Neurochemical Characterization of Brainstem Pro-Opiomelanocortin Cells

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Genetic research has revealed pro-opiomelanocortin (POMC) to be a fundamental regulator of energy balance and body weight in mammals. Within the brain, POMC is primarily expressed in the arcuate nucleus of the hypothalamus (ARC), while a smaller population exists in the brainstem nucleus of the solitary tract (POMCNTS). We performed a neurochemical characterization of this understudied population of POMC cells using transgenic mice expressing green fluorescent protein (eGFP) under the control of a POMC promoter/enhancer (Pomc eGFP). Expression of endogenous Pomc mRNA in the nucleus of the solitary tract (NTS) Pomc eGFP cells was confirmed using fluorescence-activating cell sorting (FACS) followed by quantitative PCR. In situ hybridization histochemistry of endogenous Pomc mRNA and immunohistochemical analysis of eGFP revealed that POMC is primarily localized within the caudal NTS. Neurochemical analysis indicated that POMCNTS is not co-expressed with tyrosine hydroxylase (TH), glucagon-like peptide 1 (GLP-1), cholecystokinin (CCK), brain-derived neurotrophic factor (BDNF), nesfatin, nitric oxide synthase 1 (nNOS), seipin, or choline acetyltransferase (ChAT) cells, whereas 100% of POMCNTS is co-expressed with transcription factor paired-like homeobox2b (Phox2b). We observed that 20% of POMCNTS cells express receptors for adipocyte hormone leptin (LepRbs) using a Pomc eGFP:LepRbCre:tdTom double-reporter line. Elevations in endogenous or exogenous leptin levels increased the in vivo activity (c-FOS) of a small subset of POMCNTS cells. Using ex vivo slice electrophysiology, we observed that this effect of leptin on POMCNTS cell activity is postsynaptic. These findings reveal that a subset of POMCNTS cells are responsive to both changes in energy status and the adipocyte hormone leptin, findings of relevance to the neurobiology of obesity. (Endocrinology 161: 1–13, 2020)

Key Words: Pomc, leptin receptor, NTS, obesity

The rapid rise in the prevalence of obesity has emphasized the need for a greater understanding of the neurobiological mechanisms that underlie energy homeostasis and body weight. Circulating nutritional cues and neuromodulatory signals are integrated within the brain to regulate energy balance. The central melanocortin system is a critical point of convergence for many of these signals and has a fundamental role in regulating body weight. This pathway is comprised of the endogenous melanocortin agonists derived from POMC, which yield the signaling products α-melanocyte stimulating hormone (α-MSH), β-MSH, γ-MSH, adrenocorticotropic hormone (ACTH), and β-endorphin (1). Brain POMC peptides α-MSH, β-MSH, and γ-MSH compete for action with the endogenous melanocortin...
receptor antagonist/inverse agonist agouti-related peptide (AgRP) at melanocortin-3 and -4 receptors (MC3R, MC4R) (2), with MC4Rs predominantly linked to energy balance and body weight regulation (3–5). In the adult brain, POMC is expressed in the arcuate nucleus of the hypothalamus (POMC ARC) and the brainstem nucleus of the solitary tract (POMC NTS) (6, 7). However, during development, POMC is transiently expressed in at least 60 additional brain regions within cells that are not fated to be POMC (8, 9). Accordingly, studies employing Pome CRE transgenic approaches may involve recombination in off-target sites within the brain and peripheral tissues and should be interpreted accordingly.

Brain infusion of α-MSH or synthetic MC4R agonists reduce food intake and body weight, increase energy expenditure, and improve glucose homeostasis (10–12). Complementing these pharmacological studies, loss-of-function mutations of Pome or Mc4r, or over-expression of Agrp, promote hyperphagia, obesity, and insulin resistance in multiple species, including zebrafish, mice, dogs, and man, illustrating the strong translational nature of this system (13–23). Furthermore, genetic haploinsufficiency of Pome/POMC in both rodents and humans is associated with preferential over-consumption of dietary fat and increased risk for diet-induced obesity (DIO) (24, 25). The melanocortin system has therefore garnered substantial interest as a potential therapeutic target for obesity and the prevention of type 2 diabetes (DIO) (24, 25). The melanocortin system has therefore garnered substantial interest as a potential therapeutic target for obesity and the prevention of type 2 diabetes.

Though POMC ARC neurons have been well characterized (28, 29), less attention has focused on the smaller population of POMC cells localized in the NTS. POMC NTS neurons are anatomically localized to impact energy homeostasis given that (1) the NTS is a primary integrator of multiple metabolic cues (30–34), and (2) POMC NTS cell activity is modulated in response to the firing of vagal afferent and ingestive-related signals (30, 31, 35). Indeed, chemogenetic activation of POMC NTS neurons results in a suppression of feeding and an enhancement of short-term satiety (36). A recent report indicated that POMC NTS is required for the acute anorectic effect of obesity medication 5-HT2C R agonist lorcaserin (37). However, what has not been established is whether other neuropeptides/neurotransmitters implicated in energy homeostasis are co-expressed with POMC NTS and the direct endogenous regulators of POMC NTS neuron activity.

Specifically, the NTS contains other appetite-regulating neuropeptides and neurotransmitters such as cholecystokinin (CCK) (38, 39), glucagon like peptide-1 (GLP-1) (40, 41), catecholamines (39, 42), brain-derived neurotrophic factor (BDNF) (43), and nesfatin (44). Previous reports indicate that receptors (LepRs) for the adipocyte hormone leptin are co-expressed with a subset of POMC NTS neurons using a Pome GFP mouse line (43, 45), though others have not found evidence for this using a Pome CRE line (46). In both mice and humans, the absence of LepRb/LEPRB leads to morbid obesity, hyperphagia, insulin resistance, and decreased energy expenditure, amongst other symptoms (47–49). Illustrating that the specific subset of LepRb co-expressed with brain POMC is involved in this metabolic phenotype, selective inactivation of LepRb only in POMC cells produces a milder version of this phenotype (50, 51). However, this Cre/Lox approach does not distinguish between LepRs expressed within POMC in the ARC or NTS. Here we aimed to clarify the distribution, neurochemical identify, and leptin responsiveness of POMC NTS.

### Material and Methods

#### Animals

Male and female Pome-enhanced green florescent protein (Pome GFP; kindly provided by Prof. Richard Simerly and Prof. Malcolm Low) (52), LepRb-Ires-Cre::Kosa26-eGFP (LepRb CRE::eGFP) (53) and LepRb-Ires-CreItdTOMATO (LepRbdTOMATO; kindly provided by Prof. Joel Elmquist and Prof. Jeffrey Friedman) (54) mice were used. A Pome GFP::LepRbdTOM double-reporter line was produced by crossing homozygous Pome GFP and LepRbdTOM mice. All mice were maintained on a 24-hour, 12-hour light cycle with ad libitum access to a standard laboratory chow diet and water unless indicated otherwise. All procedures performed were in accordance with the UK Animals (Scientific Procedures) Act, 1986 and with appropriate ethical approval.

#### Immunofluorescent histochemistry

Mice were deeply and terminally anesthetized with pentobarbital (50 mg/kg i.p.) and transcardially perfused with diethylpyrocarbonate (DEPC)-treated phosphate buffered saline (PBS) followed by 10% neutral buffered formalin (Sigma-Aldrich, Gillingham, UK). Brains were extracted, postfixed in diethylpyrocarbonate (DEPC)-treated phosphate buffered saline (PBS) for 1–2 days at 4°C. Brains were sectioned at 25 μm on a freezing sliding microtome and collected in 5 equal series. Free-floating NTS sections were washed in PBS and incubated for 1 hour with blocking buffer (2% bovine serum albumin with 0.25% Triton X-100 in PBS). Sections were then incubated overnight at 4°C in blocking buffer with a primary antibody: chicken anti-GFP (1:500, Abcam, Cambridge, UK [RRID: AB_2737429 (57)]), rabbit anti-mCherry (1:1000, Rockland Immunochemicals, Limerick, PA [RRID: AB_2614470 (56)]), rabbit antinesfatin (1:1000, Phoenix Pharmaceuticals, Burlingame, CA [RRID: AB_2737429 (57)]), mouse anti-tyrosine hydroxylase (TH; 1:1000, Chemicon, Temecula, CA [RRID: AB_390204 (58)]), goat antiantheline

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acetyltransferase (ChAT; 1:1000, Millipore, Billerica, MA [RRID: AB_2079751 (59)]), rabbit antinitrice oxide synthase (nNOS; 1:1000, Immunostar, Hudson, WI [RRID: AB_572255 (60)]), rabbit antitestin antibody (1:1000, Dr. D. Ito, Keio University School of Medicine, Japan [61, 62] [RRID: AB_2819210 (63)]), and rabbit antipaired-like homeobox 2b (Phox2b; 1:1000, Abcam, Cambridge, UK [RRID: AB_10675986 (64)]). The tissue was subsequently washed in PBS and incubated for 1 hour with the corresponding secondary Alexa Fluor antibodies (1:500, ThermoFisher, Paisley, UK [RRID: AB_2340375 (65), RRID: AB_141637 (66), RRID: AB_141633 (67), RRID: AB_142540 (68)]). Sections were mounted onto microscope slides and visualized under an Axioskop II microscope (Carl Zeiss, Oberkochen, Germany) and images were taken with an AxioCam (Carl Zeiss, Oberkochen, Germany) digital camera. Sections containing the NTS were assigned a bregma level and boundaries of the NTS delineated based on neuroarchitecture and a mouse brain atlas (69). The number of POMC-eGFP immunoreactive (IR) cells, neurochemically defined cells, and double-labeled cells falling within the defined regions were counted and expressed as a percentage of total POMC-eGFP-IR expressing cells in that brain slice.

cFOS immunohistochemistry

Pomc-eGFP mice were injected with mouse recombinant leptin (5 mg/kg, i.p., Merck, Whitehouse Station, NJ) or vehicle during the light cycle and food was removed. Two hours later, mice were deeply anesthetized with pentobarbitone (50 mg/kg i.p.) and transcardially perfused with DEPC-treated PBS followed by 10% neutral buffered formalin. Another cohort of Pomc-eGFP mice were fed ad libitum (n = 4), 12-hour fasted overnight (n = 5) or 12-hour fasted overnight followed by a 2-hour light cycle refeeding (n = 5). Mice were then injected with deep terminal anesthesia and transcardially perfused with DEPC-treated PBS followed by 10% neutral buffered formalin. Brains were extracted and tissue prepared as described above. Free-floating NTS sections were processed at room temperature. Tissue was washed in PBS and then treated for 30 minutes with 0.3% H₂O₂ in PBS. Tissue was then washed in PBS, blocked for 1 hour in blocking solution (0.25% Triton X-100 and 3% normal donkey serum in PBS) and incubated overnight in primary antibody rabbit anti-c-fos added to blocking solution (cFOS; 1:5000, Calbiochem, Watford, UK [RRID: AB_2106755 (70)]). The sections were next incubated in biotinylated rabbit antigoat secondary antibody (1:1000, Vector Laboratories, Peterborough, UK [RRID: AB_2336126 (73)]) in blocking buffer for 1 hour. Sections were then washed in PBS and incubated for 1 hour in VectaStain ABC reagent and chromogenic detection was conducted using DAB reagent (Vector Laboratories, Peterborough, UK). Sections were mounted onto microscope slides and air dried. Slides were dipped in photographic emulsion (Kodak, Rochester, NY) and stored at 4°C for 2 weeks before being developed in D-19 developer and fixer (Kodak). Double-labeled cells were recorded if GFP-IR-positive cell bodies contained overlying black grains that were in a quantity greater than 3 times the background and conformed to the shape of the GFP-IR cell bodies.

In situ hybridization histochemistry and IHC

In situ hybridization histochemistry (ISHH) was conducted as previously described (43). Briefly, mice were injected with deep terminal anesthesia and transcardially perfused with DEPC-treated PBS followed by 10% neutral buffered formalin. Brains were extracted and tissue prepared as described above. Radiolabelled riboprobes specific to the mRNA sequences of POMC, PPG, BDNF, and CCK were used to detect gene expression. Linearized recombinant plasmids were subjected to in vitro transcription with a T7 RNA polymerase (Ambion Inc., Austin, TX) in the presence of 35S-labeled UTP. cRNA riboprobes were diluted to 2 x 10⁷ cpm/ml in a hybridization solution. 35S-labeled Pomc was examined within adjacent brainstem sections ranging from -6.36 to -8.24 from bregma of 2- to 6-month-old male and female wild type C57BL/6 (n = 7) and Pomc-eGFP (n = 7) mice. Sections mounted onto microscope slides were placed with Carestream Kodak Biomax MR single emulsion film (Sigma) in a light tight box for 5 days. Films were scanned and manually analyzed, confirming 35S Pomc within the NTS. High-resolution images were generated using an AxioCam HRC (Carl Zeiss) interface with a brightfield Axioskop II microscope (Carl Zeiss).

Following ISHH, free-floating tissue processed for dual-histochemical staining was washed in PBS before commencement of the IHC protocol. Sections were treated for 30 minutes in 0.3% H₂O₂ in PBS, rinsed in PBS, and blocked in 0.5% BSA/0.5% TritonX-100 in PBS for 1 hour. Sections were incubated in blocking buffer containing goat anti-GFP antibody (1:1000, Abcam, Cambridge, UK [RRID: AB_304897 (72)]) overnight. Sections were washed in PBS and a biotinylated rabbit antigoat secondary antibody (1:1000, Vector Laboratories, Peterborough, UK [RRID: AB_2336126 (73)]) in blocking buffer for 1 hour. Sections were then washed in PBS and incubated for 1 hour in VectaStain ABC reagent and chromogenic detection was conducted using DAB reagent (Vector Laboratories, Peterborough, UK). Sections were mounted onto microscope slides and air dried. Slides were dipped in photographic emulsion (Kodak, Rochester, NY) and stored at 4°C for 2 weeks before being developed in D-19 developer and fixer (Kodak). Double-labeled cells were recorded if GFP-IR-positive cell bodies contained overlying black grains that were in a quantity greater than 3 times the background and conformed to the shape of the GFP-IR cell bodies.

Isolation of NTS POMC-GFP cells with FACS

Four-week-old male and female ad libitum–fed Pomc-eGFP mice (n = 6) were sacrificed between 9:00 and 10:00 AM. The NTS was microdissected into ice cold dissociation buffer consisting of 0.36% glucose (Sigma, Gillingham, UK), 2 x 10⁻⁴% phenol red solution (Sigma), and 1 mM HEPES buffer (Sigma) in HBSS solution (Invitrogen, Paisley, UK). 10X K/ Mg solution consisting of 0.19% kynurenic acid (Sigma), 5 x 10⁻⁴% phenol red solution (Sigma), and 5 mM HEPES buffer (Sigma), and 0.1M MgCl₂ (Sigma), pH 7.5, was added before use. Dissociation media was replaced with 1 ml prewarmed 20 U/ml papain solution consisting of 20X L-cysteine solution (Sigma), papain solution (Sigma), and dissociation...
medium (containing 10X KCl/Mg) and nuclei were incubated at 37°C for 30 minutes. Papain solution was replaced with 1 ml prewarmed 10 mg/ml trypsin inhibitor solution (Sigma, diluted in dissociation media) and the nuclei incubated at 37°C for 10 minutes. Trypsin inhibitor was removed and nuclei were washed with 1 ml ice cold PBS (Sigma) with 2% FCS (P.A.A. laboratories, Ltd., Yeovil, UK). Phosphate buffered saline was replaced with 2 ml PBS with 2% FCS and the solution triturated. Samples were filtered through a 70 μm cell strainer (BD Falcon, Tewksbury, MA). Fluorescence-activating cell sorting was performed using an Influx Cell Sorter (BD Biosciences, San Jose, CA) utilizing a previous established method (31, 32). Cell sorting was set according to cell size (FSC), cell granularity (SSC), FSC pulse-width for singlets, and fluorescence at 488 nm/532 nm for GFP and 647/670 nm for nuclear stain with Draq7 (Biotostat, Shepshead, Leicester, UK). Pools of GFP-positive (GFP+) and GFP-negative (GFP−) cells were sorted into a plate containing RLT lysis buffer (Qiagen, Manchester, UK) and RNA was isolated using RNeasy Plus Micro Kit (Qiagen). Reverse transcription and whole transcriptome amplification were performed using Nugen Ovation Pico WTA system V2 according to the manufacturer’s instructions. 

**Electrophysiology**

Standard current and voltage clamp whole-cell patch clamp electrophysiology recordings were made from POMC−NTS cells. Specifically, Pomc−GFP mice (6–10 weeks old) were injected with a terminal dose of pentobarbitone (50 mg/kg, i.p.). The blood was collected in EDTA-coated tubes (Startedt AG & Co., Numbrecht, Germany). To separate plasma, whole blood was centrifuged at 3500 rpm for 15 minutes at 4°C. Leptin concentrations in serum samples was determined using Mouse Leptin Quantikine® ELISA (R&D Systems, Abington, UK) according to the manufacturer’s protocol at room temperature. Briefly, the kit equilibrated for 30 minutes at room temperature. Assay diluent RD1W (50 μl) was added to each well and the plate was covered to protect it from light exposure and left for 30 minutes. Finally, the reaction was stopped by adding 100 μl of stop solution, initiating a color change from blue to yellow. The plate was mixed by gentle tapping and the absorbance was then measured within 30 minutes on an EnVision® Multilabel Plate Reader (Perkin Elmer, Waltham, MA), measuring the absorbance at 450 nm and subtracting the absorbance at 540 nm/570 nm. The serum leptin levels in each group were determined using the standard curve obtained from the leptin standards provided.

**Statistics**

Data were analyzed with t-test or one-way ANOVA followed by Tukey’s post hoc tests, where appropriate. For all analyses, significance was assigned at P < 0.05. Data are presented as mean ± SEM.

**Results**

**Pomc mRNA and Pomc−GFP distribution in the NTS**

POMC is an essential regulator of energy homeostasis and body weight, and POMC neurons within the ARC have been well characterized (28, 29). POMC cells...
are also localized within the NTS. Using in situ hybridization with a $^{35}$S-labelled Pomc riboprobe, endogenous Pomc mRNA expression was visualized within the NTS of wild-type male and female mice on a C57BL/6 background (n = 7) and PomceGFP mice (n = 7). These findings were reproduced in PomceGFP mice (n = 7). Representative photomicrographs of GFP immunofluorescence (IF) in adult male and female PomceGFP mice (n = 20) also identified that the most abundant distribution of GFP-IR cells is between -7.5 to -7.8 from bregma. Expression of Pomc mRNA in GFP cells in extracted NTS of PomceGFP mice was confirmed using fluorescence-activating cell sorting (FACS) followed by qPCR analysis. Pomc and Gfp mRNA were normalized to that of the housekeeping gene Gapdh. Expression of Pomc and Gfp mRNA is expressed as a percentage of that determined in GFP-positive (GFP+) cells and compared to GFP-negative (GFP-) cells. CC, central canal, scale bar B 500 μm; scale bar C 125 μm.

To overcome these technical difficulties we employed a Pomc eGFP reporter mouse line to map the distribution of individual POMC cells within the brainstem. Expression of GFP protein confirmed that the majority of brainstem POMC cells sit within caudal NTS (-7.5 to -7.8 from bregma; Fig. 1C).

**NTS validation of PomceGFP mouse line**

To confirm the expression of Pomc mRNA within eGFP cells, the NTS was microdissected from PomceGFP mice (n = 6), and FACS followed by Pomc and Gfp qPCR was performed (Fig. 1D). One-hundred percent
of GFP-positive cells expressed Pomc mRNA as compared to 8% of GFP-negative cells. Similarly, 99% of GFP-positive cells expressed Gfp mRNA as compared to 10% of GFP-negative cells. These data provide the first NTS validation of the PomceGFP line and verify the expression of endogenous POMCNTS.

**Neurochemical characterization of POMC<sub>NTS</sub> neurons**

The NTS has a regulatory role in a large number of physiological processes. As a consequence of this functional heterogeneity, this nucleus is home to numerous distinct neuronal populations. To characterize POMC<sub>NTS</sub> cells, we examined the level of co-expression between PomceGFP and other neurochemicals and receptors implicated in the regulation of energy balance. We observed that POMC<sub>NTS</sub> cells do not co-localize with catecholamines epinephrine or norepinephrine using TH to visualize this subset of cells (Fig. 2A). Similarly, PomceGFP was not co-expressed with the neuropeptide nesfatin-1 (Fig. 2B) or the neurotransmitter acetylcholine using choline acetyltransferase (ChAT; Fig. 2C). PomceGFP was expressed in a distinct population to the protein seipin associated with lipodystrophy (Fig. 2D) and the enzyme nitric oxide synthase 1 (nNOS; Fig. 2E). Likewise, PomceGFP was not co-localized with neuropeptides involved in the reduction of food intake, preproglucagon (PPG)/GLP-1 (Fig. 2F). Dual IHC and ISHH analysis of adult male and female PomceGFP mice demonstrated the absence of GFP-IR co-expression (brown cytoplasmic stain) with 35S preproglucagon (Ppg) (Fig. 2F), 35S cholecystokinin (Cck) (Fig. 2G) or 35S brain derived neurotrophic factor (Bdnf) mRNA (black grains) (Fig. 2H). I: Double-IF analysis in adult male and female PomceGFP:LepRb:GFP mice (n = 9) revealed a subset of POMC-expressing neurons (green) were co-expressed with LepRb-expressing cells (red). J: In PomceGFP mice (n = 4) and LepRb:GFP mice (n = 4) (K), all GFP-IR cells (green) were Phox2b-IR positive (red). L: Schematic illustrating overlap of POMC, Phox2b, and LepRb in the NTS. Level of NTS presented in (A–K), -7.56 to -7.76 from bregma. Arrows represent dual-labeled cells. CC, central canal; scale bar, 50 μm applies to (A–K).
(Fig. 2F), CCK (Fig. 2G), or BDNF (Fig. 2H), as revealed with immunohistochemistry combined with in situ hybridization. Thus, PomcGFP neurons appear to reside in a distinct subgroup within the NTS and do not co-express other well-characterized regulators of energy homeostasis.

We then examined potential endogenous regulators of POMCNTS. Some previous reports indicate that leptin administration increases a marker of leptin signal transduction (pSTAT) in PomcGFP cells (45), thereby providing evidence of co-localization. To facilitate the visualization of POMC and LepRb cells and to quantify co-expression, we crossed LepRbtdTomato mice with PomcGFP mice to create a double reporter line (PomcGFP:LepRbtdTomato). We found that 20.6% ± 2.14 of POMC NTS cells co-localized with LepRb tdTomato (Fig. 2I). Co-localization was highest at -7.64 and -7.76 from bregma, the subregion of the NTS we found to express the majority of POMC cells (Fig. 1C). All PomcGFP cells co-expressed Phox2b, a transcription factor associated with the formation and development of the NTS (74) (Fig. 2J). Using LepRbCRE:eGFP mice to visualize LepRbNTS expression, we observed that all LepRbNTS cells also expressed Phox2b (Fig. 2K and 2L).

PomcGFP cells increase their activity in response to food intake

Given that a subset of POMCNTS cells co-express LepRb, we postulated that this subgroup should be responsive to leptin. Fasting has been shown to affect the concentrations of various circulating hormones, including reducing leptin (75). We dark cycle fasted mice, dark cycle fasted and then re-fed mice, or ad libitum fed mice and measured serum leptin and the activity of POMCNTS cells using FOS-IR (Fig. 3). The NTS and blood was collected 2 to 4 hours following the onset of the light cycle. As expected, fasting significantly reduced leptin levels (0.56 ± 0.30 ng/ml, n = 4) and fasting followed by a 2-hour bout of refeeding significantly increased leptin levels (3.44 ± 0.82 ng/ml, n = 8; F2,19 = 4.64, P = 0.023; Fig. 3E). A significant difference in leptin levels between the refed group and the fed group (1.58 ± 0.32 ng/ml, n = 9) was not detected. Refeeding (n = 9) also significantly increased the number of FOS-IR-positive cells within the NTS compared to the fasted state or fed state (Fig. 3E). Significantly more NTS PomcGFP neurons expressed FOS-IR in mice that had been fasted and then refed (21.34 ± 6.91 cells) compared to mice in the fasted (0.93 ± 0.42 cells) or fed state (1.29 ± 0.54 cells; F2,11 = 7.55, P = 0.008, n = 4–5 per group; Fig. 3A–3D). These findings suggest that a subset of POMCNTS cells are responsive to nutritional state and changes in hormones such as endogenous leptin levels.

Leptin activates a subset of POMCNTS neurons

To gain further insight into the physiological role of the LepRb expression on POMCNTS cell activity, we examined the effect of peripheral administration of leptin. Consistent with the fluctuations of endogenous leptin described above, we observed that leptin (5 mg/kg, i.p.) increased FOS-IR within the NTS compared to saline treatment (Fig. 4A). We examined the effect specifically in POMCNTS cells and found that leptin increased...
Figure 4. *Pomc*<sub>GFP</sub> cells are responsive to changes in exogenous leptin levels. A–C: Leptin treatment (5 mg/kg, i.p.) in *Pomc*<sub>GFP</sub> mice increased FOS-IR within GFP-IR (A–B) and non-GFP-IR NTS cells (C) compared to saline treatment (n = 10). Level of NTS presented in A, -7.56 to -7.76 from bregma. D: Representative current clamp recording of a *Pomc*<sub>GFP</sub> cell. E–F: Bath application of leptin (100–250 nM) increased the membrane potential of 4 out of 10 Pomc<sub>GFP</sub> cells and reduced the membrane potential of 1 cell. G: Representative current clamp recording of a Pomc<sub>GFP</sub> cell in the presence of synaptic blockers (1 μM tetrodotoxin, 3 μM strychnine, 50 μM picrotoxin, 50 μM D-AP5, 10 μM CNQX). H–I: Bath application of leptin (250–500 nM) depolarised and increased the membrane potential of 7 of 30 Pomc<sub>GFP</sub> cells and inhibitory effects were observed in 3 cells. Arrows represent dual-labeled cells. CC, central canal; scale bar A, 50 μm. Data are presented as mean ± SEM. **P < 0.01, ****P < 0.0001.
We report that POMC NTS cells are primarily localized within the hindbrain for the regulation of food intake via peptide product α-MSH and for the induction of analgesia via peptide product β-endorphin. The melanocortin system also appears to play a role in blood pressure and heart rate. Compared to equally obese control subjects, the prevalence of hypertension in MC4R-deficient people was significantly lower, and MC4R-deficient patients exhibited lower increases in heart rate upon waking (78). Though lacking direct co-expression, POMCNTS cells may form local interactions with neighboring DVC TH, GLP-1, CCK, BDNF, nesfatin, nNOS, seipin, and/or ChAT cells to impact homeostasis, analgesia, and/or blood pressure.

In support of system connectivity, CCK increases the firing rate of POMCNTS cells (30). Though CCK is widely expressed within the CNS, recent reports support a functional role of the subpopulation of CCK-positive neurons within the NTS in feeding behavior and body weight regulation. Specifically, chemogenetic or optogenetic activation of CCKNTS neurons potently reduces food intake and body weight (38, 39). This effect appears to be mediated via transmitter release in the paraventricular nucleus of the hypothalamus (PVH) and parabrachial nucleus (PBN) given that selective optogenetic activation of CCKNTS axon terminals within these regions reduces feeding (38, 39). A subset of CCKNTS cells co-express PPG/GLP-1 (43). Like CCKNTS, chemogenetic activation of PPG/GLP-1NTS cells also suppresses acute feeding (41).

Nesfatin-1 is a peptide and neuropeptide first identified in 2006 and observed to reduce food intake (79). NesfatinNTS cells are responsive to CCK-8 and gastric distention (80–82). It is therefore possible that CCKNTS not only impacts feeding via a PVH and PBN circuit, but also via a local interaction with nesfatin and POMC. Providing support for potential cardiovascular function, NTS microinfusion of nesfatin-1 increases blood pressure and heart rate (80). A subset of NesfatinNTS cells co-express GABA and the majority of the dorsal motor nucleus of the vagus (DMX) nesfatin cells co-express ChAT. NesfatinDMX cells innervate the stomach (80).

One of the best described cell types within the NTS modulating feeding behavior are those expressing the catecholamines. Similar to our findings, Fan and colleagues reported no overlap between the expression of POMC and TH in the NTS (31). Like POMCNTS cells, vagal afferents also directly innervate THNTS cells (83) and similar to nesfatinNTS, THNTS are responsive to gastric distension (84). Direct chemogenetic or optogenetic activation of noradrenergic dopamine β-hydroxylase (DBH)-expressing NTS neurons also decreases food intake and body weight (39). Supporting a cardiovascular function, DBH conjugated to the neurotoxin saporin,

**Discussion**

Obesity has emerged as a key challenge to human health, making it essential that the neurobiology underpinning energy homeostasis is clarified to foster the identification of new strategies to prevent and treat this condition. Genetic analysis has revealed that a functioning melanocortin system is necessary for healthy body weight in multiple species. Specifically, genetic disruption of POMC/Pomc and MC4R/Mc4r promotes severe hyperphagia and obesity (76). Within the adult brain POMC is predominantly expressed within the ARC, and the function of POMCARC has been extensively characterized. Here we investigated the smaller and less well-studied population within the NTS.

**Distribution of POMCNTS**

Low levels of endogenous Pomc expression within the NTS have hampered the study of this subpopulation. To overcome these technical restrictions, we utilized a reporter mouse line that allowed us to map, quantify, and characterize these cells. Here we provide an instrumental validation of the expression of endogenous POMC mRNA in eGFP cells in the PomceGFP mouse line. We report that POMCNTS cells are primarily localized within the commissural NTS at the level of the AP. Though other energy balance modulating neurons are present within the caudal DVC, we observed a lack of co-localisation with CCK, GLP-1, TH, BDNF, nesfatin, nNOS, seipin, or ChAT-containing cells. POMCNTS cells are activated by visceral afferents and chemogenetic activation of POMCNTS decreases acute food intake and produces opioid analgesia and bradycardia (30, 36, 77). This suggests that POMCNTS cells may constitute a distinct hub within the hindbrain for the regulation of food intake via peptide product α-MSH and for the induction of analgesia via peptide product β-endorphin. The melanocortin system also appears to play a role in blood pressure and heart rate. Compared to equally obese control subjects, the prevalence of hypertension in MC4R-deficient people was significantly lower, and MC4R-deficient patients exhibited lower increases in heart rate upon waking (78). Though lacking direct co-expression, POMCNTS cells may form local interactions with neighboring DVC TH, GLP-1, CCK, BDNF, nesfatin, nNOS, seipin, and/or ChAT cells to impact homeostasis, analgesia, and/or blood pressure.

In support of system connectivity, CCK increases the firing rate of POMCNTS cells (30). Though CCK is widely expressed within the CNS, recent reports support a functional role of the subpopulation of CCK-positive neurons within the NTS in feeding behavior and body weight regulation. Specifically, chemogenetic or optogenetic activation of CCKNTS neurons potently reduces food intake and body weight (38, 39). This effect appears to be mediated via transmitter release in the paraventricular nucleus of the hypothalamus (PVH) and parabrachial nucleus (PBN) given that selective optogenetic activation of CCKNTS axon terminals within these regions reduces feeding (38, 39). A subset of CCKNTS cells co-express PPG/GLP-1 (43). Like CCKNTS, chemogenetic activation of PPG/GLP-1NTS cells also suppresses acute feeding (41).

Nesfatin-1 is a peptide and neuropeptide first identified in 2006 and observed to reduce food intake (79). NesfatinNTS cells are responsive to CCK-8 and gastric distention (80–82). It is therefore possible that CCKNTS not only impacts feeding via a PVH and PBN circuit, but also via a local interaction with nesfatin and POMC. Providing support for potential cardiovascular function, NTS microinfusion of nesfatin-1 increases blood pressure and heart rate (80). A subset of NesfatinNTS cells co-express GABA and the majority of the dorsal motor nucleus of the vagus (DMX) nesfatin cells co-express ChAT. NesfatinDMX cells innervate the stomach (80).

One of the best described cell types within the NTS modulating feeding behavior are those expressing the catecholamines. Similar to our findings, Fan and colleagues reported no overlap between the expression of POMC and TH in the NTS (31). Like POMCNTS cells, vagal afferents also directly innervate THNTS cells (83) and similar to nesfatinNTS, THNTS are responsive to gastric distension (84). Direct chemogenetic or optogenetic activation of noradrenergic dopamine β-hydroxylase (DBH)-expressing NTS neurons also decreases food intake and body weight (39). Supporting a cardiovascular function, DBH conjugated to the neurotoxin saporin,
but not the neurotoxin 6-hydroxydopamine (6-OHDA) infused into the NTS, causes myocardial lesions and in some cases sudden death (85, 86).

As observed in POMC deficiency, genetic alterations in BDNF in humans is linked to elevated food intake and obesity (87, 88). BDNF function is best characterized within the ventromedial hypothalamus (VMH) (89). BDNF signaling within the NTS is essential to life, as the knockout of its receptor TrkB within the NTS is lethal (90). Heterozygous mice with partial knockdown are hyperphagic but display a normal body weight (90). Additional research is required to define a function for BDNFNTS.

Despite being known primarily for its role in adipocyte differentiation, the protein seipin is expressed within the NTS; however, its function within this region has yet to be fully explored (62). nNOS plays a role in a variety of processes, including blood pressure, energy homeostasis, and synaptic plasticity. Viral knockdown of nNOSNTS in rats inhibited sympathetically mediated baroreflex (91), though food intake and body weight in these rats was not reported and remains to be investigated. Thus, the NTS harbors a variety of factors involved in homeostatic regulation and future study is warranted to unpack potential local interactions and their functional implications.

Though POMCNTS cells do not co-express CCK, GLP-1, TH, BDNF, nesfatin, seipin, or nNOS, 100% of POMCNTS co-express Phox2b. Phox2b is a transcription factor that is required for the embryonic development of the autonomic nervous system. The Phox2bCRE line is frequently used as a broad NTS histochemical marker or to genetically alter cells within the NTS. Functionally, subsets of Phox2b cells have been reported to be involved in central excitatory relays of the sympathetic baroreflex and transmit peripheral chemoreceptor information to the retrotrapezoid nucleus (92, 93). Moreover, a recent study revealed that a subset of Phox2bNTS neurons act as central respiratory chemoreceptors (94).

Modulation of POMCNTS

In line with previous findings (31), we observed that the activity (as detected by FOS-IR) of a small subset of POMC-eGFPNTS cells is activated by a feeding bout. In the present report, we employed an acute fast followed by 2 hours of refeeding. In the earlier report, POMC-eGFP mice were on a restricted feeding schedule of 5 hours per day (31). The proportion of POMCNTS cells activated following refeeding was greater than that observed in response to leptin treatment, suggesting that other homeostatic factors modulate the activity of POMCNTS cells. We found that POMCNTS cells expressing LepRbs were primarily concentrated -7.56 to -7.92 from bregma, an area where POMC neurons have been shown to respond to dietary amino acids (95, 96). A study by Grill and colleagues provides support that LepRbs within the NTS are required for appropriate energy homeostasis (97). Specifically, they observed that viral knockdown of LepRb within the NTS increased food intake, body weight, and adiposity in rats. Phox2bCRE:LepRb flox'd mice were hyperphagic, displayed increased food intake after fasting, and gained weight at a faster rate than wild-type controls. Phox2bCRE:LepRb flox'd mice also exhibited an increased metabolic rate independent of changes in locomotor activity and normal glucose homeostasis (98). These data suggest that leptin signaling within the NTS is required for normal feeding and body weight in rodents and that a subset of POMCNTS cells are regulated by leptin.

In line with other earlier work, we observed increased FOS-IR in a subpopulation of POMCNTS cells following acute leptin treatment (45, 99). However, our results do not coincide with similar experiments utilising a PomcCRE, driven reporter line (46). As the PomeGFP and the PomcCRE reporter lines appear to label nonoverlapping neuronal populations within the NTS (8), it is likely that the cells characterized here and in references 45 and 99 represent a different population to those studied in reference 46. To further investigate the mechanism by which POMCNTS neurons respond to leptin, we employed whole cell patch clamp electrophysiology. Leptin’s effects on neuronal excitability in the rat brainstem are varied and appear to encompass cells that are inhibited, excited, or nonresponsive (100, 101). Approximately half of the unidentified neurons described in these studies became hyperpolarized upon leptin application, while a smaller proportion (13%) showed an increase in membrane potential (100, 101).

We provide some of the first insights into the effect of leptin on PomeGFP cells. We found that leptin increased the firing rate of approximately a quarter of PomeGFP cells, a pattern similar to the proportion of POMCNTS FOS-IR-positive cells. As the membrane potential increase endured in the presence of synaptic blockers, we conclude that POMCNTS cells possess the required cellular machinery to respond directly to circulating levels of this hormone. However, the effects observed were small and warrant further investigation with different concentrations of leptin and different electrophysiological techniques to further clarify both the network and direct effects of leptin on PomeGFP cell activity. TRPC channels are responsible for the activation of POMC-ARC neurons by leptin (102). The precise electrophysiological mechanism and the current responsible for POMCNTS effects also remain to be elucidated.
We recently reported that approximately 40% of POMC-NTS cells co-express the 2c receptor subtype for the neurotransmitter serotonin (5-HT_{2cR}) (37). Moreover, we observed that POMC-NTS is essential for the appetite suppressive effects of the 5-HT_{2cR} obesity medication lorcaserin (37). The findings reported here add to the profile of POMC-NTS and its potential physiological role. Specifically, we dissect the interplay of 2 of the most essential players in body weight regulation, the melanocortin and leptin systems, within the key homeostatic brain region the NTS. We reveal that POMC-NTS cells represent a segregated class of leptin responsive neurons that do not co-localize other established NTS metabolic regulators. These findings provide new insights into the neuroendocrinology of appetite and have implications for the neurobiology of obesity.

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Additional Information

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