brown) coats are hypermethylated. Graph (B) shows the distribution of the coat colors between the 2 groups, un-supplemented (gray bars) and supplemented (black bars). [4]

suggest that prenatal malnutrition can lead to differential methylation in regions that are critical for early development and metabolic pathways [3].

One study uses the viable yellow agouti (A^{vy}) mouse model, to examine if CpG methylation is critical in nutrient-induced phenotypic alterations [4]. The agouti gene is unique because it encodes a molecule that switches hair growth from black (a allele) to yellow (A allele) partly due to the environment [4]. The A^{vy} epiallele is the product of the insertion of a retrotransposon at the 5' of the A allele upstream from the start of transcription [4]. These researchers looked at homozygous a/a females that were assigned to either a diet supplemented with methyl donors, cofactors folic acid, vitamin B12, choline chloride, and anhydrous betaine or an un-supplemented diet starting two weeks before and throughout pregnancy [4]. Because they were analyzing A^{vy}/a mice, which have varying phenotypes, it was important to classify the coat colors. When examining the differences in the coats between the two groups, there was a significant increase in supplemented offspring with the brown phenotype ($P = 0.008$) and increased DNA methylation (Figure 8A, B) [4]. This was confirmed by examining the CpG methylation at seven sites in the offspring [4]. Additionally, the coat color and the methylation patterns were maintained throughout adulthood, even in different tissues [4]. Exposing these A^{vy} mice to a diet that supplemented methyl donors in early development shifted the epigenotype that still affected the adult phenotype [4]. While the previous studies focused on lack of nutrients can affect DNA methylation, this one demonstrated that an increase in nutrients can also affect methylation patterns even into adulthood.

Insulin Growth Factor II & Imprinting Control Region 1

Figure 9. Pictures Chromosome 11 (p15.5). The red box displays the H19/IGF2 Imprinting Control Region 1. https://genome.ucsc.edu

As mentioned previously, IGF2 is epigenetically regulated. It is also a protein hormone that plays a critical role in the regulation of cell proliferation, growth, migration, and differentiation [17]. Additionally, it is also predominantly expressed during early embryonic/fetal development, and in adults, IGF2 is expressed in the liver and plasma [17]. From this information alone, it can make sense how important this gene is for early development.

The imprinting domain associated with IGF2 genes is known as Imprinting Control Region 1 (IRC1) (Figure 9) [17]. IRC1 is a differentially methylated region that regulates the expression of H19 and IGF2 genes [17]. Upstream of these two genes is their shared enhancer. On the paternal allele, IRC1 is methylated, which prevents the CTCF protein from binding [17]. This leads to IGF2 being activated and H19 silenced [17]. On the maternal allele, ICR1 is not methylated and the CTCF protein can bind, creating a chromatin insulator [17]. This then leads to IGF2 being silenced and H19 activated [17].

Furthermore, Silver-Russell syndrome is a condition defined by extreme intrauterine growth retardation and poor postnatal growth where 20-60% of cases are due to the hypomethylation at H19 and IGF2 [18]. While the study mentioned earlier that found

hypomethylation at the IGF2 DMR did not see cases of Silver-Russell syndrome, I believe it is still important to see the similarity between the two.

Discussion

While the results of these studies had some similarities, there is quite a bit that they do not have in common. However, it is important to note the gaps in the literature when it comes to epigenetic mechanisms and how they relate to health years later. What we can conclude from these studies is that embryonic development is a very critical stage and adverse environmental conditions cause changes to some extent in the genome.

As mentioned earlier, there are two specific points where DNA methylation is changing, first at fertilization and then at the blastocyst stage. Additionally, research has found that the methylation status of the embryo highly resembles that of the oocyte. This leads me to question a few different things. One mainly is if the mother experiences famine for some time before fertilization, could it change the DNA methylation status of the oocyte and consequently the embryo? This is something I would like to research further.

Additionally, as one of the articles mentioned, they believed that hypomethylation of IGF2 was due to there being a lack of methyl donors from the diet. Initially, this made logical sense, especially when in another study they found that increasing methyl donors in the diet found an increase in methylation at the epiallele A^{vy} in mice. Both IGF2 and A^{vy} are epigenetically regulated, however, the other loci mentioned, such as Hnf4a, INSR, and CPT1A have not. Furthermore, Hnf4a and CPT1A showed downregulation due to hyper-methylation when lacking methyl donors from the diet. These results do not exactly line up with the hypothesis that the amount of methyl donors in the diet has a positive relationship with DNA methylation levels. I wonder if this is true for epigenetically regulated loci and if there is another reason for changes in the methylation status in Hnf4a and CPT1A besides famine during early development.

It is important to note that other factors could be contributing to changes in methylation status. One of these is stress. For both humans and mice alike, starvation can cause stress. Additionally, the women affected by the Dutch hunger winter most likely experienced stress for a multitude of reasons, for example, the stress over the war and the cold temperatures [19]. Furthermore, there have been statements that when the famine was at its worst, some began eating toxic food substitutes such as tulip bulbs [19]. All these factors could end up playing a role in the results of some of these studies and should be considered when interpreting causality.

Lastly, the relationship between the environment and genetics is very complicated. As shown in Figure 10, in-utero exposure does not mean a certain phenotype will be present. Genetic differences between individuals can affect transcription factor binding by remodeling epigenetic marks and consequently affect gene expression (figure 10b) [2]. Additionally, after birth, we are still experiencing environmental exposures. Exposures in-utero that cause

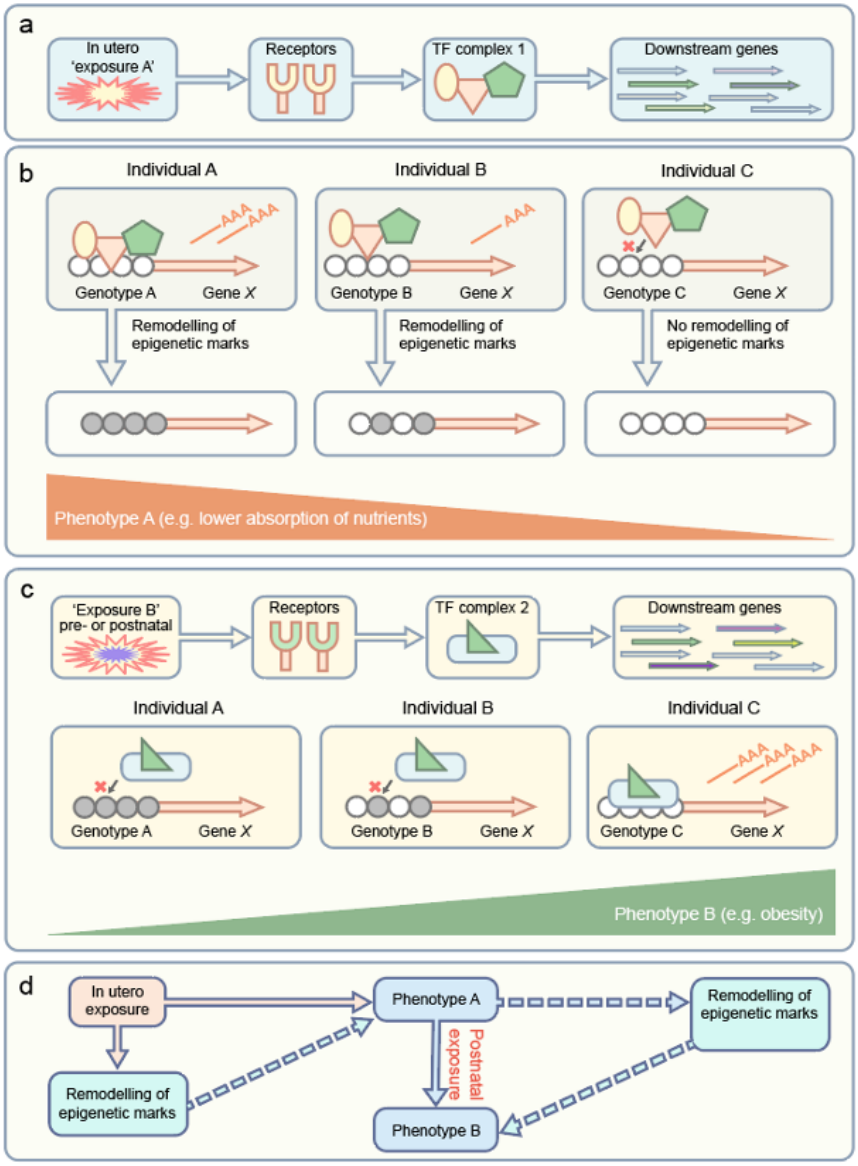

Figure 10. Panel (a) displays how exposures in-utero can lead to activation of transcriptional regulators and downstream genes. Panel (b) shows how genotype differences can impact transcription factor binding and gene expression (—AAA is mRNA). Panel (c) is similar to that of (a) and (b) but it displays environmental exposures and their effect on gene expression in postnatal life (grey circles indicate epigenetic marks such as DNA methylation). Panel (d) is a model of how an in-utero exposure can affect the phenotype and susceptibility to a disease depending on postnatal exposures. Dashed lines have not been proven but show the possible contribution to changes in phenotypes. [2]

epigenetic reprogramming might not make a difference until another exposure in postnatal life occurs, resulting in an altered phenotype in adult life (figure 10c, d) [2]. This makes it difficult when trying to explain causality instead of simply associations between epigenetic mechanisms, famine in-utero, and health conditions later in life.

With all of this said, famine studies such as the Dutch hunger winter strongly suggest that undernutrition during early gestation affects health in later life (the developmental origins of health and disease hypothesis). However, I do not believe a clear epigenetic link has been made to fully support this hypothesis. Numerous studies see the associations between changes in DNA methylation and the adverse health conditions of those apart from the Dutch hunger winter cohort, but this was a very specific group of individuals. The timing of the famine and the point of gestation seems to play a very critical role. However, so does the severity of exposure and genetic background. Linking prenatal undernutrition and epigenetic mechanisms is not easy, especially since research regarding humans can only be observational with no manipulations due to it being very unethical. There are many confounding variables in studies, such as those described earlier.

It would be beneficial for future research to conduct longitudinal studies with different lengths of exposure to famine. The Dutch hunger Winter affected people who quickly went from being well-nourished to a drastic famine, and then a sudden relief back to being well-nourished [1]. Additionally, most studies focus primarily on maternal influence. I believe this is a gap in the research that should be investigated. While, as mentioned earlier, the methylation levels of the embryo highly resemble the oocyte, there could potentially be an influence of sperm methylation levels as well. Lastly, in animal experiments, examining and modifying the methyl donors in the diet should be further explored. There seems to be a positive relationship between the number of methyl donors and DNA methylation of epigenetically regulated loci.

This area of research still has a long way to go. There are sufficient associations, but nothing has a distinct causality. There must be proper nutrition during early development, but that is not always the case. When epigenetic variation due to hostile exposures is found, it could act as a biomarker and help with either preventative care or corrective actions.

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Appendix I

VITA

Brooke T. Howell was born in Dallas, Texas, on July 2, 2001. She attended Rockwall-Heath High School in June 2019. The following August she entered Oklahoma State University and in May 2023 received a Bachelor of Science in Microbiology & Molecular Genetics, a Minor in Psychology, and awarded the Departmental Honors Award and the Honors College Degree. In August of 2023, she will attend MD Anderson Cancer Center School of Health Professions to receive a Bachelor of Science in Molecular Genetic Technology in August of 2024.

Appendix II

Thesis Presentation and Defense Announcement

Wednesday, April 26, 2023 at 14:28:12 Central Daylight Time

Subject: Re: 2023 OSU Undergraduate Research Symposium on Tuesday, April 18 at the ConocoPhillips Alumni Center

Date: Wednesday, April 19, 2023 at 7:37:45 AM Central Daylight Time

From: Burnap, Rob

To: Friske, Bekkah, Stubbendieck, Reed, Goyal, Tanisha, Singh, Padam, Ansari, Mehraj, Varghese, Jesna, Underhill, Simon, Pratt, Carrie, Beakley, Savannah, Burch-Konda, Jacob, George, Tyler, Mitra, Avi, Beckmann, Sabrina, Conway, Tyrrell, Cabeen, Matthew, Elshahed, Mostafa, Fathepure, Babu, Hadwiger, Jeff, Hoff, Wouter, Lutter, Erika, Morgenstein, Randy, Patrauchan, M, Prade, Rolf Alexander, Wozniak, Karen, Youssef, Noha, Zhang, Minquan, Budd, Connie, Blakley, Teresa, Coldiron, Marty, Bules, Alice, Aranda, Ramee Grace, Doranga, Sudhir, Hamm, Chris, Khadka, Rabindra, Luthra, Deepali, Maharjan, Suman, Nelson, Ben, Pan, Somalisa, Salpadoru, Tarosha, Yadav, Archana, Yahya, Amal, Jett, Clark, Ajagbe, Damilare, Dohmen, Rosalie, Hull, Kenzie, Holcomb, Christian, Nair, Ayesha, Ambriz, Adriana G, Alam, Imam, Conn, Brittney, Dasgupta, Noopur, Giri, Samikshya, Heise, Brenden, Kannon, Mamie, Braga, Reygan, Hahn, Ryan, Meili, Casey, Carder, Macy, Faulk, Aaron Scott, Fatima, Saher, Das, Niloy Kumar, Quadri, Oluwatobi, Mukherjee, Swarnali, Zhang, Yingxin, Chiconas, Alex, Kirchberger, Paul, Roper, Jess, Jones, Adrienne, Marley, Garry, Workman, Claire, Wilson, Kevin Scott

Dear colleagues,
I'd like to draw your attention to two undergraduate honors thesis presentations to be held Wednesday afternoon in our conference room, 305 Life Sciences, East:

3:00-3:30
John H Dorlon IV
Constructing and Deploying an improved CRISPR Cas12a System for Synechococcus elongatus sp. PCC 7942

4:00-4:30
Brooke Howell
Epigenetics vs. Prenatal Famine

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