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Hypothalamic cellular changes in neuroendocrine disorders

Human postmortem studies

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Publication date

2024

[Link to publication](#)

Citation for published version (APA):

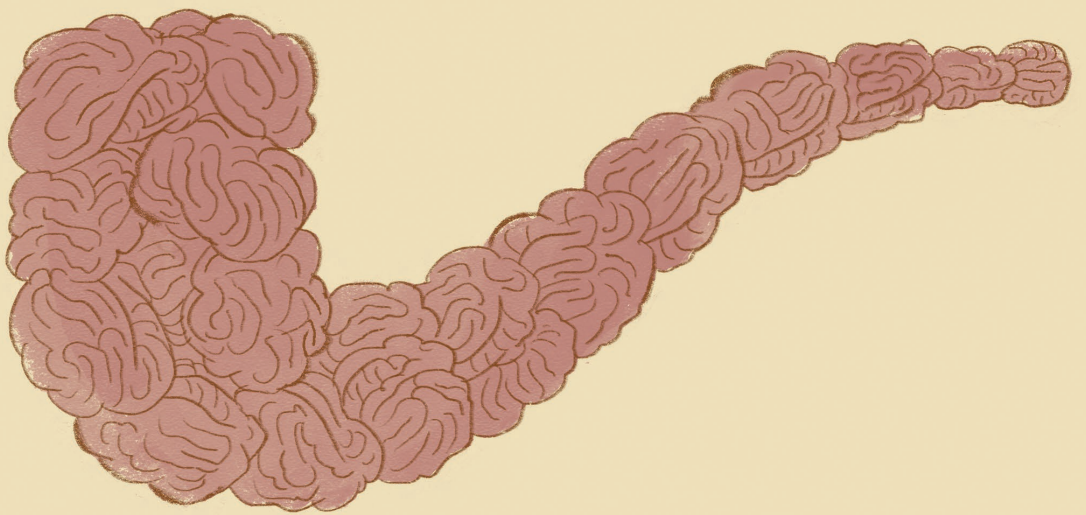
Corrêa da Silva, F. (2024). *Hypothalamic cellular changes in neuroendocrine disorders: Human postmortem studies*. [Thesis, fully internal, Universiteit van Amsterdam].

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Chapter 8

General Discussion

The hypothalamus is a small diencephalic structure that is crucial for survival of the individual and regulates a multitude of physiological processes. Diverse hypothalamic nuclei act as fundamental integrators of vegetative and peripheral cues directly coordinating reproduction, osmotic balance, stress responses, energy homeostasis, glucose homeostasis and circadian rhythms (Sternson, 2013). Specialized hypothalamic neural populations are responsible for these outputs based on internal and endocrine inputs, finely regulating homeostasis through behavioral, autonomic, or neuroendocrine modulations (van den Beld et al., 2018). Extensive research from the past decades refined our comprehension of the participation of the hypothalamus in metabolic regulation. Hypothalamic dysfunction emerged as a mechanistic link between a number of neuroendocrine disorders, including obesity, type 2 diabetes mellitus (T2DM), and Prader-Willi Syndrome (PWS) (Bochukova et al., 2018; Yeo et al., 1998; Correa-da-Silva et al., 2023).

To date, obesity is one of the most well-studied neuroendocrine diseases for which many genetic, cellular, and environmental pathogenic components have been identified (Farooqi et al., 2006; Roberto et al., 2015; Clement et al., 1998). Large population studies show that genetic variants associated with body weight regulation are predominantly associated with the central nervous system (CNS) (Locke et al., 2015). Multiple neural pathways involved in the physiological and hedonic components of eating were unveiled, and prominent attention has been given to neuronal populations located in the arcuate nucleus of the hypothalamus (Arc; infundibular nucleus – INF – in humans) (Krude et al., 1998; Horvath et al., 1992). Two functionally distinct appetite-regulating neuronal populations of the Arc coordinate energy homeostasis in response to peripheral nutrient-state signals by modulating appropriate responses, such as food seeking behavior, temperature fluctuations, and insulin secretion (Gropp et al., 2005; Balthasar et al., 2005; Campbell et al., 2017).

Resident neurons in the Arc, such as the anorexigenic pro-opiomelanocortin-expressing (POMC-expressing) neurons, undergo a drastic circuitry remodeling upon chronic exposure to obesogenic cues. These alterations include synaptic reorganization, changed electrophysiological properties, and impaired neural function; however, ultimately these changes may result in neuronal death (Horvath et al., 2010; Moraes et al., 2009; Yi et al., 2017). Initial genetic studies revealed that mutations in the melanocortin 4 receptor (MC4R), one of the receptors for POMC-derived peptides, are the most

common cause of monogenic obesity in humans, resulting in a chronic orexigenic state (Farooqi et al., 2006; Yeo et al., 1998). Likewise, mutations in leptin and its receptor leads to early-onset morbid obesity (Krude et al., 1998). Those observations stimulated research in animal models, further exploring leptin- and POMC-related neural pathways in the framework of obesity (Maffei et al., 1995; Challis et al., 2004). Moreover, technical, and methodological advances allowed the identification of other hypothalamic neural populations beyond the Arc involved in metabolic regulation, with special highlights to the paraventricular nucleus of the hypothalamus (PVN) and the lateral hypothalamic area (LHA) (Atasoy et al., 2012). Neurons in these areas are responsive to both afferent signals from the Arc, as well as peripheral cues (Ionescu et al., 1989; Qualls-Creekmore and Munzberg, 2018; Slomp et al., 2023). Our current understanding is that obesity dampens the capacity of the CNS to integrate and react appropriately to circulating nutritional and endocrine cues (Patel and Abate, 2013; Berbari et al., 2013).

Under homeostatic conditions, neurons establish a constant and dynamic interaction with glial cells resulting in optimal CNS functioning. Astrocytes constitute one of the major glial populations and provide metabolic and trophic support to neurons (Banker, 1980). Abnormal neuron-glia interaction underlies disruption of the anorexic circuitry through a multitude of mechanisms, predominantly mediated by astrocytes and microglial cells (Kalin et al., 2015). Data from neuroimaging studies also point to an altered hypothalamic microstructure in obese humans compared to lean controls, and independent findings support the idea of hypothalamic reactive gliosis in human obesity (Thaler et al., 2012). Hypothalamic astrocytes control the interstitial levels of neurotransmitters and, more recently, astrocytic gliotransmission has emerged as a modulatory node in neuroendocrine networks in control of energy homeostasis (Fuente-Martin et al., 2012; Sa et al., 2023). Astrocytic-mediated gliovascular coupling is also disrupted upon consumption of energy-dense diets and contributes to the functional impairment of hypothalamic neural populations (Garcia-Caceres et al., 2016; Gruber et al., 2021; Delle et al., 2023). Neurovascular remodeling in obesity enables the entry of neurotoxic molecules from the periphery into the CNS, affecting neural responsiveness to nutritional cues and tissue waste clearance (Benoit et al., 2009; Banks et al., 2015; Delle et al., 2023). Lastly, a subset of hypothalamic astroglia also produces inflammatory mediators during overnutrition (BahniwalLittle and Klegeris, 2017), in synergism with microglia cells.

Microglia are the CNS resident immune cell population, and they coordinate a great range of homeostatic functions in the CNS, ranging from synaptic pruning to tissue clearance (Kierdorf and Prinz, 2017). Microglia-associated changes are considered one of the major contributors and inductors of hypothalamic neuronal dysfunction (Reis et al., 2015; Gao et al., 2017a; Yi et al., 2017; Bocarsly et al., 2015). Under metabolic stress, dietary components and imbalanced endocrine signaling triggers an inflammatory response in microglia (Valdearcos et al., 2014; Gao et al., 2017a; Gao et al., 2018b). It is noteworthy that microglial inflammatory changes are persistent throughout body weight fluctuations and precede any phenotypic alterations associated with obesity (Thaler et al., 2012). Hampered microglial phagocytic capacity is also reported in murine models of obesity, together with elevated cytokine production (Gao et al., 2017b; Wang et al., 2021). This translates into accumulation of unwanted particles and cellular waste within the hypothalamic microenvironment. Moreover, recent evidence shows that obesity affects the function of other glial cell types in the hypothalamus, including tanycytes and oligodendrocytes. This may alter the secretion of neuroendocrine factors through defective tanycytic transport (Muller-Fielitz et al., 2017; Duquenne et al., 2021), and hamper the metabolic support that oligodendrocytes provide to neurons (Djogo et al., 2016; Ou et al., 2019). In summary, data from animal models show that prolonged changes in hypothalamic microstructure and cellular composition are intimately associated with obesity.

The large majority of research in the metabolism field has been conducted in murine models exposed to obesogenic diets. However, these models have intrinsic flaws and cannot fully recapitulate the human condition, especially regarding genetic heterogeneity. Pending questions such as whether the same neurobiological alterations associated with obesity can also be found in other metabolic disorders remain to be elucidated. Experimental limitations such as the influence of maternal metabolic imprinting, consistency of lifestyle choices (*i.e.*, exercises and dietary choices), the microbiome and genetic variation are usually not possible to be equated to the fullest in human studies (Lewis, 2002). In this context, studies using postmortem human material have proven to be representative for pathological stages of numerous diseases, including the ones of neuroendocrine nature. For instance, such studies have shown the association of the body mass index (BMI) with number of hypothalamic neurons in the control of energy homeostasis, and confirmed animal findings of loss of appetite-curbing

neurons in obesity (Alkemade et al., 2012). Furthermore, hypothalamic microgliosis has also been observed in humans, yet little is understood about its temporal basis and causality (Baufeld et al., 2016). Whether neuron-glia interactions are a fundamental part of pathophysiological alterations in human metabolic diseases as seen in animal studies remains to be elucidated.

The aim of this thesis was to finely dissect the molecular and cellular drivers of hypothalamic abnormalities associated with these disorders, with a main focus on the alterations that take place in glial cells. We investigated molecular and cellular changes in human postmortem material, to better understand the translational relevance of evidence derived from animal studies.

1 THE NEUROENDOCRINE BASIS OF PRADER-WILLI SYNDROME

PWS was the first human imprinted disorder to be described and it is associated with lack of expression of genes in the paternally acquired chromosome 15 q11-q13 (Cassidy et al., 2012; Holm et al., 1993). Up to date, no animal model can fully recapitulate the PWS phenotype, and some of the attempts have generated contradictory phenotypes, such as accentuated leanness (Zahova and Isles, 2021). These data indicate some degree of synergism and interaction among the PWS-causative genes. This is supported by the fact that larger deletion genetic subtypes lead to worse clinical outcomes (Butler et al., 2004). Microdeletions in the PWS genomic area affecting single or a few of the PWS loci lead to a PWS-like phenotype (Schulze et al., 1996; Cao et al., 2017; McCarthy et al., 2018). PWS clinical manifestations are extensive, and include uncontrollable hyperphagia and morbid obesity, delayed puberty, abnormal growth and body composition, and cognitive impairment (Cassidy et al., 2012). PWS symptomatology is, at least partially, of hypothalamic etiology, and numerous examples of neuroendocrine pathway disruptions underlie the clinical manifestations of the disease, such as growth hormone (GH) deficiency, central adrenal insufficiency, and hypogonadism (Muller, 1997; Grugni et al., 2013; Aycan and Bas, 2014). To our knowledge, research of hypothalamic dysfunction in PWS has not yet explored in depth the role of glial cells in its pathogenesis, leaving a gap in our understanding of the disease.

To understand the potential role of glial malfunctioning in this disorder, we analyzed hypothalamic postmortem material of PWS individuals at molecular and cellular levels. First, in **Chapter 3** we focused on hypothalamic structures involved in the control of biological rhythm generation, based on observations of deteriorated circadian rhythm outputs in PWS individuals (Vgontzas et al., 1996; Manni et al., 2001; Butler et al., 2002). The aim of this study was to determine whether PWS pathophysiology affects the numbers and functionality of the hypothalamic pacemaker cells. Next, we aimed to understand the cellular basis that underlies the phenotypic severity differences described in PWS sub-genotypes. We evaluated numeric and functional changes in distinct hypothalamic cell types, including neurons, astrocytes, microglia, and oligodendrocytes.

Circadian rhythmicity comprises the cyclic behavioral and physiological variations that are needed to accommodate changes in the environmental states to which organisms are submitted to (Hurd and Ralph, 1998; Ouyang et al., 1998). It affects virtually all physiological systems, translating into oscillations in endocrine, metabolic, immune and neurological mediators (Logan and McClung, 2019). Temporal physiological and behavioral organization is conferred through synchronization of rhythms dictated by a central pacemaker, the suprachiasmatic nucleus (SCN), and its cellular molecular clocks (Reppert and Weaver, 2002). Circadian disturbances are observed in a plethora of neurological and psychiatric disorders and are often associated with abnormal SCN cytoarchitecture (Zhou et al., 2001; Liu et al., 2000; Aziz et al., 2010; De Pablo-Fernandez et al., 2018). Sleep disturbances are the most evident clinical outcome of circadian misalignment in PWS (Vgontzas et al., 1996; Manni et al., 2001; Butler et al., 2002; Lassi et al., 2016). Whether those misalignments result from disruption of the intrinsic clock machinery or emerged as a consequence of PWS symptomatology remains unknown.

To understand whether circadian desynchronization in PWS is driven by intrinsic SCN mechanisms, we evaluated the expression of PWS causative genes at single cell resolution in the murine SCN. Our results showed a strong neural signature for three PWS-related protein coding genes: *Magel2*, *Necdin* and *Snrpn*. Of those, *Magel2* and *Necdin* were previously shown to be involved to some extent in circadian rhythmicity (Kozlov et al., 2007; Lu Dong and Li, 2020). To our knowledge, we are the first to report a potential role for *Snrpn* in biological rhythms. Overall, glial cells showed a more discreet expression level of genes in the PWS genomic region. Because PWS has distinct genetic subtypes, we included in our analysis genes related to PWS Type 1 (PWS T1) deletion, which compromises four extra genes in relation to the typical PWS Type 2 (PWS T2)

(Butler et al., 2004). We found no empirical suggestion for worsened circadian outcomes in PWS T1 subjects, which was consistent with low expression levels of PWS T1 exclusive genes in the SCN. These data are the first line of evidence indicating that PWS circadian abnormalities might be driven by intrinsic SCN factors.

Circadian adaptations are mediated by the SCN, which integrates environmental cues, such as the solar day, and transmits temporal representations to other physiological systems. It has been shown that the SCN timekeeping robustness is sustained even in *ex vivo* conditions, as demonstrated by organotropic SCN slices (Lehman et al., 1995; Jansen Van der Zee and Gerkema, 1999). Extensive research has examined the role of SCN neural machinery in adaptive and homeostatic circadian programming, especially through studies in animals where the SCN was ablated (Lehman et al., 1995; Marchant and Mistlberger, 1997). Recent state-of-the-art technology expanded the initial observations that AVP-containing neurons in the SCN are pivotal pacemaker cells (Mieda et al., 2015; Tsuno et al., 2023). Neurological conditions which include circadian disruption are often associated with reduced numbers of SCN AVP-containing cells (Liu et al., 2000; van Wamelen et al., 2013; Hogenboom et al., 2019). Interestingly, our data point to increased numbers of AVP-containing neurons in the SCN of PWS subjects, like what is observed in depression patients (Zhou et al., 2001). We found that vasoactive intestinal polypeptide-containing (VIP-containing) neurons were unaltered, suggesting a selective effect of PWS pathology on AVP-expressing cells. It is worth noting that both neuronal subtypes express similar levels of PWS causative genes in mice, as seen by our single cell RNA-sequencing analysis. As PWS neurons have defective production and secretion of neuropeptides (Chen et al., 2020), increased AVP-ir parameters may reflect impaired neuropeptidergic release. Our data also suggest at least a partial AVP neuronal dysfunction, as we observed increased AGEs content within the AVP domain in the SCN of PWS patients. Nevertheless, altered AVP content in the SCN implies an impaired capacity of the CNS to convey temporal programs to downstream tissues.

Glial cells have been shown to play a role in the maintenance of effective central clock machinery, especially astrocytes (Tso et al., 2017; Brancaccio et al., 2019; Brancaccio et al., 2017). These studies elegantly demonstrated that astroglia actively shape and participate in the generation of biological rhythms in mice. Reduced SCN astrocytic counts concomitant with circadian imbalance have been previously reported in a variety of human conditions (Hogenboom et al., 2019; Stopa et al., 1999). PWS is associated with a generalized hypothalamic astrocytic loss (Bochukova et al., 2018), and therefore this is

not limited to the SCN. Moreover, similar to our findings in the PVN of T2DM individuals, we found overrepresentation of components of the glymphatic system (GS). Taken together, these findings point to a greater AGEs SCN content in PWS, and we speculate that GS activity emerges as an adaptive response to metabolic waste. SCN microglia were unaltered in PWS, like previous reported data in T2DM (Hogenboom et al., 2019). This suggests that the human hypothalamus partitions waste clearance differently than shown in murine models, which are heavily microglia-centered (Podlesny-Drabiniok, Marcora and Goate, 2020). Thus, our results indicate an abnormal cytoarchitecture of the SCN of PWS subjects, affecting primarily AVP-containing neurons and astroglia.

Circadian timing is essential for neuroendocrine function, as widely demonstrated by diurnal periodicity of numerous hormones (Everett and Sawyer, 1950; Boyar et al., 1976; Plant, 1981). In fact, SCN neurons establish contact with neuroendocrine cells (van der Beek et al., 1993; Kalsbeek et al., 1996; Palm et al., 1999; Miller et al., 2006), evidencing the importance of circadian variation to endocrine function. Many of those reports focus on reproduction-controlling neurons, which are impaired in PWS (Hirsch et al., 2015). Moreover, rhythmicity is also sustained at the cellular level by a network of transcriptional factors, the clock genes, which creates cyclic waves of transcription in virtually every cell (Konopka and Benzer, 1971). Previously published data suggested increased levels of expression of the period circadian regulator 1, *Per1*, in the hypothalamus of PWS subjects (Bochukova et al., 2018). To our knowledge, our study is the first to demonstrate the neuroanatomical basis for circadian disruptions in PWS. Our results suggest that disruption in the SCN functionality might contribute to other phenotypic traits of PWS, beyond sleep abnormalities. In theory, these results open the door for novel therapeutic avenues in PWS, namely circadian-based therapies, such as timed exposure to light, time-restricted eating, and melatonin administration. Evidence from the clinical setting points to symptom attenuation in patients with Alzheimer's Disease (AD) patients upon some of those therapies (Figueiro et al., 2014; Riemersma-van der Lek et al., 2008).

Following our findings in **Chapter 3**, we concentrated our efforts on understanding the hypothalamic molecular and cellular basis of PWS phenotypic traits. In **Chapter 4**, we focused on the potential effect of PWS pathophysiology in hypothalamic perineuronal nets (PNNs), which are specialized structures of extracellular matrix in the CNS (Celio et al., 1998; Viggiano Ibrahim and Celio, 2000). Those structures are largely explored in the context of cortical and subcortical areas (Xu et al., 2003; Carulli et al., 2010; Vo et al., 2013; Gao et al., 2018a; Fawcett Oohashi and Pizzorusso, 2019), but emerging evidence

demonstrates their participation in hypothalamic energy homeostasis control (Alonge et al., 2020; Mirzadeh et al., 2019). PNNs are pivotal modulators of a multitude of neuronal functions, with special attention to synaptic organization and plasticity (Srinivasan Schachner and Catterall, 1998; Kochlamazashvili et al., 2010; Lensjo et al., 2017). Loss of PNNs is observed in several neuropathologies, such as Alzheimer's disease and epilepsy, and their diminished abundance is often connected to abnormal synaptogenesis and plasticity in circuitry specific to those disorders (Rogers et al., 2018; Alcaide et al., 2019; BaigWilcock and Love, 2005).

Transcriptional analysis of PWS hypothalami revealed downregulation of neuron-enriched genes compared to controls, with emphasis to transcripts involved in neurogenesis, neurotransmitter release and synaptic plasticity regulation (Bochukova et al., 2018). The presence and abundance of PNNs in the human hypothalamus is virtually unexplored, with exception of a few reports (Alonge et al., 2020; Mirzadeh et al., 2019; Zhang et al., 2021). Mirzadeh and colleagues demonstrate the presence of a subpopulation of orexigenic neurons that are enmeshed by the PNN component *Wisteria floribunda* (WFA). Namely, Neuropeptide Y-/Agouti Related Protein-containing neurons (NPY-/AgRP-) were described (Mirzadeh et al., 2019). Whether other neuronal populations are also surrounded by PNNs or if PNNs are affected in human pathological states remains undetermined. To understand if PNNs are affected by PWS pathophysiology and, potentially, can affect synaptic plasticity of neurons in control of energy homeostasis, we profiled WFA-positive structures in the INF of PWS and controls.

PNNs assembly occurs in postnatal development and is essential for restraining the maximal neural plasticity associated with embryonic and early stages of development of the CNS. Curiously, our data indicates that hypothalamic PNNs abundance is not age-dependent in controls in opposition to what has previously been described for other brain regions (Pizzorusso et al., 2002; Lensjo et al., 2017). This supports the notion that PNNs are highly heterogeneous structures, with distinct molecular composition and spatiotemporal patterns (Lupori et al., 2023). We observed a drastic reduction of PNNs in the INF of PWS subjects in comparison to controls, supporting previous findings of defective synaptic homeostasis in PWS (Bochukova et al., 2018; Soeda et al., 2023). Conjectural analysis of our data points out that PWS INF neurons are structurally immature, with potential repercussions to their functionality. The precise contribution of hypothalamic PNNs to energy homeostasis is still poorly explored, but initial results suggest an active role in coordination of glucose homeostasis and feeding behavior

(Alonge et al., 2020; Mirzadeh et al., 2019). One of the limitations of our study is the undefined neuropeptidergic signature of INF WFA-positive neurons, hampering our ability to propose mechanisms by which loss of WFA-associated structures contribute to PWS symptomatology. Previous findings show that NPY/AgRP neurons are enmeshed by the cardinal PNN marker, WFA, in humans (Mirzadeh et al., 2019). Those neurons antagonize the anorexigenic neuronal population characterized by POMC expression and activation of NPY/AgRP neurons leads to promotion of feeding behavior and dampens energy expenditure (Baskin Breininger and Schwartz, 1999; Larsen et al., 1999). Thus, it is reasonable to speculate that reduction in hypothalamic PNNs might be linked to the severe hyperphagia that PWS individuals experience.

Next, we dwelled into the investigation of alterations that might underlie distinct phenotypic severity in PWS deletions subtypes. Notably, individuals with PWS T1 deletions as compared with PWS T2 deletions exhibit more pronounced physiological and cognitive abnormalities such as compulsive behaviors, obsessive thoughts, self-injury, cognitive impairment, and disruptions in visual processing (Butler et al., 2004; Milner et al., 2005; Hartley et al., 2005). In **Chapter 5**, we systematically analyzed the transcriptional profile and cellular composition of hypothalamic nuclei that compose the mediobasal hypothalamus (MBH). As the MBH harbors neurons in control of metabolism, various behaviors, and social cognition, we hypothesized that worsened phenotypic severity of PWS T1 compared with T2 is linked to more drastic cellular disruptions. Through comprehensive transcriptomic analyses and cell-specific protein expression profiling in neurons, glial cells, and white matter, we uncovered significant disparities in gene expression and cellular functional outcomes in PWS genetic subtypes. Notably, our findings highlight a dysfunctional microglial phagolysosome and altered neural communication as pivotal contributors to the heightened phenotypic severity observed in patients carrying PWS T1 deletion.

Neurodegenerative diseases are often associated with accumulation of neurotoxic proteins, which may lead to neural dysfunction and death (Menzies et al., 2017). Robust evidence from PWS animal models and postmortem human material show that neural populations in the MBH are heavily affected by PWS pathophysiology (Swaab Purba and Hofman, 1995; Goldstone et al., 2002; Mercer et al., 2013; Poley-Wolf et al., 2018; Bochukova et al., 2018). Despite the well-established role of glial cells in neurodegeneration, little is known about their role in the context of PWS. A recent report demonstrated increased microglia-related mediators in the hypothalamus of

PWS compared to controls consistent with non-genetic obesity (Bochukova et al., 2018). However, whether microglial activation differs between different PWS subgenotypes or it is associated with specific hypothalamic domains remains elusive. Our work demonstrates that PWS T2 individuals have classical features of microglial activation, such as microgliosis, similar to non-genetic obesity (Baufeld et al., 2016). Microglial activation seems to be restricted to the MBH, given our SCN findings in Chapter 3. Microglia of PWS T1 subjects show a generalized severe morphological disruption, characterized fragmentation of processes' and discontinuation of soma-ramifications, contrary to our observations in PWS T2 microglia. Those changes were not exclusive to the hypothalamus, they were also observed in the hippocampus of the same subjects. This morphological disruption is termed cytorrhesis and has been previously described in the context of AD and aging (Streit et al., 2004; Streit et al., 2009). Although it is not possible to establish whether microglial activation emerges as a consequence of the obese phenotype in PWS T2 individuals. Dysmorphic microglia are already present as early as 6 months of age in PWS T1, which precedes hyperphagia and obesity (Miller et al., 2011). Furthermore, comparisons of the transcriptional signature of PWS T1 and T2 hypothalami demonstrated a downregulation of cytoskeleton-related transcripts and process in PWS T1. Finally, our results in experimental animals demonstrate that microglial dimorphism can be rooted to the lack of the gene *Cyfp1*, one of the PWS T1 exclusive genes. *Cyfp1*-haploinsufficient rats and microglia-specific *Cyfp1* knockout mice also present with microglial morphological disruptions.

Microglial morphological disruption translates into lesser immunosurveillance, as indicated by impaired autophagic flux in PWS T1. Once again, our molecular analyses were aligned with the morphometric characterization. Moreover, microglia cells are not only disease-associated. Beyond removal of threatening agents, they actively release trophic factors, shape circuits, and provide protection against oxidative stress and excitotoxicity (Kierdorf and Prinz, 2017). Cytorrhesis is the ultimate state of cellular senescence (Neumann et al., 2023), indicating that the PWS T1 hypothalami are deprived of microglial trophic support. Diverse endogenous mechanisms promote CNS tissue clearance, both in microglia-dependent ways, such as phagocytosis, or extrusion of unwanted extracellular particles by the GS (Iliff et al., 2012; Podlesny-DrabiniokMarcora and Goate, 2020). Our examination of the GS in PWS T1 and T2 hypothalami showed enhanced GS activity in the MBH of PWS T1 subjects, which could be due to a compensatory mechanism for microglial malfunctioning. As mentioned earlier, increased GS activity as an adaptive

response to tissue injury seems to be region specific, since in the SCN (**Chapter 3**) we detected it irrespective of subgenotypes. Taken together, these findings suggest that the combination of dystrophic microglial profiles and accumulation of interstitial waste might amplify phenotypic severity in PWS T1.

Optimal CNS function relies on the ability of neurons to communicate with each other. Therefore, we assessed neuronal communication through evaluation of a synaptic marker, synaptophysin, evaluation of neuropeptidergic profiles and integrity of the fornix. Our observations point out that PWS T2 hypothalami have diminished content of energy homeostasis-controlling neuropeptides, but unchanged levels of expression of synaptophysin and unaltered fornical microstructure compared to controls. In contrast, PWS T1 has a marked reduction in synaptophysin expression and abnormal microstructure of the fornix compared to controls. These data provide additional insights to the worsened PWS T1 phenotype, as synaptophysin knockout animals have behavioral inflexibility and cognitive defects (Schmitt et al., 2009; Tarpey et al., 2009). Moreover, the fornix is the major output tract from the hippocampus linking the limbic system to the hypothalamus (Ou et al., 2023). Abnormalities in the fornical structure have been shown to be linked to memory defects and cognitive deviances (Cummings, 1994; Zhuang et al., 2013), which are exacerbated in PWS T1 in comparison to PWS T2 subjects (Butler et al., 2004). *Cyfp1* has been previously implicated in myelination capacity and neuron-neuron communication (De Rubeis et al., 2013; Dominguez-Iturza et al., 2019; Silva et al., 2019), reinforcing the causative role of this gene in PWS T1 phenotypic determination.

Our findings carry potential implications for PWS therapeutic avenues. The distinct molecular and cellular signature in the hypothalami of PWS T1 and T2 advocate for the use of personalized medicine strategies targeting each subgenotype. Of note, fornical deep brain stimulation has been extensively debated in other neurological disorders, such as AD (Leoutsakos et al., 2018). Outcomes from clinical trials have shown successful alleviation of AD symptomatology, such as cognitive decline (Laxton et al., 2010). However, competing reports suggest that this therapeutic route needs optimization, possibly explained by non-consistent electrode placement, and consequent targeted networks, in different studies (Li et al., 2020). Speculative interpretation of our results indicates that fornical deep brain stimulation might ameliorate PWS T2 symptomatology, but not PWS T1, given the fornix structural deterioration observed in this group. T1-deletion personalized strategies might require restoring microglial homeostatic function. A

recent report suggested systemic hematopoietic cell transplantation as a possibility for microglial replacement in the context of AD (Yoo et al., 2023). The implementation of personalized interventions for distinct subgenotypes in PWS could lead to a more assertive targeting of the disease-modifying aspects of each subgenotype.

2 DISRUPTED NEUROENDOCRINE SYSTEMS IN T2DM

Obesity is a significant risk factor for development of T2DM (Khaodhiar McCowen and Blackburn, 1999). Thus, reasonable speculation points to at least a partial overlap of cellular and molecular mechanisms for both diseases. To this date, there is no animal model that can fully represent the human T2DM pathophysiology. Impaired glucose regulation in murine models is often achieved by introduction of obesogenic diets that mimic a human western-style hypercaloric diet (Speakman, 2019). Moreover, genetic rodent diabetic models are derived from mutations in the leptin signaling pathway (Lee et al., 1996; Takaya et al., 1996), that are shown not to be a primary cause in humans (Taylor, 2012). T2DM is characterized by disruptions in glucose homeostasis due to defective insulin signaling in metabolic-relevant organs, including the hypothalamus. (Taylor, 2012). Likewise, to what is observed in obese individuals, evidence from neuroimaging studies demonstrate brain structural and metabolic alterations in T2DM subjects (Rosenbaum et al., 2022). However, those studies fail to provide spatial resolution to these alterations, and whether these metabolic disruptions are rooted in selective neuronal populations or in a generalized hypothalamic malfunction is undetermined. To better understand the hypothalamic alterations that underlie T2DM pathogenesis, our group has resorted to the use of postmortem tissue (Alkemade et al., 2012; Yi et al., 2012; Hogenboom et al., 2019; Kalsbeek et al., 2020), allowing for spatial resolution, (*i.e.*, where potential alterations take place), and a retrograde analysis of medical records. Previous findings have pointed to a neuropeptidergic imbalance in the hypothalamus of T2DM subjects in a similar fashion to what is observed in obesity (Alkemade et al., 2012; Kalsbeek et al., 2020).

In this thesis we proposed to investigate the impact of T2DM pathophysiology on key glucoregulatory neural populations and homeostatic features of glia cells. In **Chapter 6**, we profiled hypothalamic lipid droplets (LD), inspired by previous reports demonstrating a strong connection between lipid metabolism, inflammation, and

insulin resistance in peripheral tissues (Sanjabi et al., 2015; van Dierendonck et al., 2022). We compared the distribution of the LD organelle in both mice and humans and found that LDs are preferentially present in the hypothalamic third ventricle tanycytic layer in homeostatic conditions. Previous studies point to a dysfunction in the lipid metabolism taking place in the CNS of metabolically diseased mice (Timper et al., 2018; Varela et al., 2021). Furthermore, a robust amount of evidence demonstrates that sutured lipid species trigger, at least partially, the hypothalamic remodeling observed in obesity (Benoit et al., 2009; Valdearcos et al., 2014; Melo et al., 2020).

We hypothesized that an obesogenic diet would prompt dynamic changes in the ventricular LD content, and impact regional lipid metabolism in the hypothalamus. Indeed, our results revealed that high fat fed mice showed increased hypothalamic content of LD, especially in cells that line the third ventricle. This tanycytic response to metabolic perturbations might indicate an adaptive mechanism buffering lipotoxicity, similar to what is observed in the periphery (Khatua et al., 2021). Our observations also suggest that the changes in the third ventricle wall might contribute to the cellular metabolic stress that appetite-curbing neurons suffer upon exposure to obesogenic cues (Timper et al., 2018). A study by Shen et al. showed that astrocytic lipid metabolism governs body weight gain and glucose homeostasis, and can impact POMC neurons function (Shen et al., 2008), supporting our findings. Interestingly we showed no correlation between BMI and hypothalamic ventricular LD content in humans. Of importance, our analysis was restricted to a limited number of individuals and increased sample size might refine our understanding on human hypothalamic lipid biology. In T2DM, LD content was reduced in comparison to controls, suggesting an opposite metabolic remodeling than the one observed in animal models of obesity (Sanjabi et al., 2015). Studies that focused on cortical areas demonstrate a role for LD accumulation in microglial cells, and a direct relationship with pathogenic outcomes, such as cognitive decline (Lee et al., 2023). In the hypothalamus, LD presence in the parenchyma was extremely low, and our analyses did not show LD presence in the human microglia. It is worth mentioning that the cells in the ventricular wall and in the brain parenchyma are interconnected through a vascular network, which allows cerebral blood and cerebrospinal fluid (CSF) flow (Eide et al., 2021; Göbel et al., 2020). The reduction in LD we observed in T2DM individuals might be indicative of a disruption in these gliovascular units since cellular metabolism heavily supports those functions. In fact, previous findings of our group reported hypothalamic hypervascularization in the INF of T2DM patients (Yi et al., 2012),

reinforcing this hypothesis. Independent observations demonstrated that T2DM is associated with increased protein levels in the CSF (Kobessho et al., 2008), suggesting that gliovascular remodeling also extends to the dynamics of CSF flow in this disease. The exact mechanism and physiological consequences behind those changes remain to be elucidated.

The PVN harbors key glucoregulatory and neuroendocrine neural populations and functions as an integrator of hypothalamic and extra-hypothalamic inputs (Ionescu et al., 1989; Biag et al., 2012). To better understand the impact of T2DM pathogenesis in the hypothalamus, we profiled the neuro-glio-vascular composition of the PVN of T2DM subjects. In Chapter 7, we report a drastic reduction of oxytocin-containing (Oxt-) neurons in the PVN of T2DM subjects. Oxt is a well-recognized neuroendocrine mediator, and it is released from neurohypophyseal terminals in response to a variety of stimuli. Central Oxt signaling regulates a multitude of physiological processes, and undoubtedly impacts feeding behavior and glycemic control (Atasoy et al., 2012). Evidence from murine models, non-human primates and humans consistently show that Oxt administration leads to reduction in glycaemia (Altszuler and Hampshire, 1981; Bjorkstrand Eriksson and Uvnas-Moberg, 1996; Lawson et al., 2015; Blevins et al., 2015). Oxt knockout mice are obese and glucose intolerant, even in standard chow-fed conditions (Camerino, 2009). Therefore, reduced numbers of Oxt neurons in T2DM individuals are coherent with the clinical outcomes of this disorder and support previous observations of lesser serum levels of Oxt in T2DM subjects (Qian et al., 2014; Al-Rawashdeh et al., 2017).

Our analysis also revealed that T2DM does not affect the numbers of AVP- and corticotrophin releasing hormone-containing (CRH-containing) neurons, suggesting a selective effect on the Oxt-expressing neuronal population. Dysregulations of the hypothalamic-pituitary axis (HPA) are extensively reported in animal models of T2DM, and a direct link with glucose intolerance and insulin resistance has been established (Andrews et al., 2002; Lucassen and Cizza, 2012; Di Dalmazi et al., 2012). Therefore, it is not unreasonable to conjecture that CRH neurons, which are central mediators of the HPA axis (Vale et al., 1981), may be affected by T2DM pathophysiology. Evidence from animal models show that the oxytocinergic secretory activity can diminish the response of the HPA axis to a given stressor (Lang et al., 1983; Legros, 1992). Thus, even though we found no numeric changes of CRH-containing neurons, reduced Oxt levels might indirectly contribute to persistent activation of the HPA in T2DM.

Imbalanced autonomic hypothalamic output is observed in T2DM subjects, partially attributed to hyperinsulinemia and/or insulin resistance (Rowe et al., 1981; Lembo et al., 1992; Vollenweider et al., 1993; Freeman, 2014; Gudbjornsdottir et al., 1994). These disruptions can lead to adverse clinical outcomes, for instance, in the gastrointestinal, cardiovascular, and endocrine systems (Ryder et al., 1990; Huggett et al., 2003). Since the pre-autonomic PVN neuronal populations modulate parasympathetic and sympathetic outflow (Busnardo et al., 2010; Buijs et al., 2003), our results also contribute to the understanding of autonomic-related endocrine abnormalities in T2DM. Despite immense efforts, the neuropeptidergic identity of autonomic neurons is still not known. Recently, a transneural network connecting PVN Oxt neurons to the endocrine pancreas was described and functionally characterized (Papazoglou et al., 2022). Moreover, previous studies have demonstrated that a subpopulation of PVN Oxt neurons contributes to the sympathetic innervation of the liver and adipose tissue (Stanley et al., 2010; Buijs et al., 2003). These results indicate that PVN Oxt cells may be involved in glucoregulation through autonomic innervations. Thus, reduced numbers of PVN Oxt neurons might underlie the increased sympathetic outflow observed in T2DM individuals.

Because of the neural changes observed, we also profiled the PVN glial and vascular composition. Insulin astrocytic signaling can dictate body weight gain and glucose homeostasis (Garcia-Caceres et al., 2016; Herrera Moro Chao et al., 2022). Therefore, it was expected that T2DM-related alterations are associated with alterations in astroglia. Interestingly, we observed reduced numbers of astrocytes and augmented vasculature in the PVN. Evidence from chronically diabetic rats shows a similar astroglial reduction (Lechuga-Sancho et al., 2006), suggesting lack of astrocytic trophic support to oxytocinergic cells, associated with disrupted glucose homeostasis. It is important to highlight that those findings are based on immunoreactivity of the cardinal astrocyte marker glial fibrillary acid protein (GFAP). Recent methodological advances in state-of-art technologies allowed the visualization of astrocytic transcriptional and molecular diversity at single cell resolution beyond GFAP (Khakh and Sofroniew, 2015; Endo et al., 2022). The comprehension of astrocytic subpopulations affected by T2DM pathophysiology might provide insightful information on T2DM-associated neurodegeneration, similar to recent discoveries in murine models of obesity (Lutomska et al., 2022). Lastly, augmented vascularization in the PVN suggests a generalized hypothalamic angiopathy in T2DM, potentially mediated by glial cells.

To understand hypothalamic astrocytic reactivity in diabetic subjects, we profiled aquaporin 4-positive (AQP4-positive) astroglia. These cells constitute the GS, and therefore form a network of cells that coordinate interstitial clearance through fluid interchange in perivascular spaces (Iliff et al., 2012; Mestre et al., 2018). The hypothalamic GS is virtually unexplored in metabolic disorders (Delle et al., 2023), and, to our knowledge, our work is the first to explore it in the human condition. Different neuropathologies have been associated with dysfunctions in the GS, especially in cortical areas (Aoki-Yoshino et al., 2005; Yang et al., 2011; Peng et al., 2023; SmithDuan and Verkman, 2019). In contrast to our results on GFAP-positive astrocytes, we found an increased representation of AQP4 astroglia. Speculative interpretation of those results indicates that in the T2DM condition there is accumulation of metabolic and interstitial waste in the hypothalamus. This is supported by previous reports demonstrating hypothalamic accumulation of advanced glycation end products (AGEs) in high fat diet-fed (HFD-fed) mice (Gao et al., 2017a). AGEs are macromolecules with pathogenic significance in T2DM and are used as a proxy for cellular dysfunction in diverse tissues (Reddy et al., 1995). Increased GS activity might emerge as a response to formation and accumulation of different AGEs. In fact, AGEs formation occurs through a non-enzymatic modification of macromolecules. As lipid species might participate of AGEs formation (Fu et al., 1996), it is possible that the dynamic changes we previously observed in LD content are also implicated in fueling the AGE pathways.

Extensive research has demonstrated the role of microglia-derived inflammatory mediators in hypothalamic dysfunction in obesity, both in animal models (De Souza et al., 2005; Thaler et al., 2012; Gao et al., 2014) and humans (Baufeld et al., 2016; Melo et al., 2020). It is important to stress that increased microglial activity in human obesity is not fully understood and is predominantly observed in the chronic stages of the disease. Therefore, there is a lack in temporal and causal basis, and speculative interpretation points to a mechanism similar to what is described in animal models, centered in the chronic production of neurotoxic mediators. Hypothalamic microgliosis is commonly used as a proxy for increased local proinflammatory tonus (Thaler et al., 2012; Berkseth et al., 2014; Gao et al., 2018b). Previous observations from our lab show that T2DM does not elicit microgliosis in the human hypothalamus (Hogenboom et al., 2019; Kalsbeek et al., 2020), despite comparable loss of key metabolism-controlling neurons in obesity (Kalsbeek et al., 2020; Lechner et al., 2023). This difference might be rooted in distinct immune phenotypes between rodents and humans (Vijayan et al., 2019; Medetgul-

Ernar and Davis, 2022), and divergence of neural pathophysiological mechanisms behind neurodegeneration in each condition. Strikingly, recent data from mice elegantly show that hypothalamic microglia participate in glucose metabolism in a body weight-independent manner (Douglass et al., 2023). In this study, the authors report that microglial inflammatory mediators act on glucose-sensing neurons, amplifying insulin secretion via parasympathetic circuitry, irrespective of HFD-feeding. Their results indicate that microglial reactivity is necessary for euglycemia, compatible with previous observations (Winkler et al., 2019). However, which factors orchestrate microglial activation to coordinate glycaemia are not yet fully understood. As microglial immunosurveillance and phagocytic capacity are unaltered in aglycemic conditions (Bernier et al., 2020), glucose itself might not be the primordial driver here. These findings seem to be consistent with our observations, where neither numeric nor functional changes in microglia were detected in the suprachiasmatic nucleus (SCN), INF and PVN of T2DM individuals (Kalsbeek et al., 2020; Hogenboom et al., 2019). Cautious interpretation of these data is necessary, as our analysis does not fully partition the impact of body weight in T2DM or control subjects, and it is impossible to determine whether microgliosis took place at earlier points of the disease. Our data on the hypothalamic GS suggest that the human brain might have a different functional organization of waste clearance than rodents. Associated with increased production of cytokines, murine microglia dampen their phagocytic capacity upon exposure to obesogenic cues (Gao et al., 2017b; Gao et al., 2018b; Wang et al., 2021; Milanova et al., 2022). This results in reduced ability for waste removal, which contributes to neuronal dysfunction (FrickerOliva-Martin and Brown, 2012). Our data show that microglial phagocytic function in the PVN is unaffected by T2DM pathology. However, enhancement of GS activity can be the primary mechanism for waste clearance in this pathogenic state or it can emerge in response to microglial hypoactivity. Further research is necessary for a full understanding of the cellular basis of hypothalamic dysfunction and its phenotypic consequences in T2DM.

Our results show that T2DM leads to defective neuroendocrine systems in T2DM, which are fundamental for insulin sensitivity and body weight maintenance. Our investigations revealed oxytocinergic alterations, and this thesis provides insights into the cellular alterations that might underlie neuroendocrine abnormalities in T2DM. Our data provides ample results in support of the hypothesis that disruption of the neuroglia-vascular unit culminates in the pathophysiological alterations related to T2DM.

3 OXYTOCIN AS A THERAPEUTIC NODE IN T2DM AND PWS

Metabolic disorders have reached epidemic levels and have become a major cause of morbidity and mortality worldwide (Chew et al., 2023). Substantial efforts have been made in the past decades to combat obesity and, by consequence, its comorbidities like T2DM, beyond lifestyle and behavioral interventions. Until recent years, the development of pharmacotherapeutic agents for the treatment of obesity were modest and underperformed surgical interventions, such as gastric bypass (Boyers et al., 2021). Numerous efforts focused on endocrine pathways associated with the central control of metabolism, with special attention to leptin-, ghrelin- and melanocortin-related pathways (Barnett et al., 2010; Lee et al., 2016; Collet et al., 2017). Currently, therapies which target endogenous mechanisms of nutrient-stimulating hormones in control of energy homeostasis emerged as promising agents in suppressing hyperphagia and increase energy expenditure (Coskun et al., 2022; Jastreboff et al., 2023). One of the most promising medication classes now are the glucagon like peptide 1 receptor (GLP-1R) agonists, with several agents commercially available (Muller et al., 2019). Interestingly, some initial data indicate that those pharmacological agents also hold therapeutic value for monogenetic forms of obesity (Iepsen et al., 2018). Whether this is true for polygenic cases, such as PWS, is still poorly understood. It is noteworthy that those endocrine agonists are expected to compose a life-long treatment plan, potentially due to irreversibility of hypothalamic damage elicited by metabolic disorders (Wilding et al., 2021). However, it is possible to speculate that upon achievement of body weight stability and normoglycemic state, a comprehensive plan that includes behavioral and less potent pharmacological interventions should be considered.

Animal models have yielded robust evidence into the translational potential of Oxt in the treatment of a variety of pathologies. Diverse patient populations which have abnormal or reduced oxytocinergic signaling might benefit from exogenous Oxt administration. Given the magnitude of effects observed in mice, numerous interventions were posed to non-human primates and humans, targeting a broad range of pathologies such as autism spectrum disorder and metabolic diseases (Blevins et al., 2015; Thienel et al., 2016; Sikich et al., 2021). Our data demonstrated a clear deficiency of Oxt in two neuroendocrine disorders, T2DM and PWS, indicating a potential therapeutic avenue. In fact, Oxt therapy has been considered in both contexts previously (Zhang et al., 2013;

Correa-da-Silva et al., 2021), but great variability on administration route, number of doses and administration dosage hampered the significance and reproducibility of the findings (McCormackBlevins and Lawson, 2020). Moreover, the vast majority of studies do not equate the effect of circadian and/or ultradian rhythms in exogenous Oxt administration, despite increasing evidence of a marked circadian pattern for homeostatic Oxt secretion and signaling (AmicoSeif and Robinson, 1981; Zhang and Cai, 2011). Lastly, a number of trials with Oxt intervention for non-genetic metabolic disorders were performed exclusively in males (McCormackBlevins and Lawson, 2020), limiting the clinical significance of those findings.

Interventional studies of Oxt administration in humans demonstrate a clear anorectic and weight loss induction effect, in both control and obese subjects (Ott et al., 2013; Hsu et al., 2018; BurmesterHiggs and Terry, 2018; Plessow et al., 2018). These data confirm the large body of evidence from animal studies that showed the importance of oxytocinergic signaling in the physiological and hedonic control of feeding behavior (Blevins Schwartz and Baskin, 2004; Atasoy et al., 2012). Furthermore, a potent beneficial effect on glucose homeostasis was described, especially in young healthy men (Chiodera et al., 1984; Paolisso et al., 1988; Klement et al., 2017). Curiously, the effects of exogenous Oxt administration in glucoregulation seem to be restricted to normal weighted subjects (Zhang et al., 2013; Brede et al., 2019). Those results indicate that pronounced obesity might be associated with molecular resistance to the Oxt signal, similar to what has been observed for other energy-controlling hormones such as insulin, leptin and ghrelin (El-Haschimi et al., 2000; Saltiel and Kahn, 2001; CuiLopez and Rahmouni, 2017). Therefore, Oxt,-based therapies for T2DM might be a more suitable approach in the context of body weight and glucose levels maintenance.

Oxt has multiple physiological functions, ranging from lactation, parturition, social cognition to global metabolism control (Baskaran et al., 2017). Oxt deficiency appeared as one of the first targets for therapeutic interventions in PWS, following early reports of reduced numbers of Oxt-containing neurons in the PVN of PWS individuals (Swaab Purba and Hofman, 1995). Detailed work in PWS animal models and human postmortem hypothalamic material have confirmed those observations (Bochukova et al., 2018; Schaller et al., 2010; Meziane et al., 2015). Oxt-based interventions emerged as a promising therapeutic node in PWS, with potential beneficial effects on metabolism and behavioral deviances. To this date, five studies proposed to evaluate the clinical

potential of Oxt in PWS pathophysiology (Rice et al., 2018). All of them had the same administration route (nasal spray) which facilitates comparison among the findings. The studies, however, varied in administered doses, age of the participants and the outcomes that were measured. Limited sample size and experimental design flaws, like the lack of control group (Tauber et al., 2017) or lack of statistical analysis (Miller et al., 2017), limit the interpretation of some of those findings. Exogenous Oxt improved social emotions and cognition in PWS individuals (Tauber et al., 2011; Kuppens Donze and Hokken-Koelega, 2016). Kuppens et al. report that Oxt administration has no effect in PWS individuals older than 11 years old, whereas Tauber and colleagues worked with adults (Tauber et al., 2011; KuppensDonze and Hokken-Koelega, 2016). Finally, no effects on hyperphagia or global metabolism were achieved (Tauber et al., 2011; Einfeld et al., 2014), except on children under 11 years old (Kuppens Donze and Hokken-Koelega, 2016). Together, these data do not provide sufficient evidence that intranasal Oxt administration may serve as an effective therapeutic avenue for PWS.

The lack of positive read outs in the aforementioned trials does not disprove the hypothesis that Oxt abnormalities underlie the PWS phenotypic traits. The conduction of a randomized, double-blind, placebo-controlled clinical trial of Oxt administration would provide robust information on the therapeutic value of exogenous Oxt administration for disease-modifying strategies in the context of PWS. The comprehension of the oxytocinergic anatomical projections that are defective in PWS might also contribute to potential designs of novel therapies involving Oxt (Althammer et al., 2022). In fact, increased serum levels of Oxt in PWS children (Johnson et al., 2016) suggests a compensatory production of this neuropeptide to some degree. It is important to mention that initial evidence suggests that Oxt can be also produced in peripheral structures, such as the gastrointestinal tract in humans (Ohlsson et al., 2006). Whether increased Oxt plasma levels are contributed by extra hypothalamic systems remains unexplored. Alternatively, Oxt signal transduction might be impaired in PWS, which is supported by recent findings of reduced Oxt receptor expression in the CNS of PWS individuals (Bittel et al., 2007). In this case, administration of Oxt would not mediate significant disease-modifying milestones. Further research is necessary to reach a precise determination of the therapeutic value of Oxt in PWS, and to evaluate the optimal conditions for such treatment (*i.e.*, most appropriate age, most effective combination of therapies).

LIMITATIONS OF THIS THESIS

To understand the molecular and cellular basis of neurological disorders, we took advantage of postmortem human brain tissue samples. The use of material of this nature allows for a great range of experimental techniques to be employed in consecutive sections of the same individual. This creates a potential for comprehensive determination of molecular and cellular changes that underlie a disease. However, there are inherent limitations to this model. Intrinsic differences between the living brain and postmortem material have been reported (Liharska et al., 2023). However, there are no options for non-invasive and/or safe acquisition of hypothalamic tissue in live subjects. Combined with the fact that animal models fail to fully recapitulate the diseases investigated in this thesis, the use of human postmortem material becomes the best model as a proxy to the living brain. Moreover, there is great variability in human studies driven by genetic heterogeneity, different lifestyles, and previous medical conditions. To address this, we impose a range of selection criteria that might act to reduce confounding factors in our groups. Those include a balanced gender proportion among controls and subjects of interest, and matched age and tissue processing parameters, such as fixation time. Future studies should consider larger sample sizes, pending on appropriate capacity of well-matched groups.

It is important to address that retrograde analysis of medical history of the individuals included in this thesis was possible, but the clinical complexity of PWS and T2DM still posed a significant challenge. T2DM is considered a progressive condition, suggesting that duration of the disease might influence our results. However, because symptoms can be minimal or unnoticed, a precise determination of this cofounder was not possible. Moreover, we were unable to fully address the impact of antidiabetic drugs in our studies, due to a limitation of sample size. In the context of PWS, we faced limitations on the number of samples due to lack of availability. This forced us to pool children and young adults, which might impact the measurement of our final outcomes. Moreover, our results must be interpreted in the light of PWS clinical complexities. Those include diversity of treatments that those patients might have undergone and the impact of failure of other physiological systems in this pathology other than in the CNS .

Histological analyses were conducted in sections adjacent to the region with the highest count of specific neuronal populations for each hypothalamic nucleus (*i.e.*, Oxt for the PVN, and NPY for the INF). Those sections were considered as a proxy for the whole nuclei, like previously published research (Alkemade et al., 2012; Yi et al., 2012; Hogenboom et al., 2019; Kalsbeek et al., 2020; Guo et al., 2022). However, emerging evidence points to great functional and molecular diversity of both neurons and glial cells (HealyZia and Plemel, 2022; Chen et al., 2017). To what extent this heterogeneity occurs in the human homeostatic and pathological condition is currently under investigation. Moreover, we took advantage of general markers for glial cells, analyzing pan astroglial and microglial markers (*i.e.*, Iba1 and GFAP). Therefore, we cannot fully exclude alterations in specific hypothalamic domains or the participation of discreet subpopulations in pathogenic events explored here. Concomitant research must be conducted in order to find suitable markers to further unravel human hypothalamic dysfunction.

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