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**Title:**

A mouse model of adipocyte mTORC1 activation increases milk fat.

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**Declaration of Interests**

The authors have no competing interests to declare.

**Abstract:**

Changes in the mammary gland biology during pregnancy and lactation and the interplay between mammary epithelial cells and adipocytes remain largely unknown. Mammary adipocytes are thought to "disappear" during lactation, and their contribution to milk composition is still not fully understood. A major nutrient sensor in most tissues is the mechanistic target of rapamycin 1 (mTORC1). To understand the role of mammary glands in sensing maternal nutritional status, we aimed to understand the effect of adipocyte mTORC1 hyperactivation on mammary gland function, milk composition, and offspring outcome in an adiponectin-Cre *Tsc1/2* knockout mouse model. Knockout (KO) and wild type (WT) C57BL/J6 female mice were mated with KO or WT males at 6-8 weeks of age. Data on maternal body mass composition during pregnancy and lactation, pup survival and weight, litter numbers, milk volume production, milk composition and lipidomic analysis, and mammary gland weights and histology were assessed. We used RNA sequencing to investigate mammary gland gene expression. Our results show that female pups born to KO dams are heavier, with KO dams having higher milk fat composition. Additionally, KO dams had lower percentage saturated fatty acids, higher percentage of monounsaturated fatty acids, and lower milk omega6:omega3 ratio a. Gene expression showed 112 upregulated and 153 downregulated genes in the mammary glands and differentially expressed metabolic pathways. These results suggest suggests a key role of mammary adipocyte mTORC1 in mammary gland function, milk composition, and offspring health.

**Key words**: Mammary glands, Milk composition, Adipocytes, mTORC1, Obesity

**1.0 Introduction**

Maternal obesity increased by 11% from 2016 to 2019 and has reached 29% (1). Maternal weight can increase maternal mortality risk and pregnancy complications including gestational diabetes (2). According to the Developmental Origins of Health and Disease theory, the health of the offspring is highly influenced by intrauterine and early postnatal exposures (3). Maternal obesity can impact offspring health during *in utero* development and can increase risk of fetal macrosomia (4). During early postnatal life and the critical lactation window of development, maternal obesity can impair the ability to initiate and sustain breastfeeding and can alter milk composition (5). However, the mechanisms by which maternal obesity affects lactation ability and offspring health during lactation remain less clear.

Successful lactation requires the full development and differentiation of the mammary glands in preparation for milk production and secretion (6, 7). The mammary gland is composed of adipocytes and alveolar cells. Mammary adipocytes form a major proportion of the mammary gland and are necessary for proper gland development and proliferation (8, 9). During pregnancy and lactation, the mammary adipocytes undergo transformation and almost disappear due to de-differentiation to support lactation and epithelial cell expansion at the expense of the mammary fat pad (10). The mammary adipocytes within closer proximity to the alveolar epithelial cells are thought to provide a primary source of lipids for milk production (10). When the offspring is weaned or lactation is ceased, the mammary adipocytes then re-differentiate and expand reverting to their original form during the involution process (10). Although the mammary fat pad undergoes restructuring during pregnancy and lactation, the exact fate of these fat cells and the mechanisms regulating their transformation are less clear.

Given their role in maturation, development, and function of the mammary gland, mammary adipocytes are crucial for successful lactation. Maternal obesity can affect lactation onset and duration. Initiation of lactation is delayed in pre-pregnancy obese or overweight women (11) while the duration of breastfeeding for 6 months or more is shorter (12). The probability of early weaning at 3 months postpartum was highest for infants of obese mothers (13). In addition to altering lactation initiation and duration, maternal obesity can impact milk composition. Maternal weight, body mass index, fat mass, and fat mass percentage were positively correlated with total and true milk protein content at 3 months postpartum (14). Maternal weight and body mass index were positively correlated with milk fat content at 1 month postpartum (14). Furthermore, the fatty acid composition showed a higher omega6:omega3 ratio in milk of obese women compared to their non-obese counterparts (15).

Obese subjects that had excess fat mass showed increased activity of the mechanistic target of rapamycin complex 1 (mTORC1) in the visceral fat compartment (16). mTORC1 is a critical nutrient sensor and a main regulator of protein and lipid synthesis (17, 18). In the presence of anabolic signals like insulin, energy abundance, and amino acid availability, mTORC1 function is upregulated via the Akt pathway (19). mTORC1 promotes lipogenesis and adipogenesis and inhibits lipolysis (17, 20). Hyperactivation of mTORC1 in the mammary glands has been studied in the context of breast cancer (21), but little is known about its role in macronutrient synthesis in the mammary gland during lactation (22). Using a murine genetic model, we show that chronic mTORC1 activation in maternal adipocytes via deletion of its upstream negative regulator, *Tsc1*, increased milk fat composition and alters milk lipid profile, reduced gene expression of immune response pathways in the mammary glands, and increased weight of lactating offspring.

**2.0 Materials and Methods**

**2.1 Animals**

All mice were purchased from the Jackson Laboratory. All mice were fed a normal chow diet with *ad libitum* access to food and water.

To hyperactivate adipocyte mTORC1 and generate an adipose-specific *Tsc1* knockout, we used the Cre-loxP recombination technology. *Tsc1* fl/fl mice with flanked *Tsc1* gene exons 17 and 18 were crossed with *Adipoq*-Cre mice expressing the adipocyte-specific constitutive Cre recombinase controlled by adiponectin gene promoter. The parental strains (F0) for this experiment were 6-8 week old male *Tsc1* fl/fl ;Tg/+ or *Tsc1* fl/fl ;+/+ crossed with 6-8 week old female *Tsc1* fl/fl ;+/+ or *Tsc1* fl/fl ;Tg/+, respectively. The offspring (F1) were a combination of knockout (KO, fl/fl;Tg/+) and phenotypically wild-type (WT, fl/fl;+/+) at an expected ratio of 1:1. The knockout of the floxed alleles are driven by Adiponectin-Cre (23, 24), which is expressed in all adipocyte lineages (brown, white and mammary adipocytes) as shown in Wang et al. (25). As such one limitation of this approach is that all adipocytes are affected, not just mammary adipocytes (for which there is no known specific Cre driver). All mice were bred in our facility at the University of Michigan. All animal procedures were carried out in accordance with the National Institute of Health guide for the care and use of laboratory animals and was approved by the University of Michigan Institutional Animal Care and Use Committee prior to the work being performed.

Mice had *ad libitum* access to normal chow diet and water. Male breeders were removed from the cage after 16 days of mating to avoid the occurrence of a second pregnancy.We checked for litters on a daily basis after 2.5 weeks of mating. The number of pups born was recorded to determine maternal fertility and pup viability. After delivery (delivery day denoted as postnatal day 0.5, PND0.5), the dams continued to have *ad libitum* access to food and water.

Pups were sexed and culled to four animals (2 females and 2 males, when possible) per litter at PND2.5. The offspring were weighed at PND0.5, PND7.5, 14.5, 16.5. The pups underwent body composition analysis by echoMRI at PND16.5 then immediately sacrificed.

**2.2 Body Composition and Indirect Calorimetry**

In all groups, the dams underwent body mass assessment three times a week during pregnancy and lactation and on the day of delivery using magnetic resonance (EchoMRI 1100, EchoMRI, Houston, TX) to assess body composition. Mice were weighed by dynamic weighing to capture accurate weight using a digital scale. The weight was recorded along with the mouse ear tag number. The mouse was then gently placed in the MRI tube with the plunger slightly compressing along the mouse’s body to ensure restrained movement during the measurement. Fat, lean, free water and total water mass (g) were recorded for each animal. We weighed offspring and performed body mass assessment using MRI at PND16.5.

## **2.3 Sacrifice and Tissue Collection**

All animals were sacrificed using anesthetic gas inhalation (5% isoflurane drop jar) at PND16. Cervical dislocation was conducted as a secondary method to confirm euthanasia. The mice were pinned on a dissection board in a supine position. We dissected KO and WT dams by a midline incision of the skin from the rectum to the diaphragm and extracted thoracic, abdominal and inguinal mammary glands. Briefly, the peritoneum was pulled apart from the skin. The lower glands were excised carefully then weighed. Portions of the upper and lower glands were embedded in paraffin for histology, while the remaining tissue from the lower left and right mammary glands were collected in 2ml tubes and snap frozen in liquid nitrogen and later stored at -80C for molecular studies. Offspring of dams were sacrificed without tissue extraction at PND16 after body assessment measurements.

## **2.4 Determining Milk Output Volume**

At PND10.5, considered the peak of lactation (26), we determined milk output volume for the WT and KO dams. To determine milk volume, we used the weigh-suckle-weigh technique (27). Briefly, we weighed the dam separately then determined the aggregate weight of the pups. The dam and pups were then separated for two hours. During the two-hour separation, the pups were placed in a new cage and were kept warm using a heating pad. In the meantime, the dam remained in its initial cage with *ad libitum* access to normal chow diet and water. After the two-hour separation period, the dam was weighed again and the aggregate weight of the pups was measured. The pups were then returned to the dam’s cage and were allowed to nurse for one hour undisturbed. At the end of the nursing timepoint, the dam was weighed again and the aggregate weight of the pups was determined. After this one-hour nursing period, milk volume was determined as the weight change of the pups after nursing and after the 2-hour separation. The difference in the dam’s weight after nursing and after the 2-hour separation was calculated to further ascertain the dam’s milk supply.

## **2.5 Determining Milk Composition**

On PND16.5, we collected milk samples (~0.5ml) from the nursing dams. Briefly, we anesthetized the dam after two hours of separation from the pups by intraperitoneal injection of Ketamine (0.1275g/kg body weight). We then performed an intraperitoneal injection of oxytocin into the forelimb (2U/dam) to induce milk production. The dam’s nipples were manually squeezed to promote milk letdown, and the milk was collected into a 1.5 ml tube via suction. After milking was complete, the dam was immediately sacrificed using isoflurane and a secondary measure of cervical dislocation. We then dissected the dam by a midline incision of the skin, extracted thoracic, abdominal and inguinal mammary glands. The lower mammary gland pads were weighed. A small section of the lower mammary glands was saved for paraffin embedding for histology while the rest was snap frozen in liquid nitrogen and cryopreserved. Milk protein composition was analyzed using SDS-PAGE gels and diluted milk samples (4-fold dilution).

## **2.6 Determining Milk Protein Concentrations**

Milk samples collected from WT and KO dams were assessed for protein content. Milk was diluted to a factor of 4 (1:3 in PBS+EDTA). Skimmed milk was collected after centrifuging. Samples were heated to ~95C and loading cocktail was added onto the plastic plate with the gel along with a ladder. Gels were stained by Coomassie blue and quantified by near-infra-red imaging. Imaging was done using LiCOR Odyssey to determine protein levels of whey acidic protein, alpha casein, beta casein, lactoferrin, and serum albumin identified based on known molecular weights.

## **2.7 Determining Milk Fat Content**

Milk samples collected from WT and KO dams were assessed for fat content by the creamatocrit method using a hematocrit centrifuge (28). Briefly, samples were diluted to a factor of 4 (1:3 in PBS). Diluted samples were transferred into plain micro-hematocrit glass capillary tubes. The tubes were sealed from one end using Critoseal. The tubes were later placed in CritSpin mini-creamatocrit spinner. Samples were centrifuged for 8 cycles of 120 seconds per cycle for a total spin time of 16 minutes. The capillary formed layers of white fat and non-fat milk. The distance of the fat layer was measured in millimeters (mm) accurately using a 150 mm dial caliper (General Tools and Instruments 6” Dial Caliper, 2011). The total volume of milk (fat + non-fat milk) was also measured in mm. Percentage of fat was determined with respect to the total milk volume.

## **2.8 RNA Sequencing**

Using the lower right mammary gland tissues collected from the dams, we assessed whole-transcriptome RNA expression using five wild-type and six knockout samples. RNA samples were prepared from the mouse tissues using the PureLink RNA Mini Kit. Briefly, tissues were cut on dry ice to ~50mg samples then homogenized and treated to collect the purified RNA. The RNA was quantified using a nanodrop and purity was verified by an Agilent Bioanalyzer. All samples had a RNA integrity number (RIN) higher than 7.5. Library preparation and next generation sequencing was conducted by the Advanced Genomics Core at the University of Michigan. Paired-end poly-A mRNA libraries were generated and sequenced to an average depth of 57M (range 46M-69M) reads/sample on Illumina NovaSeq platform. Reads were aligned to the mouse reference genome GRCm38.p6 using Salmon v 1.3.0 (29) with the gc-bias and validateMappings flags. Mapping efficiency was 54.8% (sample range 53-56.6%). Transcript-level data was reduced to gene-level data via tximeta v1.8.4 (30) and txiimport v1.18.0 (31) prior to analysis by DESeq2 v1.30.1 (32). To determine differential expressed genes we evaluated 14242 genes, excluding those with low or no read counts, identifying 265 differentially expressed genes (q<0.05). Full gene expression results are reported in Supplementary Table 1. For gene set enrichment analyses, we used ClusterProfiler v3.16 after ranking genes by fold change and analyzing relative to Gene Ontologies. Similarities between enriched gene sets were calculated by Jaccard distances. Gene set enrichment results are presented in Supplementary Table 2. Data are available from GEO at accession number XXXX

## **2.9 Western Blotting**

Using the lower right mammary gland tissues collected from the dams, we assessed TSC1/2 protein levels and mTORC1 activity to confirm knockout in mammary glands as a whole tissue and specifically in mammary adipocytes. To better determine the site of the knockout, a separate cohort of KO and WT dams were bred for this purpose. The mammary gland fat and stromal vascular fraction (SVF) were separated. Genotyping was separately done on the glandular and SVF compartments to verify knockout specificity in the mammary gland. Briefly, a portion of the whole lower right mammary gland, the SVF, and the fat samples was boiled and loaded into different wells with a ladder control. Proteins were transferred to nitrocellulose overnight. The matrix was stained for total protein using Revert total protein and scanned by LiCOR to normalize against total protein. Samples were incubated with the primary then the secondary antibodies. Briefly, antibodies against TSC1/2, total and phosphorylated mTORC1 targets (S6K, 4EBP1, S6) and regulators (Akt, IRS) were used.

**2.10 Lipidomic Analysis**

Lipidomic analyses were done by the Biomedical Research Core Facilities at the University of Michigan. Briefly, milk samples were frozen at -80°C until analysis to prevent lipid hydrolysis. and peroxidation. Samples were quickly thawed once for lipidomic analysis without undergoing multiple freeze-thaw cycles. Long chain fatty acid concentrations were determined by gas chromatography using an assay developed and optimized to analyze human milk in consultation with the University of Michigan Regional Comprehensive Metabolomics Resource Core. Results were reported on 33 lipid classes from C14:0 to C24:1. Lipidomic analysis methods include sample extraction, semi-purification and derivatization followed by fatty acid measurement by gas chromatography (GC) using an Agilent GC equipped with flame ionization detector. The coefficient of variation for lipidomic analysis is 2.5-3.6%.

## **2.11 Histology**

Mammary glands collected from WT and KO dams were embedded in paraffin and Hematoxylin and Eosin (H&E) stained at the Rogel Cancer Center’s Tissue and Molecular Pathology. Slides were blindly assessed for adipocyte size and count.

**2.12 Mammary Gland Adipocyte Sizing and Counting**

Mammary gland adipocytes were quantified using the software Image J. The adipocyte tools plugin was also downloaded and added to the program. This plugin provided the parameters p, processing adipocyte segmentations options, and s, simple adipocyte segmentation options. In analyzing our images the parameters for p were set at min 40, max 1000, and dilates 30, and the parameters for s were set at min 600 and max 1500. First, p was used to process the image, and then s was subsequently used. Once these two parameters were set on the image, manual addition and deletion were performed to ensure adipocytes were properly counted. Once all the adipocytes were accounted for, they were quantified using the measurement method within Image J. The numbers provided were then used to assess if there were any differences between KO and WT adipocytes within the mammary gland.

## **2.13 Statistical Analysis**

All statistical analyses were performed using R, version 4.0. For longitudinal measurements including body composition, food intake, and pup weight gain, data were analyzed using mixed linear models. Statistical significance was designated at p<0.05. We tested for sex-differences in all outcomes and report modifying effects of sex only when significant.

**3.0 Results**

To understand how activation of mTORC1 in adipocytes affects lactation we evaluated pregnant mice that were wild-type (*Tsc1fl/fl; Adipoq-CreTg/+*) andknockout(*Tsc1fl/fl; Adipoq-CreTg/+*). In this model all adipocytes, including all white and brown adipocyte depots and mammary adipocytes are ablated for TSC1 and are predicted to have activation of mTORC1. KO (n=6) and WT (n=5) virgin dams were mated with a male having the opposite genotype, and dams and their offspring were monitored throughout lactation (See Figure 1A).



Figure 1: Dams and pups were monitored throughout lactation. Pup births and weights were measured on postnatal day (PND) 0.5. Pups were culled at PND4. Pups weights were assessed on PND7.5, 14.5 and 16.5. Milk volume was measured on PND10.5 using the weigh-suckle-weigh method. On PND16.5,milk was collected from dams and mammary glands extracted. Maternal body composition was measured on PND0.5 after delivery and every Monday, Wednesday, and Friday thereafter until and including PND16.5.

## **3.1 Maternal Body Composition Was Similar during Pregnancy and Lactation in Adipocyte *Tsc1* Knockout Mice**

Dam body composition was measured every Monday, Wednesday, and Friday during pregnancy and lactation and on the days of delivery and sacrifice. Body weights were comparable between dams (Figure 2A). Lean mass was also comparable between KO and WT dams (Figure 2B). KO dams had a slightly lower fat mass during pregnancy and during lactation (Figure 2C). While WT dams lost fat mass gradually during lactation, KO dams gained fat mass (Figure 2D, d=0.125g/day, p<0.001). Consistent with this, KO and WT dams had similar food intake during pregnancy. However, during lactation KO dams had lower food intake compared to WT dams (Figure 2E, d=6.34g/day, p=0.0113). We assessed litter sizes by which the average litter size from KO and WT dams was similar (Figure 2F). Pups were culled to four pups per dam to normalize milk supply.

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Figure 2: Maternal body composition during gestation and lactation, food intake, and litter size of WT and KO dams. (A) Maternal body weights. (B) Maternal lean mass. (C) Maternal fat mass. (D) Maternal fat mass change from the day of delivery until PND16.5. (E) Average weekly food intake. (F) Litter size of WT and KO dam.

## **3.2 Mammary Gland Weights of KO Dams were Lighter**

Based on these changes in milk composition, we next examined the mammary glands from the adipocyte *Tsc1* knockout dams. At PND16.5, the lower abdominal and inguinal mammary glands were collected and weighed from KO and WT dams. The right lower mammary glands of KO dams were significantly lighter than those of WT dams (Figure 3, d=20.68%, p=0.042). Left lower mammary glands of KO dams significantly weighed less than those of WT dams (Figure 3, d= 28.75%, p=0.001).

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Figure 3: Mammary glands collected from lactating WT and KO dams on PND16.5 showing significant reductions in weight of left and right mammary glands of KO dams.

## **3.3 Adipocyte Size, Count, and Area**

After determining differences in mammary gland weights, we then performed histological analyses to quantify the number of mammary gland adipocytes, measure their size, and calculate their area. Using ImageJ Software, KO mammary glands had slightly more adipocytes compared to the WT. Additionally, the adipocytes of the KO glands showed a trend of being larger than adipocytes of the WT. The percentage area of the adipocytes from the total mammary gland was higher in the KO glands compared to the WT.

## **3.4 Pups Born to Adipocyte *Tsc1* Dams are Heavier During Peak Lactation.**

To evaluate effects of mammary gland changes on the offspring we monitored growth of pups during lactation. There was no significant difference in pup weight at birth (PND0.5) but the KO pups were trending to be slightly heavier than the WT pups. At PND7.5, females born to KO dams were heavier than females born to WT dams (Figure 4, d=9.3%, p=0.**044**), but weights of males born to KO or WT mothers were not significantly different (Figure 4). At PND14.5 and PND16.5, there were no weight differences between groups or sexes. We hypothesize that this is because at later time points the pups are eating more chow-based food and relying less on maternal lactation.

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Figure 4: Pup weights during lactation. Weights of male and female offspring of WT and KO dams at PND7.5.

## **3.5 Adipocyte *Tsc1* Dams Produce Similar Volumes of Milk, but with Higher Milk Fat.**

Based on the changes in offspring weight and mammary gland size and histology, we calculated the mass of milk produced per dam via the weigh-suckle-weigh technique. This was calculated by a two-hour separation period and then as the difference between pup weight after nursing for one hour and pup weight before nursing. As shown in Figure 5A, this was not significantly different between groups. Similar data were obtained by measuring the weight of the dams pre- and post- lactation. To test milk composition, milk was extracted from dams at PND 16.5. Creamatocrit fat analysis revealed that milk of KO dams had higher fat percentage than milk of WT dams (Figure 5B, d=34.07%, p=0.024).Using a milk gel, we quantified total protein and major milk proteins based on known molecular weights. Milk proteins including alpha-Casein, beta-Casein, lactoferrin, whey alpha protein (WAP), and albumin were similar between milk of KO and WT dams.

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Figure 5: Milk production and fat composition. (A) Weight of milk produced by WT and KO dams assessed by pup weight gain after an hour of nursing was similar between pups of WT and KO dams. (B) Fat composition of milk from KO dams is higher than fat composition of milk from WT dams.

## **3.6 Adipocyte *Tsc1* Knockout Alters Fatty Acid Composition in Milk**

After determining a higher milk fat percentage in milk of KO dams, we assessed the quality of the fat using lipidomics. Lipidomic analyses of the milk samples collected from PND16.5 showed a healthier milk fat composition in the KO milk compared to the WT. KO dams produced milk with lower percentage of saturated fatty acid (SFA) (Figure 6A, d=10.9%, p=0.008), higher percentage of monounsaturated fatty (MUFA) (Figure 6B, d=11.75%, p=0.009), and similar percentages of polyunsaturated fatty acids (Figure 6C). The MUFA/SFA ratio showed higher rate of C16:0 conversion from a SFA to MUFA which could explain the differential SFA and MUFA percentages (Figure 6D, d=23.67%, p=0.004). Further analysis of omega-3 and omega-6 composition showed that KO milk had higher percentage of omega-3 (Figure 6E, d=28.46%, p=0.013), higher percentage of Docosahexaenoic acid (DHA) (Figure 6F, d=42.36%, p=0.031), similar percentage of omega-6 (Figure 6G), and a lower omega-6:omega3 ratio (Figure 6H, d=30.85%, p=0.008).

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| A | B |
| C    E    G | D    F    H |

Figure 5: Milk fat lipidomic analysis. (A) Lower average %SFA in milk of KO. (B) Higher average %MUFA in milk of KO. (C)Similar average %PUFA in milk of KO and WT. (D) Higher MUFA/SFA ratio in milk of KO. (E) Higher %omega-3 fatty acids in milk of KO. (F)Higher %Docosahexaenoic acid (DHA), an omega-3 metabolite, in milk of KO. (G) Comparable omega-6 fatty acid composition in milk of KO and WT. (H) Lower omega-6:omega-3 ratio in milk of KO.

## **3.7 RNA Sequencing Reveals Suppressed Expression of Adaptive Immune Markers and Increased Expression of Muscle Biosynthesis Genes**

To understand the mechanisms by which adipocyte mTORC1 activation affects mammary gland gene expression we performed bulk RNAseq on mammary gland explants from lactating wild-type and knockout dams. We identified 139 significantly differentially expressed genes between these groups (Figure 7A-B, and Supplementary Table 1). Among the most highly expressed genes in the mammary gland are secreted milk proteins. These transcripts are not significantly altered by adipocyte *Tsc1* knockout, but trend downwards (Figure 7C). Several markers of adipogenesis and PPARg were upregulated including *Plin4, Adipoq, Cav2,* and *Fabp4*, consistent with increased adipocyte numbers (Figure 7D). Furthermore, several genes involved in eicosanoid signaling were also significantly upregulated including the enzymes *Plcb1*, *Ephx2*, and *Pla2g4a* as well as the prostaglandin receptor *Ptger3*, whereas *Ptgs1* was downregulated (Figure 7E). This is consistent with elevations in DHA in the breastmilk. Gene set enrichment analyses identified two clusters of significantly differentially expressed ontologies, related to downregulation of adaptive immune differentiation and function, and another related to upregulation of striated muscle differentiation (Figure 7F and Supplementary Table 2).

**4.0 Discussion**

Here, we show that hyperactivation of mTORC1 in adipocytes increases weight of female offspring through higher energy intake from fat. Milk composition analyses revealed higher milk fat percentage and a healthy lipid profile in our knockout model. This could be the main driver of the excess weight seen in the offspring nursing from KO dams. We demonstrate that mTORC1 hyperactivation in adipocytes causes reductions in mammary gland weight which can be caused by the increased fatty acid release into the epithelial ducts and the milk. We further find an increase in the mammary adipocytes number, size and percent area. RNA sequencing revealed potential mechanisms by which adipocytes capacity to produce and secrete fat into the milk can be promoted via reduced lipolysis and increased transport of fatty acids. Additionally, our model reveals differentially expressed pathways in the mammary glands which can influence offspring immunity.

mTORC1 is a nutrient sensor and is crucial for proliferation and growth. Our data revealed that mTORC1 hyperactivation in adipocytes caused reductions in mammary gland weight. This could be explained by the increased fat content in milk from KO dams suggesting that mammary gland weights could be reduced due to the increased emptying of their content into the milk in KO dams. Our results are consistent with the idea that mTORC1 increases lipid synthesis which is incorporated into milk composition and can be causing reduced mammary gland weights.

Based on our findings, the increased milk fat content could be driven by the increased expression of Fabp4, fatty acid binding protein 4, which allows uptake of free fatty acids into adipocytes. This could lead to increased uptake of fatty acids by the mammary adipocytes along with an increased capacity to produce and release fat into the epithelial ducts. Another mechanism that can conserve the mammary adipocytes is the increased expression of Plin4, perilipin 4, which promotes lipid coating and protection against lipolysis. This could be protective for the mammary adipocytes to conserve their size and number, as evident by higher adipocyte count and size in KO mammary glands. Additionally, the reduced expression of the lipid metabolism pathways shows lower expression of Pla2g gene family, phospholipase A2 group, which promotes hydrolysis of triglycerides at the sn-2 position to yield free fatty acids. This can also be predictive of the higher omega-3 content we see in the milk of KO dams, primarily due to the reduced lipolytic capacity to metabolize omega-3 fatty acids. The increased DHA percentage we show in the KO milk could be further due to the reduced activity of Pla2g. We expected EPA to DHA converting gene Elovl2 to be upregulated, due to the higher DHA levels. Elovl2 expression was increased in the KO showing that the increased conversion of EPA to DHA could be the primary factor in increasing DHA levels.

Additionally, and supporting our finding, transgenic pregnant mice with activated AKT in the mammary epithelial cells showed distended alveoli during lactation and a higher lipid droplet composition and size in the mammary epithelial during gestation and lactation (39). Milk composition from these transgenic mice revealed higher fat percentage (39). AKT, upstream of mTORC1, may play a significant role in regulating mammary gland differentiation and lipid and protein synthesis (39) which is concordant with our findings that milk from dams with mTORC1 hyperactivation had increased milk fat composition.

Our study is the first to examine the effects of mTORC1 hyperactivation in an adiponectin-Cre *Tsc1/2* knockout mouse model on mammary gland function and histology, and milk composition.

**5.0 Conclusions**

Our novel findings show that hyperactivation of mTORC1 activity in adipocytes of pregnant and lactating dams can impact milk composition, offspring weight, and mammary gland gene expression. These findings are crucial to better understand the effects of nutrient sensing in the mammary gland on milk production and composition and offspring health. Our data supports our hypothesis that mTORC1 hyperactivation in adipocytes increases mammary adipocyte capacity to produce fat and secrete it into the produced milk. The mechanisms by which mTORC1 could be influencing mammary gland function and milk secretion is insightful for future research addressing the effects of maternal obesity on lactation and infant health. We present data, for the first time, demonstrating the milk nutritional composition may reveal a higher energy density but a healthier overall lipid composition. This warrants further studies to unravel the mechanisms by which mammary adipocyte nutrient sensing pathways can affect offspring health through lactational programming.

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