Neuromedin U-homolog Microcircuit Connects Chemosensory and Neuroendocrine Systems in *Drosophila*

Schlegel Philipp[1], Texada Michael J.[2], Miroschnikow Anton[1], Peters Marc[1], Schneider-Mizell Casey M.[2], Lacin Haluk[2], Li Feng[2], Fetter Richard D.[2], Truman James W.[2], Cardona Albert[2], Pankratz Michael J.[1,*]

1 Department of Molecular Brain Physiology and Behavior, LIMES Institute, Bonn, Germany
2 HHMI Janelia Research Campus, Ashburn, VA, USA

*** pankratz@uni-bonn.de**

Abstract

Neuromedin U (NMU) is a potent regulator of food intake and activity in mammals. While some downstream targets of NMU have been localized, connectivity of the neural circuits employing this neuropeptide is largely unknown. In *Drosophila*, neurons producing the homologous neuropeptide hugin regulate feeding and locomotion in a similar manner and project to structures of the central nervous system analogous to those in which NMU is found. Here, we use EM reconstruction and receptor expression analysis to map the connectome of hugin-producing neurons in the *Drosophila* larval central nervous system. We show that hugin-producing neurons establish distinct units that are reciprocally connected and share connectivity motifs. One of these units simultaneously employs synaptic as well as peptide-receptor connections to target neuroendocrine cells (NSCs) of the pars intercerebralis, the *Drosophila* analog of the hypothalamus. These NSCs produce CRH- and insulin-like peptides which are homologs of downstream targets of NMU. Furthermore, most of the hugin-producing neurons, including those that target the NSCs, receive inputs from chemosensory neurons in the subesophageal zone, the brain stem analog in *Drosophila*. Our data positions hugin neurons as part of a novel sensory-to-endocrine network that may reflect the way NMU operates in mammals. We propose that the hugin neurons interconnecting chemosensory and neuroendocrine organs are part of a physiological control system that has been conserved not only at functional and molecular levels, but at the network architecture level as well.

Introduction

Multiple studies have demonstrated functional conservation of fundamental hormonal systems for metabolic regulation in mammals and *Drosophila*, including insulin [1, 2], glucagon [3, 4], and leptin [5]. In addition to these predominantly peripherally released peptides there is a range of neuropeptides that are employed within the central nervous systems (CNS) of vertebrates and have homologs in invertebrates, e.g. NPY, CRH, oxytocin/vasopressin [6–10]. Among these, neuromedin U (NMU) is known for its profound effects on feeding behavior and activity. NMU inhibits feeding behavior [11, 12], promotes physical activity [13, 14], and is involved in energy

homeostasis [15,16] and stress response [17,18]. The *Drosophila* homolog of NMU, hugin, has recently gained traction due to similar effects on behavior in the fly. Increased hugin signaling inhibits food intake and promotes locomotion [19,20]. In addition, both neuropeptides are also found in analogous regions of the mammalian/*Drosophila* CNS. NMU is widely distributed in the CNS, with high levels in the arcuate nucleus of the hypothalamus, the pituitary, the medulla oblongata of the brain stem, and the spinal cord [11,21–23]. Hugin is produced by neurons in the subesophageal zone (brain stem) that project to the ring gland (pituitary gland), the pars intercerebralis (hypothalamus) and ventral nerve cord (spinal cord) [24]. Based on morphological, genetic and functional similarities, these regions of the fly brain were suggested to correspond to aforementioned regions of NMU occurrence [25,26] (Fig. 1). Consequently, NMU/hugin has previously been referred to as a clear example of evolutionary constancy of peptide function [27].

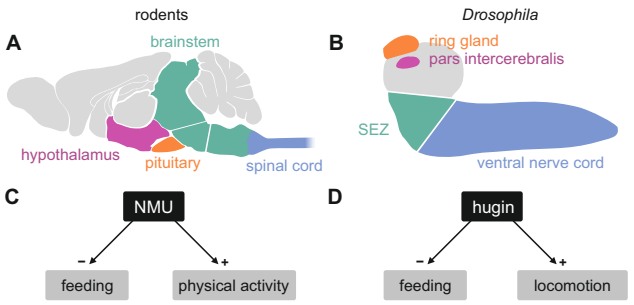

Figure 1. Comparison of mammalian neuromedin U and *Drosophila* hugin. A, Distribution of neuromedin U (NMU) in the rodent CNS. NMU peptide, NMU-expressing cells and NMU-positive fibers are found in brain stem, hypothalamus, pituitary and spinal cord. **B**, Similarly, *hugin* is expressed by neurons in the subesophageal zone (SEZ) that project into the pars intercerebralis, ring gland and ventral nerve cord. Note that analogous regions in A and B are given corresponding colors. **C,D**, Increased NMU and hugin signaling has similar effects: feeding behavior is decreased whereas physical activity/locomotion is increased.

Although functional and morphological aspects of neurons employing either neuropeptide have been extensively studied in the past, their connectivity is mostly unknown. While large scale connectomic analyses in vertebrates remain challenging, generation of high resolution connectomes has recently become feasible in *Drosophila* [28–31]. We took advantage of this and performed an integrated analysis of synaptic and G-protein coupled receptor (GPCR)-mediated connectivity of hugin neurons in the CNS of *Drosophila*. Our results show that hugin neurons form distinct units, demonstrating that clusters of neurons employing the same neuropeptide can be remarkably different in their synaptic connectivity. One unit of hugin neurons targets cells in the *Drosophila* analog of the mammalian hypothalamus that produce DH44 (a CRH-like peptide) and *Drosophila* insulin. Both of these peptides have mammalian homologs that are likewise downstream of NMU [32,33]. Endocrine function is essential to ensure homeostasis of the organism and coordinate fundamental behaviors, such as feeding, mating and reproduction, and acts as integrator of external and internal sensory cues [34]. Consequently, connections between sensory and endocrine systems are found across species [35–38]. We show that hugin neurons receive chemosensory input in the *Drosophila* analog of the brain stem, thereby linking chemosensory and neuroendocrine systems.

Materials and Methods

Neuronal Reconstruction.

Reconstructions were based on a ssTEM (serial section transmission electron microscope) data set comprising an entire central nervous system and the ring gland of a first-instar *Drosophila* larva. Generation of this data set was described previously by Ohyama et al (2015) [28]. Neurons' skeletons were manually reconstructed using a modified version of CATMAID (http://www.catmaid.org) [39]. Hugin-PH (pharynx) neurons were first identified by reconstructing all axons in the prothoracic accessory nerve, through which these neurons exit the CNS towards the pharynx. Similarly, hugin-RG (ring gland) were identified by reconstructing all neurosecretory cells that

target the ring gland. To find the remaining hugin neurons, neighbors of already identified hugin neurons were reconstructed. Among those, the remaining hugin neurons were unambiguously identified based on previously described morphological properties such as projection targets, dendritic arborizations, relative position to each other and prominent landmarks like antennal lobes or nerves [40, 41]. The mapped synaptic connections represent fast, chemical synapses matching previously described typical criteria: thick black active zones, pre- (e.g. T-bar, vesicles) and postsynaptic membrane specializations [42]. Hugin inputs and outputs were traced by following the pre- and postsynaptically connected neurites to the respective neurons' somata or nerve entry sites in sensory axons. Subsequently, all sensory and endocrine neurons synaptically connected to hugin neurons were fully reconstructed. Interneurons were fully reconstructed if (a) homologous neurons were found in both hemispheres/-segments (did not apply to medially unpaired neurons) and (b) at least one of the paired neurons was connected by a minimum of 3 synapses to/from hugin neurons. Neurons that did not fit either criteria were not fully reconstructed and thus excluded from statistical analysis. This resulted in the reconstruction 177 synaptic partners that together covered 90%/96% of hugin neurons' above threshold pre-/postsynaptic sites (S5 Fig). The same parameters were applied to the reconstruction of synaptic partners of medial neurosecretory cells (mNSCs). Morphological plots and example synapse's volume reconstruction were generated using custom python scripts or scripts for Blender 3D (www.blender.org). The script for a CATMAID-Blender interface is on Github https://github.com/schlegelp/CATMAID-to-Blender. See S6 Neuron atlas of all reconstructed neurons and their connectivity with hugin neurons.

Localization of DCVs in respect to synaptic sites. Due to the neuronal reconstructions' being skeletons instead of volumes, distances were measured from the center of each given dense core vesicle to the center of the closest presynaptic site along the skeleton's arbors. DCVs within 3000 nm radius around the centers of neurons' somata were excluded. Data was smoothed for graphical representation (Fig. 8D; bin size 50 nm).

Normalized connectivity similarity score. To compare connectivity between neurons (Fig. 4B), we used a modified version of the similarity score described by Jarrell et al. (2012) [43]:

$$f(A_{ik}, A_{jk}) = min(A_{ik}, A_{jk}) - C_1 max(A_{ik}, A_{jk}) e^{-C_2 min(A_{ik}, A_{jk})}$$

With the overall connectivity similarity score for vertices i and j in adjacency matrix A being the sum of $f(A_{ik}, A_{jk})$ over all connected partners k. C_1 and C_2 are variables that determine how similar two vertices have to be and how negatively a dissimilarity is punished. Values used were: $C_1 = 0.5$ and $C_2 = 1$. To simplify graphical representation, we normalized the overall similarity score to the minimal (sum of $-C_1 max(A_{ik}, A_{jk})$ over all k) and maximal (sum of $max(A_{ik}, A_{jk})$ over all k) achievable values, so that the similarity score remained between 0 and 1. Self-connections (A_{ii}/A_{jj}) and A_{ij} connections were ignored.

Synapse similarity score. To calculate similarity of synapse placement between two neurons, we calculated the synapse similarity score (Fig. 5D):

$$f(i_s, j_k) = e^{\frac{-{d_{sk}}^2}{2\sigma^2}} e^{-\frac{|n(i_s) - n(j_k)|}{n(i_s) + n(j_k)}}$$

With the overall synapse similarity score for neurons i and j being the average of $f(i_s, j_k)$ over all synapses s of i. Synapse k being the closest synapse of neuron j to

synapses s [same sign (pre-/postsynapse) only]. d_{sk} being the linear distance between synapses s and k. Variable σ determines which distance between s and k is considered as close. $n(j_k)$ and $n(i_s)$ are defined as the number of synapses of neuron j/i that are within a radius ω of synapse k and s, respectively (same sign only). This ensures that in case of a strong disparity between $n(i_s)$ and $n(j_k)$, $f(i_s, j_k)$ will be close to zero even if distance d_{sk} is very small. Values used: $\sigma = \omega = 2000$ nm.

Clustering. Clusters for dendrograms were created based on the mean distance between elements of each cluster using the average linkage clustering method. Clusters were formed at scores of 0.2 for synapse similarity score (Fig. reffig5B,E) and 0.4 for connectivity similarity score (Fig. reffig6D).

Synaptic load. Synaptic load was calculated by counting the number of synapses that constitute connections between neuron A and a given set of pre- or postsynaptic partners (e.g. sensory neurons) divided by the total number of either incoming or outgoing synaptic connections of neuron A.

Statistics. Statistical analysis was performed using custom Python scripts; graphs were generated using Sigma Plot 12.0 (www.sigmaplot.com) and edited in Adobe Corel Draw X5 (www.corel.com).

Generation of *CG8784* promoter lines.

The *CG8784-GAL4::p65* construct (Fig. 7) was created using recombineering techniques [44] in P[acman] bacterial artificial chromosome (BAC) clone CH321-45L05 [45] (obtained from Children's Hospital Oakland Research Institute, Oakland, CA), containing CG8784 within ≈80 kb of flanking genomic context. A generic landing-site vector was created by flanking the kanamycin-resistance/ streptomycin-sensitivity marker in *pSK+-rpsL-kana* [46] (obtained from AddGene.org, plasmid #20871) with 5′ and 3′ homology arms (containing *GAL4* coding sequences and *HSP70* terminator sequences, respectively) amplified from *pBPGUw* [47]. *CG8784*-specific homology arms were added to this cassette by PCR using the following primers (obtained as Ultramers from Integrated DNA Technologies, Inc., Coralville, Iowa; the lower-case portions are *CG8784*-specific targeting sequences, and the capitalized portions match the *pBPGUw* homology arms):

CG8784-F:	tggcgtggcgtggagtggatagagtccacaattaatcga cgacagctagtATGAAGCTACTGTCTTCTATCGAACAAGC
CG8784-R:	tttgccgcattacgcatacgcaatggtgtccctcaaaaa tgccatctcacGATCTAAACGAGTTTTTAAGCAAACTCACTCCC

This cassette was recombined into the BAC, replacing the coding portion of the first coding exon, and then full-length *GAL4::p65-HSP70* amplified from *pBPGAL4.2::p65Uw* [48] was recombined into the landing site in a second recombination. Introns and exons following the insertion site were retained in case they contain expression-regulatory sequences, although they are presumably no longer transcribed. Correct recombination was verified by sequencing the recombined regions, and the final BAC was integrated into the third-chromosome *attP* site *VK00033* [49] by Rainbow Transgenic Flies, Inc. (Camarillo, CA).

The *CG8784-6kb-GAL4* (S4 Fig) was created using standard restriction-digestion/ligation techniques in pCaSpeR-AUG-Gal4-X vector [50]. An approximately 6-kb promoter fragment 5′ of the first coding exon was amplified using the following primers and inserted into a pCaSpeR vector (Addgene.org, plasmid #8378) containing a start codon (AUG) and the *Gal4* gene (S4 Fig).

CG8784-6kb-F: AATATCTTG GCAACGAAGTCC
CG8784-6kb-R: AGCTGTCGTCGATTAATTGTG

This construct was integrated into the genome via P-element insertion.

Immunohistochemistry.

For antibody stainings of *CG8784-GAL4::p65*, larvae expressing *JFRC2-10xUAS-IVS-mCD8::GFP* [48] driven by *CG8784-GAL4::p65* were dissected in PBS. Brains were fixed in 4% formaldehyde in PBS for 1 h, rinsed, blocked in 5% normal goat serum, and incubated overnight at 4°C with primaries: sheep anti-GFP (AbD Serotec #4745-1051), 1:500; rabbit anti-DH44 [51] (gift of Jan Veenstra), 1:1000; rabbit anti-DILP2 [52] (gift of Jan Veenstra), 1:1000; 1:1000; and rabbit anti-DMS [53] (gift of Luc van den Bosch and Liliane Schoofs), 1:500. Tissues were rinsed and incubated overnight at 4°C in secondaries: Alexa Fluor 488 donkey anti-sheep (Jackson ImmunoResearch, #713-545-147) and rhodamine red-X donkey anti-rabbit (Jackson ImmunoResearch #711-296-152), both 1:500. Brains were rinsed and dehydrated through an ethanol-xylene series, mounted in DPX, and scanned on a Zeiss LSM 510 confocal microscope. For antibody stainings of *CG8784-6kb-GAL4*, larvae expressing *10XUAS-mCD8::GFP* (Bloomington, #32184) driven by *CG8784(6kb)-GAL4* were dissected in PBS. Brains were fixed in 4% paraformaldehyde for 30 minutes, rinsed, blocked in 5% normal goat serum, and incubated overnight at 4°C with primaries: goat anti-GFP-FITC (abcam, ab26662), 1:500; rabbit anti-DH44 (gift of Jan Veenstra), 1:1000; guinea pig anti-Dilp2 (Pankratz lab), 1:500 and rabbit anti-DMS (gift

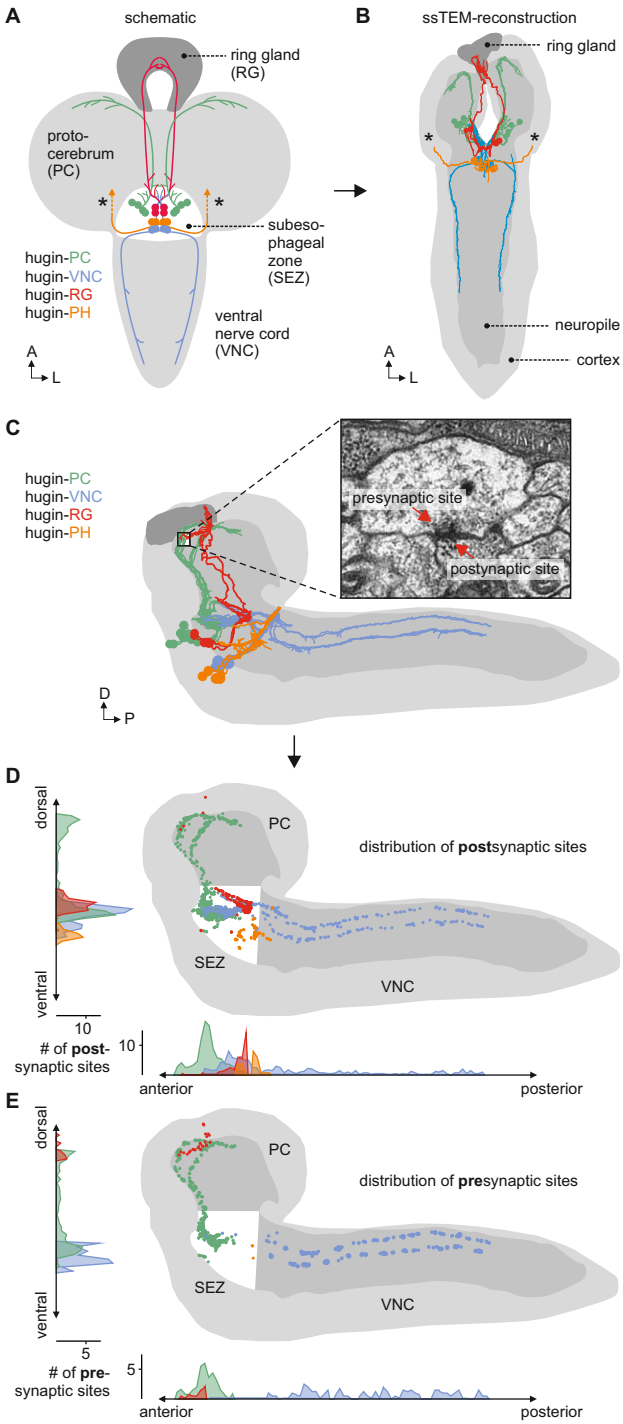

Figure 2. Morphology of hugin-producing neurons and their input and output compartments. **A**, Four morphologically distinct classes of hugin neurons: hugin-PC (protocerebrum), hugin-VNC (ventral nerve cord), hugin-RG (ring gland) and hugin-PH (pharynx, asterisks mark nerve exit sites). **B**, Reconstruction of all hugin neurons based on an entire larval brain. **C-E**, Spatial distribution of pre-/postsynaptic sites of all hugin classes. Each dot in D and E represents a single synaptic site. Graphs show distribution along dorsal-ventral and anterior-posterior axis of the CNS. Hugin interneurons (hugin-PC and hugin-VNC) show mixed input and output compartments, whereas efferent hugin neurons (hugin-RG and hugin-PH) show almost exclusively postsynaptic sites within the CNS. Note that presynaptic sites of hugin-RG neurons (E) are located in the ring gland.

of Luc van den Bosch and Liliane Schoofs), 1:500. Tissues were rinsed and incubated overnight at 4°C in secondaries: anti-rabbit Alexa Fluor 633 (Invitrogen, A-21070) and anti-guinea pig Alexa Fluor 568 (Invitrogen, A-11075), both 1:500. Brains were rinsed, mounted in Mowiol (Roth, 0713), and scanned on a Zeiss LSM 710 confocal microscope.

Results

Morphology of hugin-producing neurons and their input and output compartments.

The *hugin* gene is expressed in only 20 neurons in the CNS. This population comprises interneurons, which are confined within the CNS, as well as efferent neurons, which leave the CNS. The interneuron type can be subdivided into those projecting to the protocerebrum (hugin-PC, 8 neurons) or the ventral nerve cord (hugin-VNC, 4 neurons). The efferent type can be subdivided into those projecting to the ring gland (hugin-RG, 4 neurons) or the pharynx (hugin-PH, 4 neurons) (Fig. 2A) [41]. Based on these morphological features, we first reconstructed all hugin neurons in a ssTEM volume covering an entire larval CNS and the major neuroendocrine organ, the ring gland (Fig. 1B; see materials and methods for details). We then localized synaptic sites, which could be readily identified as optically dense structures [42]. Comparing neurons of the same class, we found the number as well as the distribution of pre- and postsynaptic sites to be very similar among hugin neurons of the same class (Fig. 2C-E). Presynaptic sites are generally defined as having small clear core vesicles (SCVs) containing classic small molecule transmitter for fast synaptic transmission close to the active zone [42]. Efferent hugin neurons (hugin-RG and hugin-PH) showed only few small presynaptic sites (< 1 average/neuron) within the CNS and we did not observe any SCVs. For hugin-RG neurons, we did find presynaptic sites but outside the CNS at their projection target, the ring gland. Many of these presynaptic sites had no corresponding postsynaptic sites in adjacent neurons. Instead they bordered haemal space indicating neuroendocrine release (S1 Fig A). The configuration of hugin-PH terminals is unknown as their peripheral target was not part of the ssTEM volume. For the interneuron classes (hugin-PC and hugin-VNC),

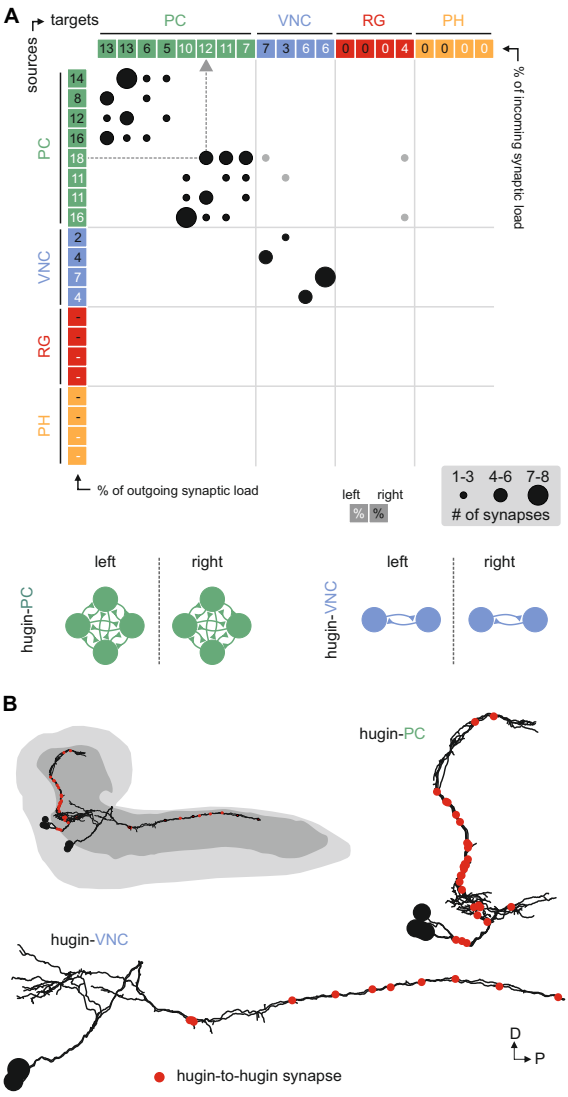

Figure 3. Hugin neurons synapse axo-axonically reciprocally within-class but not across-class. **A**, Connectivity matrix of hugin to hugin connections. Each row indicates number of synaptic connections of given hugin neuron to other hugin neurons. Connections that could not be recapitulated for both hemisegments are grayed out. Numbers in colored boxes give incoming (x-axis) and outgoing (y-axis) synaptic load (% of synapses) of the respective hugin neuron. Hugin to hugin contacts are made between hugin interneurons of the same class, not between classes (see schematic). Note that efferent hugin neurons, hugin-RG and hugin-PH, do not have presynaptic sites. **B**, Distribution of hugin-hugin synapses. Synapses connecting hugin-PC to hugin-PC and hugin-VNC to hugin-VNC neurons are axi-axonic. Only neurons of one hemisegment are shown.

we found such SCVs at larger presynaptic sites, indicating that they employ classic neurotransmitter in addition to the hugin peptide (S1 Fig B,C). Hugin-PC and hugin-VNC neurons' projections represent mixed synaptic input-output compartments as they both showed pre- as well as postsynaptic sites along their neurites (Fig. 2D,E).

All hugin neurons receive inputs within the subesophageal zone [SEZ, previously called subesophageal ganglion (SOG)], a chemosensory center that also houses the basic neuronal circuits generating feeding behavior [54]. However, only the hugin-PC neurons showed considerable numbers of synaptic outputs in the SEZ, thus making these neurons good candidates for previously reported effects on feeding [20, 55] (Fig. 2E).

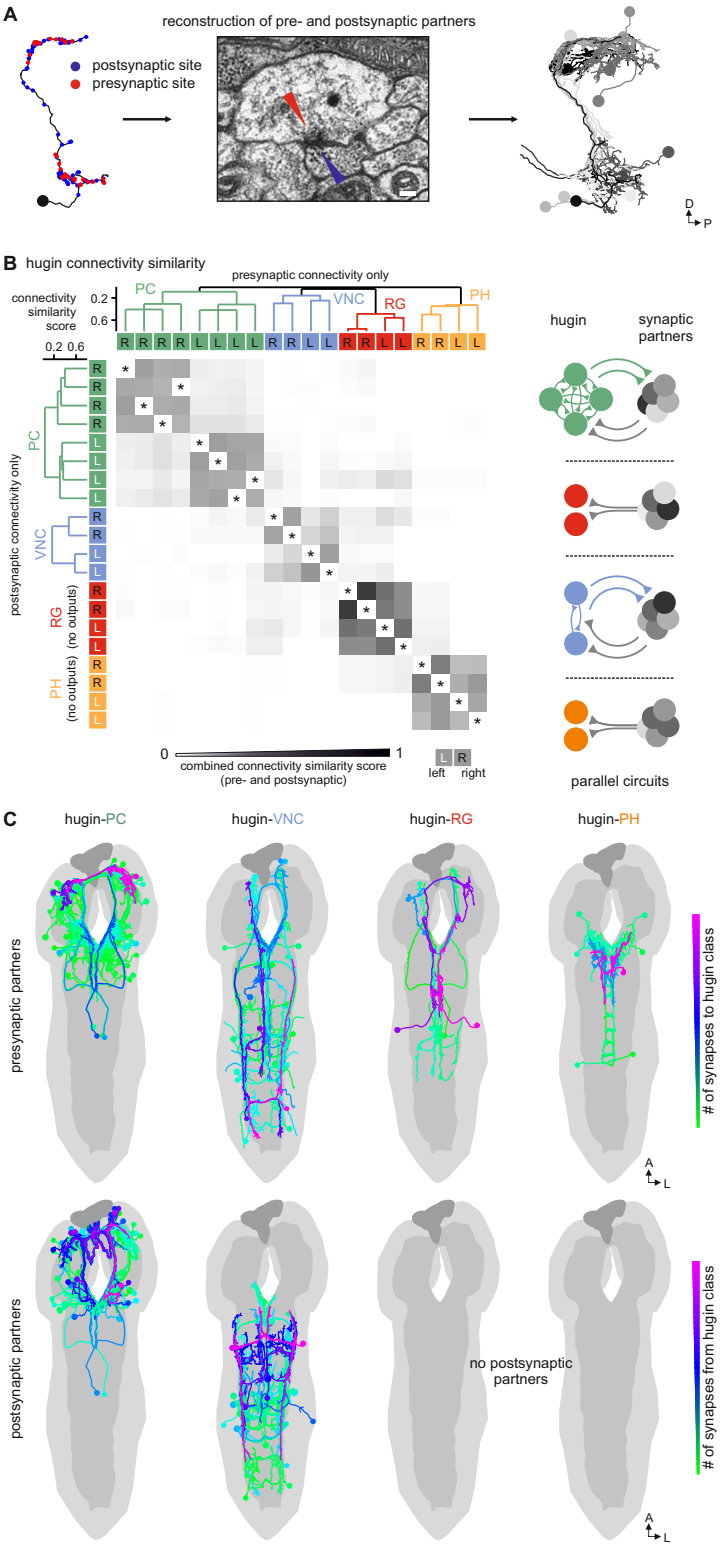

Figure 4. Each hugin class is part of a distinct micro-circuit, weakly or not at all connected to those of the other classes. **A** Exemplary pre- and postsynaptic partners of a single hugin neuron. **B**, Overlap of synaptic partners of individual hugin neurons as measured by connectivity similarity score. High similarity score indicates a large fraction of shared synaptic partners connected by similar numbers of synapses. Neurons are ordered by dendrogram of similarity score of pre- (x-axis) and postsynaptic (y-axis) partners. Matrix shows combined pre- and postsynaptic similarity score. Self-self comparisons were omitted (asterisks). Hugin classes connect to unique sets of pre- and postsynaptic partners. Neurons of each hugin class have the same synaptic partners and there is little to no overlap with other classes (see schematic). **C**, All pre- and postsynaptic partners by hugin class. Neurons are color-coded based on total number of synapses to given hugin class [minimum=1; maximum (pre-/postsynaptic): hugin-PC=52/16, hugin-VNC=21/18, hugin-RG=39/none, hugin-PH=23/none]. Hugin-RG and hugin-PH neurons do not have postsynaptic partners within the CNS.

Hugin classes form distinct units that share synaptic partners.

Reconstruction of hugin neurons and localization of synaptic sites revealed that neurons of the two interneuron classes, hugin-PC and hugin-VNC, were reciprocally connected to ipsilateral neurons of the same class (Fig. 3A, S1 Fig E,F). These axo-axonic synaptic connections made up a significant fraction of each neuron's synaptic load (% of total synapses), implying that their activity might be coordinately regulated.

We therefore further explored the different classes within the population of hugin-producing neurons, asking whether hugin classes establish functional units or whether they are independently wired. To this end, we reconstructed 177 pre- and postsynaptic partners of hugin neurons (Fig. 4A, see materials and methods for details). First, we found that neurons of the same hugin class were connected to the same pre- and postsynaptic partners. Furthermore, most synaptic partners were connected exclusively to neurons of a single hugin class (Fig. 4B). However, within each hugin class, connectivity was not entirely stereotyped as the number of synapses from/to single hugin neurons varied for each pre- or postsynaptic partner (S2 Fig). Second, pre- and postsynaptic partners of each hugin class resided in different parts of the CNS (Fig. 4C). These findings show that neurons of each hugin class form complex microcircuits that are largely separate from one another.

Hugin neurons receive chemosensory synaptic input.

Hugin neurons have a significant number of incoming synapses (63 +/- 22%) within the SEZ. This region in the CNS is analogous to the brainstem and represents a first order chemosensory center that receives input from various sensory organs [25]. We therefore searched for sensory inputs to hugin neurons and found a total of 57 afferent neurons that made synaptic contacts onto hugin neurons (Fig. 5A). Two major groups emerged: a larger, morphologically heterogeneous group consisting of afferent neurons projecting through one of the pharyngeal nerves, the antennal nerve and, unexpectedly, a second, more homogeneous group entering the CNS through abdominal (but not thoracic) nerves. We observed that the reconstructed afferent presynaptic partners of hugin neurons covered different parts of the SEZ. Thus, we sought to cluster these afferent neurons by computing the similarity in spatial distribution of their synaptic sites, termed synapse similarity score.

Clustering based on synapse similarity score resulted in 7 different groups, each of them covering distinct parts of the SEZ (Fig. 5B; see material and methods for details). To address the issue of the origin of identified sensory inputs, we compared our data with previous descriptions of larval sensory neurons. It is well established that abdominal nerves innervate internal and external sensory organs of the peripheral nervous system. This includes proprioceptive (chordotonal), tactile, nociceptive (multi dendritic neurons) and a range of sensory neurons whose function is yet unknown [56–58]. To our knowledge no abdominal sensory neurons with projections into the SEZ such as the one observed presynaptic to hugin have been described. However, the majority of afferent neurons synapsing onto hugin neurons stems from the antennal nerve. This pharyngeal nerve carries the axons of gustatory receptor neurons (GRNs) from internal pharyngeal sensilla as well as those of olfactory receptor neurons (ORNs) and other GRNs from the external sensory organs (Fig. 5C,D) [59, 60]. For ORNs, it is well established that they target specific areas of the antennal lobes - the *Drosophila* neuropil corresponding to the mammalian olfactory bulb - and thus partition this neuropil into multiple glomeruli [60]. For GRNs and their target neuropil, the SEZ, a similar organization exists although it has been studied in less detail [59, 61]. None of the afferent inputs to hugin neurons are ORNs since they are not associated with the antennal lobes (S3 Fig).

Instead, the antennal nerve neurons exhibited strong morphological similarities with the large, heterogeneous population of GRNs [59, 62]. We thus compared our groups with previously defined light microscopy-based gustatory compartments of the SEZ [59]. Groups 2 and 6, which cover the anterior-medial SEZ, likely correspond to two areas described as the target of GRNs from internal pharyngeal sensilla only (Fig. 5D). The remaining groups were either not previously described or difficult to unambiguously align with known areas. Our division into groups is also reflected at the level of their connectivity to hugin neurons: sensory neurons of group 1 have synaptic connections to both hugin-PC and hugin-VNC neurons. Groups 2-5, encompassing the previously described pharyngeal sensilla, are almost exclusively connected to hugin-PC neurons.

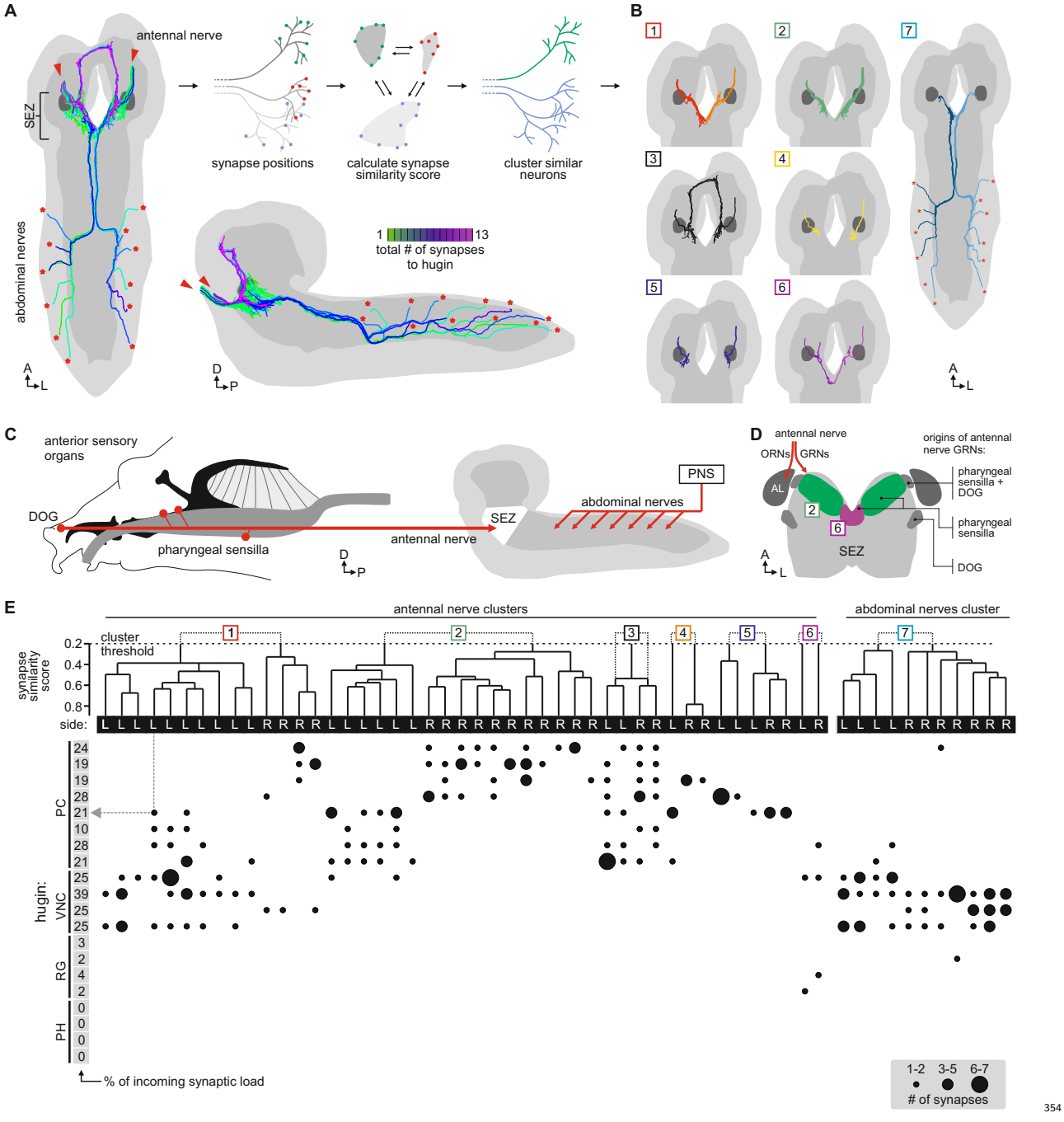

Figure 5. Each class of hugin neurons receives inputs from distinct subsets of sensory neurons. **A**, Sensory inputs to hugin neurons enter the CNS via the antennal nerve (arrowheads) and abdominal nerves (asterisks). Neurons are color-coded based on total number of synapses to hugin neurons. **B**, Morphology of sensory neurons clustered based on a synapse similarity score computed from the spatial overlap of synaptic sites between two neurons. **C**, Potential origins of sensory inputs onto hugin neurons. The antennal nerve collects sensory axons from the dorsal organ ganglion (DOG) and pharyngeal sensilla. Abdominal nerves carry afferents from the abdominal segments of the peripheral nervous system (PNS). **D**, Target areas of antennal nerve chemosensory organs in the subesophageal zone (SEZ). Olfactory receptor neurons (ORNs) terminate in the antennal lobes (AL). Gustatory receptor neurons (GRNs) from different sensory organs cover distinct parts of the SEZ. Modified from [59].**E**, Connectivity matrix of sensory neurons onto hugin. Sensory neurons are ordered by dendrogram of synapse similarity score and rearranged to pair corresponding cluster of left (L) and right (R) hemisegment. Each row of the matrix shows the number of synaptic connections onto a single hugin neuron. Numbers in gray boxes along y-axis give percentage of synaptic input onto each hugin neuron represented as one neuron per row. Shows only sensory neurons that have at least a single more-than-2-synapse connection to hugin neurons. See text for further details.

Group 6 sensory neurons make few synapses onto hugin-RG neurons. Group 7, encompassing the abdominal afferent neurons, is primarily presynaptic to hugin-VNC (Fig. 5E).

Overall, the efferent type hugin neurons, hugin-PH and hugin-RG, receive little to no sensory input. In contrast, the interneuron type hugin neurons, hugin-PC and hugin-VNC, receive a significant fraction of their individual incoming synaptic load (up to 39%) from sensory neurons. Summarizing, we found two out of four types of hugin neurons to receive synaptic input from a large heterogeneous but separable population of sensory neurons, many of which are GRNs from external and internal sensory organs.

Dual synaptic and peptide-receptor connection to the neuroendocrine system.

NMU has been well studied in the context of its effect on the hypothalamo-pituitary axis. We therefore looked for analogous motifs among the downstream targets of hugin neurons. The cluster of hugin-PC neurons project their neurites from the SEZ to the protocerebrum, terminating around the pars intercerebralis. Medial neurosecretory cells (mNSCs) in this area constitute the major neuroendocrine center in the CNS, analogous to the mammalian hypothalamus, and target the neuroendocrine organ of *Drosophila*, the ring gland [26]. Three different types of mNSCs produce distinct neuropeptides in a non-overlapping manner: 3 mNSCs produce diuretic hormone 44 (DH44), 2 mNSCs produce Dromyosuppressin (DMS) and 7 mNSCs produce *Drosophila* insulin-like peptides (Dilps, thus called insulin-producing cells [IPCs]) (Fig. 6A) [63]. We found that hugin-PC neurons make extensive synaptic connections onto most but not all of the mNSCs (Fig. 6B; S1 Fig G,H). mNSCs of the pars intercerebralis derive from the same neuroectodermal placodes and develop through symmetric cell division [64]. Among the mNSCs, IPCs have been best studied: they have ipsilateral descending arborizations into the SEZ and project contralaterally into the ring gland [2]. In contrast, morphology of DH44- or DMS-producing mNSCs has been described in less detail. We found all reconstructed mNSCs to have the exact same features, rendering them morphologically indistinguishable (Fig. 6C). To assign identities to the reconstructed mNSCs, we hypothesized that, similar to hugin neurons, the three types of mNSCs would differ in their choice of synaptic partners. We therefore reconstructed all presynaptic partners and calculated the connectivity similarity score between the mNSCs. Clustering with this similarity in connectivity resulted in three groups comprising 3, 2 and 7 neurons, coinciding with the number of neurons of the known types of mNSCs. We thus suggest that the group of 3 represents DH44-producing cells, the group of 2 represents DMS-producing cells and the group of 7 represents the IPCs (Fig. 6D).

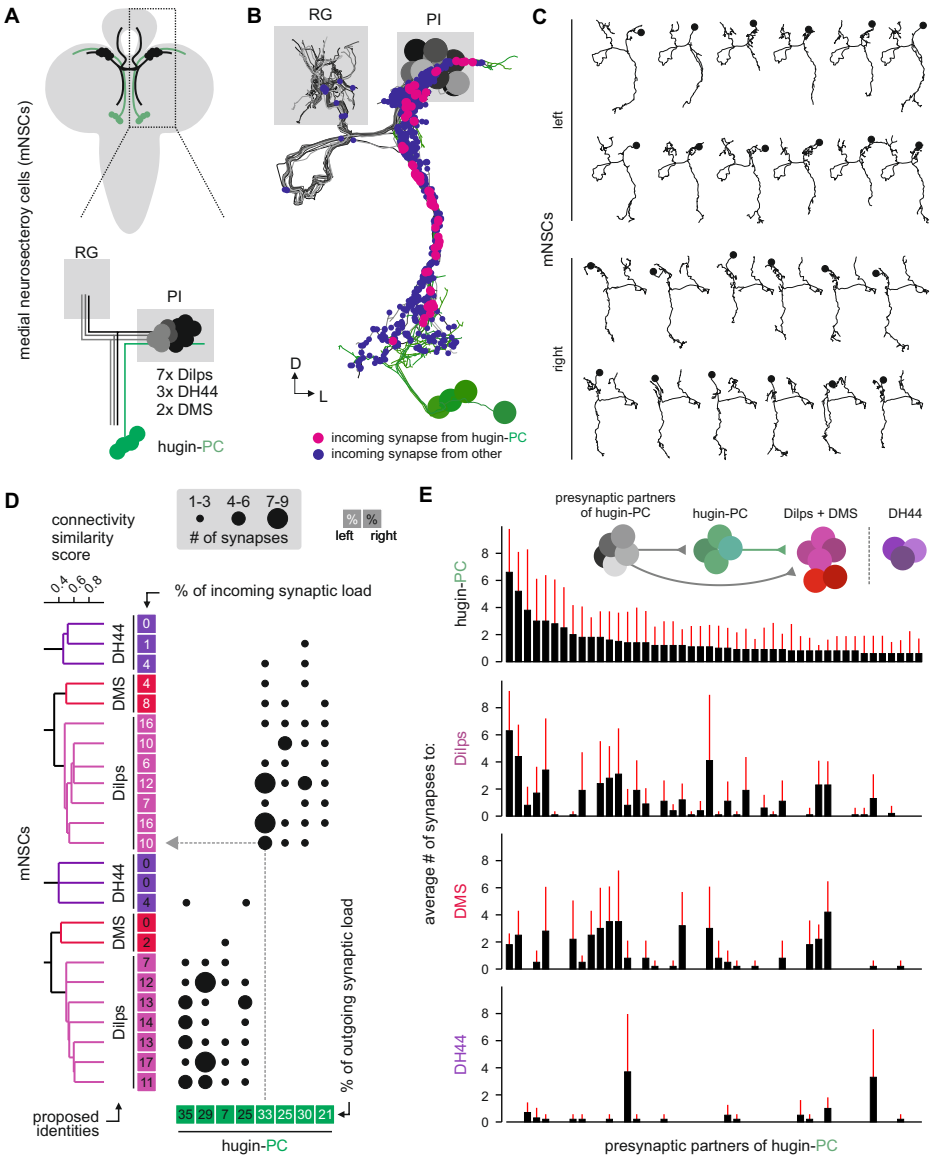

Figure 6. Hugin-PC neurons synaptically connect to all insulin-producing neurosecretory neurons. A, Schematic of medial neurosecretory cells (mNSCs) located in the pars intercerebralis (PI). mNSCs produce *Drosophila* insulin-like peptides (Dilps), diuretic hormone 44 (DH44) and Dromyosuppressin (DMS). **B**, EM-reconstruction of all mNSCs. Hugin-PC neurons make axo-axonic synapses onto mNSCs. **C**, All mNSC are sibling neurons derived from the same neuroectodermal placode via symmetric cell division. Ipsilateral siblings present similar arborizations, making morphological identification impossible. **D**, Connectivity matrix of hugin-PC to mNSCs. mNSCs are ordered by dendrogram of connectivity similarity of all presynaptic partners. Proposed identity is based on connectivity similarity clustering into groups of 3 DH44-, 2 DMS- and 7 Dilps-producing cells (see text for details). In the matrix, each row indicates number of synapses from a single hugin-PC neuron onto a mNSCs. Numbers in boxes give percentage of outgoing/incoming synaptic load (% of total synapses) represented in each column or row, respectively. **E**, Connectivity between presynaptic partners of hugin-PC neurons and mNSCs. Each column across all four graphs represents a presynaptic partner of hugin-PC. Graphs show average number of synapses to hugin-PC, DH44-, DMS- and Dilps-producing neurons of given presynaptic partner. Whiskers represent standard deviation. hugin-PC neurons share inputs with Dilps- and DMS-producing neurons but not with DH44-producing neurons.

On this basis, hugin-PC neurons make extensive synaptic contacts to the IPCs but less so to DMS- and DH44-producing mNSCs. Overall, synapses between hugin-PC neurons onto mNSCs constitute a large fraction of their respective synaptic loads (hugin-PC: up to 35%; mNSCs: up to 17%). In support of a tight interconnection between hugin neurons and these neuroendocrine neurons, we found that most of hugin-PC neurons' presynaptic partners are at the same time also presynaptic to mNSCs (Fig. 6E). These findings demonstrate that the neuroendocrine system is a major target of hugin neurons.

Unlike the small molecule messengers used for fast synaptic transmission, neuropeptides - such as hugin - are thought to be released independent of synaptic membrane specializations and are able to diffuse a considerable distance before binding their respective receptors. However, it has been proposed that neuropeptides released from most neurons act locally on cells that are either synaptically connected or immediately adjacent [65]. We therefore asked whether the synaptic connections between hugin-PC neurons and mNSCs would have a matching peptide-receptor

connection. The *hugin* gene encodes a prepropeptide that is post-translationally processed to produce an eight-amino-acid neuropeptide, termed Pyrokinin-2 (PK-2) or hugin neuropeptide [66]. This hugin neuropeptide has been shown to activate the *Drosophila* G-Protein coupled receptor (GPCR) CG8784/PK2-R1 in mammalian cell systems, but the identities of the target neurons expressing the receptor remain unknown [67]. To address this, we used two independent methods to generate transgenic fly lines, *CG8784-GAL4::p65* and *CG8784-6kb-GAL4*, driving expression under control of putative *CG8784* regulatory sequences (Fig. 7A; S4 Fig). Both *CG8784 GAL4* lines drive expression of a GFP reporter in a prominent cluster of cells in the pars intercerebralis. Double stainings show that this expression co-localizes with the peptides produced by the three types of mNSCs: Dilp2, DH44 and DMS (Fig. 7B-D; S4 Fig). These findings indicate that hugin-PC neurons employ both classical synaptic transmission and peptidergic signaling to target neurons of the neuroendocrine center.

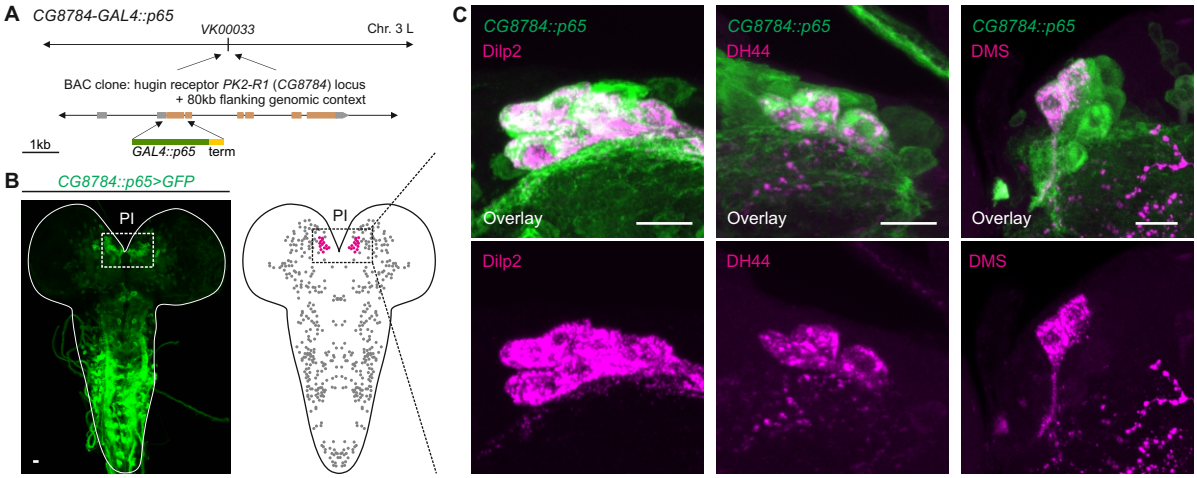

Figure 7. Hugin neurons target neurosecretory cells via peptide-receptor transmission in addition to synaptic connections. A, Promoter-based hugin receptor PK2-R1 driver line *CG8784-Gal4::p65* was generated by replacing the first coding exon of the *CG8784* loci with *GAL4* in a BAC clone containing 80kb flanking genomic context and integrating the final BAC into *attP* site *VK00033*. **B**, *CG8784-Gal4::p65* drives expression in cells of the pars intercerebralis (PI). **C**, Co-staining with *Drosophila* insulin-like peptide 2 (Dilp2), diuretic hormone 44 (DH44) and Dromyosuppressin (DMS). These peptides are produced by medial neurosecretory cells (mNSCs) in a non-overlapping manner. *CG8784-Gal4::p65* drives expression in all mNSCs of the PI. Scale bars in A and B represent 10 μm.

Neuropeptides are produced in the soma and packaged into dense core vesicles (DCVs) before being transported to their release sites [65]. We found 98% of the synapses between hugin-PC and mNSCs to have DCVs within 1000 nm radius to the presynaptic sites (average # of DCVs/synapse: 15.5), opening up the possibility of co-transmission of peptide and classical neurotransmitter [68] (Fig. 8A). Further exploring the spatial relationship between DCVs and synapses, we observed that for both interneuron type hugin classes (hugin-PC and hugin-VNC) DCVs localized close to presynaptic sites. This was often the case at local swellings along the main neurites which featured multiple pre- and postsynaptic sites, as well as close-by DCVs (Fig. 8B,C). It is conceivable that such complex local synaptic circuitry might enable local peptide release. Next, we measured the distance to the closest presynaptic site for each DCV. The majority of DCVs in hugin-PC and hugin-VNC neurons was localized within approximately 2000 nm from the next presynaptic site (Fig. 8D). However, most DCVs

were probably too distant from presynaptic sites to be synaptically released, suggesting para- and non-synaptic release [69, 70] (S1 FigD).

Taken together, these findings show that the neuroendocrine system is indeed a major downstream target of hugin neurons and that this is achieved by a combination of synaptic and GPCR-mediated peptidergic transmission (Fig. 8E).

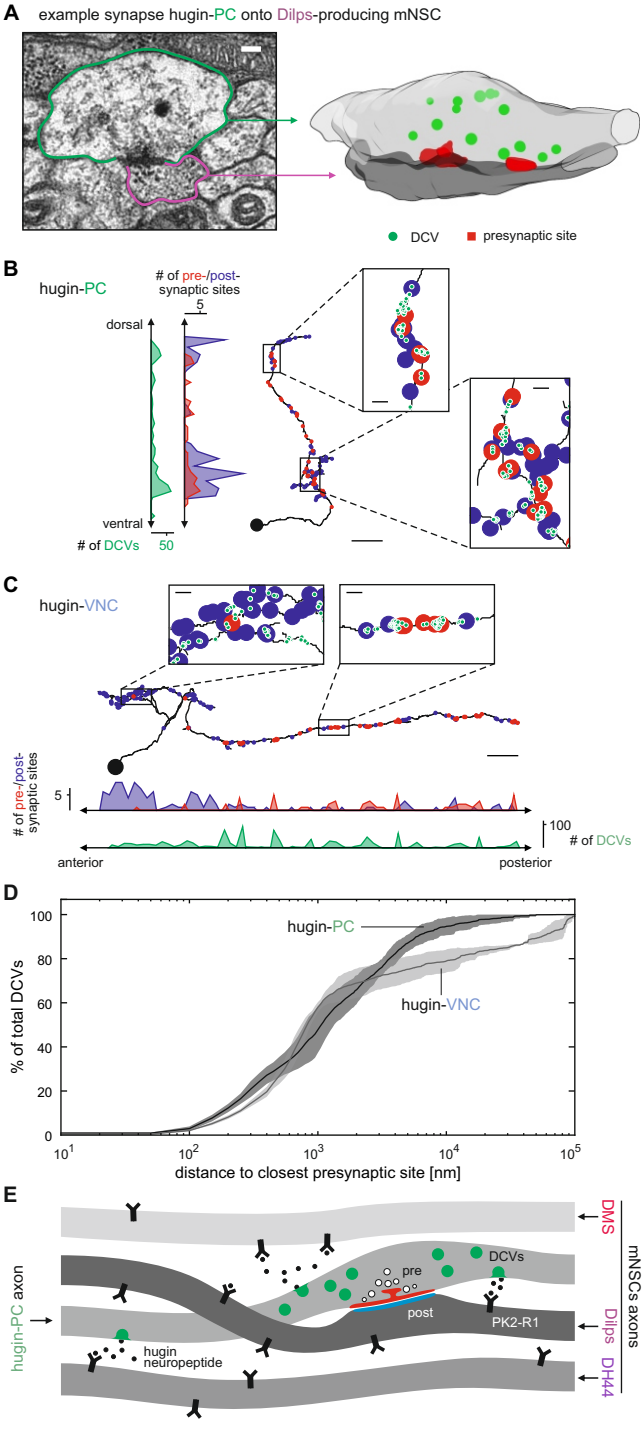

Figure 8. Dense core vesicles localize close to but not at presynaptic sites. **A**, Volume reconstruction of example synapse between hugin-PC neuron and medial neurosecretory cells (mNSCs) producing *Drosophila* insulin-like peptides (Dilps) shows dense core vesicles (DCV) in the vicinity of synaptic densities. Scale bar represents 100 μm. **B,C**, Distribution of pre- and postsynaptic sites and DCVs for a single hugin-PC (B) and hugin-VNC (C) neuron. DCVs localize close to presynaptic sites. Scale bars represent 10 μm (overview) and 1 μm (inlets). **D**, For each DCV the distances to the closest presynaptic was calculated. Graph shows percentage of DCVs within given distance to closest presynaptic site. Vesicles in the soma and the proximal part of the main neurite were excluded. Only a small fraction of DCVs are in very close proximity to presynaptic sites, indicating para- and non-synaptic rather than synaptic release. Note that hugin-RG and hugin-PH neurons were excluded due to lack of presynaptic sites within the CNS. Dashed vertical lines mark 50% fraction. Envelopes represent standard deviation. **E**, Summarizing schematic and model. Hugin-PC neurons make classical chemical synapses almost exclusively onto Dilps-producing mNSCs. Additionally, all mNSCs express hugin receptor PK2-R1 (*CG8784*) and are often in close vicinity to hugin neurites, allowing para- or non-synaptically released hugin neuropeptide to bind.

Discussion

Organizational principles of peptidergic networks.

Almost all neurons in *Drosophila* being uniquely identifiable and stereotyped enabled us to identify and reconstruct a set of 20 peptidergic neurons in an ssTEM volume spanning an entire larval CNS [71, 72]. These neurons produce the neuropeptide hugin and have previously been grouped into four classes based on their projection targets (Fig. 2A) [41]. Our analysis allows detailed comparisons between neurons of the same class to address why the CNS sustains multiple copies of morphologically very similar neurons. We found that neurons of the same morphological class (a) were very similar with respect to the distribution of synaptic sites, (b) shared a large fraction of their pre- and postsynaptic partners and (c) in case of the interneuron classes (hugin-PC and hugin-VNC), neurons were reciprocally connected along their axons with other neurons of the same class. Similar features have been described for a population of neurons which produce crustacean cardioactive peptide (CCAP) in *Drosophila* [73]. The reciprocal connections as well as the overlap in synaptic partners indicate that the activity of neurons within each interneuron class is coordinately regulated and could help sustain persistent activity within the population. In the mammalian pyramidal network of the medial prefrontal cortex, reciprocal connectivity between neurons is thought to contribute to the networks robustness by synchronizing activity within subpopulations and to support persistent activity [74]. In the hypothalamus, interconnectivity and shared synaptic inputs, as described here for each hugin class, has been demonstrated for peptidergic neurons producing gonadotropin-releasing hormone (GnRH) and oxytocin [75, 76]. Likewise, this is thought to synchronize neuronal activity and allow periodic bursting.

In addition, our results reinforce previous findings that specific phenotypes can be assigned to certain classes of hugin neurons: hugin-VNC neurons were shown to increase locomotion motor rhythms whereas the effect on feeding behavior has been attributed to one or more of the other hugin classes [20]. In accordance with this, we found that all hugin classes have their own unique sets of postsynaptic partners. This suggests that not only hugin-VNC but all hugin classes have specific, separable effects. One conceivable scenario would have been that each hugin class mediates specific aspects of an overall "hugin phenotype". This would require that under physiological conditions all hugin classes are coordinately active. However, we did not find any evidence of such coordination on the level of synaptic connectivity. Instead, each hugin class forms an independent microcircuit with its own pre- and postsynaptic partners. We thus predict that each class of hugin-producing neurons has a distinct context in which it is relevant for the organism.

Co-transmission of neuropeptide and small molecule transmitter.

A neural network is a highly dynamic structure and is subject to constant change, yet it is constrained by its connectivity and operates within the framework defined by the connections made between its neurons [77]. On one hand this connectivity is based on anatomical connections formed between members of the network, namely synapses and gap junctions. On the other hand, there are non-anatomical connections that do not require physical contact due to the signaling molecules, such as neuropeptides/-hormones, being able to travel considerable distances before binding their receptors [65]. Our current integrated analysis of the operational framework for a set of neurons genetically defined by the expression of a common neuropeptide, positions hugin-producing neurons as a novel component in the regulation of neuroendocrine

activity and the integration of sensory inputs. We show that most hugin neurons receive chemosensory input in the subesophageal zone, the brainstem analog of *Drosophila* [25]. Of these, one class is embedded into a network whose downstream targets are medial neuroendocrine cells (mNSCs) of the pars intercerebralis, a region analog to the mammalian hypothalamus [26]. We found that hugin neurons target mNSCs by two mechanisms. First, by classic synaptic transmission using a yet-to-be-identified small molecule transmitter as indicated by the occurrence of small clear core vesicles at presynaptic sites. Second, by non-anatomical transmission using a peptide-receptor connection, as demonstrated by the expression of hugin receptor PK2-R1 (*CG8784*) in mNSCs. Strikingly, while PK2-R1 is expressed in all mNSCs, synaptic connections are made only between hugin neurons and a subset of mNSCs. Given that all mNSCs are morphologically similar, this implies the involvement of cell-cell-recognition mechanisms to ensure establishment of the correct synaptic connections. This mismatch in synaptic vs. peptide targets among the NSCs suggests an intricate influence of hugin-producing neurons on this neuroendocrine center. In favor of a complex regulation is that those mNSCs that are synaptically connected to hugin neurons also express a pyrokinin-1 receptor (PK1-R, *CG9918*) which, like PK2-R1, is related to mammalian neuromedin U receptors [78–80]. There is some evidence that PK1-R might also be activated by the hugin neuropeptide, adding another regulatory layer [79].

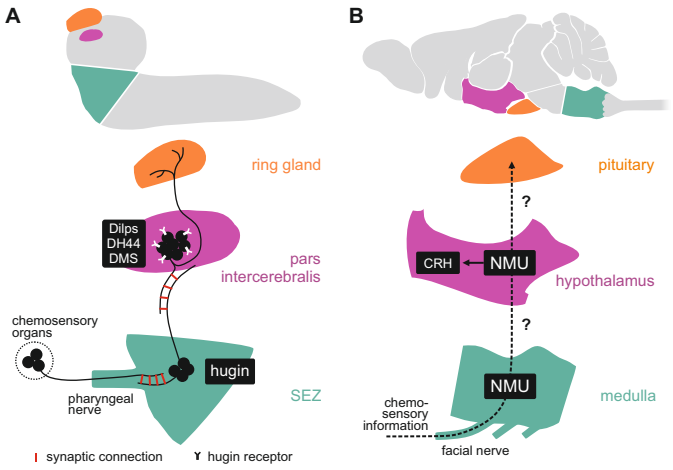

Figure 9. Summary of hugin connectivity and hypothetical implications for neuromedin U in mammals. A, Hugin neurons link chemosensory neurons that enter the subesophageal zone (SEZ) and neuroendocrine cells of the pars intercerebralis by synaptic as well as peptide-receptor connections. **B**, The effect of neuromedin U (NMU) on feeding and physical activity originates in the hypothalamus where it causes release of corticotropin-releasing hormone (CRH). CRH is a homolog of diuretic hormone 44 (DH44) in *Drosophila* which is downstream target of hugin. NMU-positive fibers have been found in a chemosensory center of the medulla. It remains to be seen if, similar to hugin neuron, NMU neurons serve as a link between chemosensory and neuroendocrine system.

The concept of multiple messenger molecules within a single neuron is well established and appears to be widespread among many organisms and neuron types [68, 81–84]. Nevertheless, there are only very few examples of simultaneous employment of neuropeptide and small molecule transmitter in which specific targets of both messengers have been investigated at single cell level. Reminiscent of our observations is the situation in the frog sympathetic ganglia, where preganglionic neurons use both acetylcholine (ACh) and a neuropeptide to target so-called C cells but only the neuropeptide additionally targets B cells. In both targets the neuropeptide elicits late, slow excitatory postsynaptic potentials [85]. It is conceivable that hugin-producing neurons act in a similar manner by exerting a slow but longer lasting effect on all mNSC and a fast, transient effect exclusively on synaptically connected mNSC.

In addition to the different timescales that neuropeptides and small molecule transmitters operate on, they can also be employed under different circumstances. It is commonly thought that low frequency neuronal activity is sufficient to trigger fast transmission using small molecule transmitters, whereas slow transmission employing neuropeptides require high frequency activity [68]. Hugin-producing neurons could employ peptidergic transmission only as a result of strong excitatory (e.g. sensory) input. However there are cases in which base activity of neurons is already sufficient for graded neuropeptide release. *Aplysia* ARC motor neurons employ ACh as well as neuropeptides and ACh is released at lower firing rates than the neuropeptide.

Nevertheless, peptide release already occurs at the lower end of the physiological activity of those neurons [86, 87]. It remains to be seen how synaptic and peptidergic transmission in hugin neurons relate to each other. The present study is one of very few detailed descriptions of differential targets of co-transmission and - to our knowledge - the first of its kind in *Drosophila*. We hope these findings in a genetically tractable organism will provide a basis for elucidating some of the intriguing modes of action of peptidergic neurons.

Hugin as functional homolog of central neuromedin U.

The mammalian homolog of hugin, neuromedin U (NMU), is found in the CNS as well as in the gastrointestinal tract [22]. Its two receptors, NMUR1 and NMUR2, show differential expression. NMUR2 is abundant in the brain and the spinal cord whereas NMUR1 is expressed in peripheral tissues, in particular in the gastrointestinal tract [88]. Both receptors mediate different effects of NMU. The peripheral NMUR1 is expressed in pancreatic islet β cells in humans and allows NMU to potently suppress glucose-induced insulin secretion [78]. The same study also showed that Limostatin (Lst) is a functional homolog of this peripheral NMU in *Drosophila*: Lst is expressed by glucose-sensing, gut-associated endocrine cells and suppresses the secretion of insulin-like peptides. The second, centrally expressed NMU receptor, NMUR2, is necessary for the effect of NMU on food intake and physical activity [18, 89]. In this context, NMU is well established as a factor in regulation of the hypothalamo-pitiutary axis [32, 33] and has a range of effects in the hypothalamus, the most important being the release of corticotropin-releasing hormone (CRH) [17, 90]. We show that a subset of hugin-producing neurons targets the pars intercerebralis, the *Drosophila* analog of the hypothalamus, in a similar fashion: neuroendocrine target cells in the pars intercerebralis produce a range of peptides, including diuretic hormone 44 which belongs to the insect CRH-like peptide family [51] (Fig. 9). Given these similarities, we argue that hugin is a functional homolog of central NMU just as Lst is a functional homolog of peripheral NMU. Demonstration that central NMU and hugin circuits share similar features beyond targeting neuroendocrine centers, e.g. the integration of chemosensory inputs, will require further studies on NMU regulation and connectivity.

Previous work on vertebrate and invertebrate neuroendocrine centers suggests that they evolved from a simple brain consisting of cells with dual sensory/neurosecretory properties, which later diversified into optimized single-function cells [36]. There is evidence that despite the increase in neuronal specialization and complexity, connections between sensory and endocrine centers have been conserved throughout evolution [35, 37, 38]. We argue that the connection between endocrine and chemosensory centers provided by hugin neurons represents such a conserved circuit that controls basic functions like feeding, locomotion, energy homeostasis and sex.

In summary, our findings should encourage research in other model systems, such as the involvement of NMU and NMU homologs in relaying chemosensory information onto endocrine systems.

Supporting Information

Please see supplemental PDF for figures.

S1 Fig

Examples of synaptic sites in the ssTEM volume. A, Presynaptic density of a hugin-RG neuron bordering haemal space within the ring gland. **B,C**, Examples of

presynaptic sites with small clear core vesicles for a hugin-PC and hugin-VNC neuron. **D**, Example of a presynaptic site with close-by dense core vesicles. **E,F**, Examples of synaptic connections between hugin neurons. **G,H**, Examples of synaptic connections from hugin-PC neurons onto insulin-producing cells (IPCs). Scale bars represent 100nm.

S2 Fig

Number of synapses constituting connections to/from a shared partners varies within each hugin class. Each data point represents a pre- or postsynaptic partner of neurons of given hugin class. Most of these partners connect to all hugin neurons of a single class but these connections vary in the number of synaptic contacts they constitute. Plotted is the average number of synapses over all hugin neurons of that class against the standard deviation.

S3 Fig

Clustered synapses of sensory inputs to hugin neurons cover discrete parts of the subesophageal zone. Distribution of synaptic sites of afferent neurons as clustered in Fig 5. Each dot indicates a synaptic site. Dot size decreases with distance to its cluster's center. Note, that the sensory neurons presynaptic to hugin neurons innervate areas medial and ventral to the antennal lobes.

S4 Fig

Hugin receptor line *CG8784-6kb-GAL4* drives expression in medial neurosecretory cells (mNSCs) of the pars intercerebralis (PI) similar to *CG8784-GAL4:p65*. **A**, Immunolabeling and semi-schematic representation of hugin receptor *CG8784-6kb-GAL4* expression pattern. In comparison with the *CG8784-GAL4:p65* BAC line (Fig. 7A,B), this line shows a more restricted expression. However, the same prominent cluster of neurons (magenta) of the PI is labeled but only few additional cells in the ventral nerve cord (grey circles). **B-D**, Double staining of *CG8784-6kb-GAL4* driving GFP expression suggests expression of *CG8784* in (B) *Drosophila* insulin-like peptide- (Dilp2), (C) diuretic hormone 44- (DH44) and (D) Dromyosuppressin-producing (DMS) mNSCs of the PI. Scale bars represent 10μm (A) and 5μm (B-D).

S5 Fig

Neurons connected by more than two synapses to hugin neurons were reliably reconstructed. **A**, Distribution of synaptic connections to/from hugin neurons. X-axis gives number of synapse per connection and y-axis occurrence. Reconstruction of the pre- or postsynaptic neuron was attempted for every hugin synapse. Red fraction was completely reconstructed, black fraction was not successfully reconstructed due to either errors/ambiguity in the ssTEM data set (e.g. missing sections) or failure to find a matching pair of neurons in both hemisegments. The fraction of unaccounted synapses strongly decreases from 2 to 3 synapses per connection. We therefore subsequently applied a threshold of at least a single more-than-two-synapses connection (did not apply to sensory neurons).**B**, Completeness of reconstruction of pre- and postsynaptic partners for each hugin neuron. Values in the table give the percentages of pre- and postsynaptic sites that connect to a above-threshold partner of hugin neurons which was successfully reconstructed.

S6 Neuron atlas

Supplementary Atlas. Morphology and connectivity of reconstructed neurons. Reconstructions of **(A)** hugin-PC, **(B)** hugin-VNC, **(C)** hugin-RG, **(D)** hugin-PH neurons, **(E)** insulin-producing cells (IPCs), **(F)** DH44-producing cells, **(G)** DMS-producing cells, **(H)** antennal nerve (AN) sensory neurons, **(I)** abdominal nerve sensory neurons, **(J)** paired interneurons and **(K)** unpaired medial interneurons. A dorsal view of each cell is shown on the left, and a frontal view on the right. Outline of the nervous system and the ring gland are shown in grey and dark grey, respectively. Number in the table is the number of synapses of given neurons onto (left) and from (right) the hugin neuron indicated in the row. Neurons are displayed as corresponding pairs of the left/right hemisegment with the exception of afferent neurons and unpaired medial interneurons.

Acknowledgments

We thank Jan Veenstra and Liliane Schoofs for their gifts of antisera, and Barret Pfeiffer and Gerry Rubin for plasmids and fly lines. We thank SFB 645 and 704, DFG Cluster of Excellence ImmunoSensation, DFG grant PA 787 and Howard Hughes Medical Institute for financial support. We also thank Lucia Torres, Gaia Tavosanis, Gáspár Jékely, Gregory Jefferis, Ingo Zinke, Andreas Schoofs, Sebastian Hückesfeld, Scott Sternson, Christian Wegener, Volker Hartenstein and Nicholas Strausfeld for critical comments on earlier versions of this manuscript. The EM image data is available via the Open Connectome Project (http://www.openconnectomeproject.org).

References

1. Ikeya T, Galic M, Belawat P, Nairz K, Hafen E. Nutrient-dependent expression of insulin-like peptides from neuroendocrine cells in the CNS contributes to growth regulation in *Drosophila*. Current biology : CB. 2002 aug;12(15):1293–300.

2. Rulifson EJ, Kim SK, Nusse R. Ablation of insulin-producing neurons in flies: growth and diabetic phenotypes. Science (New York, NY). 2002 may;296(5570):1118–20.

3. Kim SK, Rulifson EJ. Conserved mechanisms of glucose sensing and regulation by *Drosophila* corpora cardiaca cells. Nature. 2004 sep;431(7006):316–20.

4. Lee KS, You KH, Choo JK, Han YM, Yu K. *Drosophila* short neuropeptide F regulates food intake and body size. The Journal of biological chemistry. 2004 dec;279(49):50781–9.

5. Rajan A, Perrimon N. *Drosophila* cytokine unpaired 2 regulates physiological homeostasis by remotely controlling insulin secretion. Cell. 2012 sep;151(1):123–37.

6. Nässel DR. Neuropeptides in the nervous system of *Drosophila* and other insects: multiple roles as neuromodulators and neurohormones. Progress in neurobiology. 2002 oct;68(1):1–84.

7. Nässel DR, Wegener C. A comparative review of short and long neuropeptide F signaling in invertebrates: any similarities to vertebrate neuropeptide Y signaling? Peptides. 2011 mar;.

8. Grimmelikhuijzen CJP, Hauser F. Mini-review: The evolution of neuropeptide signaling. Regulatory Peptides. 2012 aug;177(SUPPL.):S6–S9.

9. Mirabeau O, Joly JS. Molecular evolution of peptidergic signaling systems in bilaterians. Proceedings of the National Academy of Sciences of the United States of America. 2013 may;110(22):E2028–37.

10. Jékely G. Global view of the evolution and diversity of metazoan neuropeptide signaling. Proceedings of the National Academy of Sciences of the United States of America. 2013;110(21):8702–7.

11. Howard AD, Wang R, Pong SS, Mellin TN, Strack A, Guan XM, et al. Identification of receptors for neuromedin U and its role in feeding. Nature. 2000;406(July):70–74.

12. Hanada R, Teranishi H, Pearson JT, Kurokawa M, Hosoda H, Fukushima N, et al. Neuromedin U has a novel anorexigenic effect independent of the leptin signaling pathway. Nature medicine. 2004;10(10):1067–1073.

13. Novak CM, Zhang M, Levine JA. Sensitivity of the hypothalamic paraventricular nucleus to the locomotor-activating effects of neuromedin U in obesity. Brain research. 2007 sep;1169(507):57–68.

14. Chiu CN, Rihel J, Lee DA, Singh C, Mosser EA, Chen S, et al. A Zebrafish Genetic Screen Identifies Neuromedin U as a Regulator of Sleep/Wake States. Neuron. 2016 feb;89(4):842–56.

15. Nakazato M, Hanada R, Murakami N, Date Y, Mondal MS, Kojima M, et al. Central effects of neuromedin U in the regulation of energy homeostasis. Biochemical and biophysical research communications. 2000 oct;277(1):191–4.

16. Ivanov TR, Lawrence CB, Stanley PJ, Luckman SM. Evaluation of neuromedin U actions in energy homeostasis and pituitary function. Endocrinology. 2002;143(10):3813–3821.

17. Hanada R, Nakazato M, Murakami N, Sakihara S, Yoshimatsu H, Toshinai K, et al. A role for neuromedin U in stress response. Biochemical and Biophysical Research Communications. 2001;289(1):225–228.

18. Zeng H, Gragerov A, Hohmann JG, Pavlova MN, Schimpf Ba, Xu H, et al. Neuromedin U receptor 2-deficient mice display differential responses in sensory perception, stress, and feeding. Molecular and Cellular Biology. 2006;26(24):9352–9363.

19. Melcher C, Bader R, Walther S, Simakov O, Pankratz MJ. Neuromedin U and its putative *Drosophila* homolog hugin. PLoS biology. 2006 mar;4(3):e68.

20. Schoofs A, Hückesfeld S, Schlegel P, Miroschnikow A, Peters M, Zeymer M, et al. Selection of Motor Programs for Suppressing Food Intake and Inducing Locomotion in the *Drosophila* Brain. PLoS Biology. 2014 jun;12(6):e1001893.

21. Domin J, Ghatei Ma, Chohan P, Bloom SR. Neuromedin U – a study of its distribution in the rat. Peptides. 1987;8(5):779–784.

22. Ballesta J, Carlei F, Bishop aE, Steel JH, Gibson SJ, Fahey M, et al. Occurrence and developmental pattern of neuromedin U-immunoreactive nerves in the gastrointestinal tract and brain of the rat. Neuroscience. 1988 jun;25(3):797–816.

23. Ivanov TR, Le Rouzic P, Stanley PJ, Ling WY, Parello R, Luckman SM. Neuromedin U neurones in the rat nucleus of the tractus solitarius are catecholaminergic and respond to peripheral cholecystokinin. Journal of Neuroendocrinology. 2004;16(7):612–619.

24. Melcher C, Pankratz MJ. Candidate gustatory interneurons modulating feeding behavior in the *Drosophila* brain. PLoS Biology. 2005 sep;3(9):1618–1629.

25. Ghysen A. The origin and evolution of the nervous system. The International journal of developmental biology. 2003;47(7-8):555–62.

26. Hartenstein V. The neuroendocrine system of invertebrates: A developmental and evolutionary perspective. Journal of Endocrinology. 2006;190(3):555–570.

27. Taghert PH, Nitabach MN. Peptide neuromodulation in invertebrate model systems. Neuron. 2012 oct;76(1):82–97.

28. Ohyama T, Schneider-Mizell CM, Fetter RD, Aleman JV, Franconville R, Rivera-Alba M, et al. A multilevel multimodal circuit enhances action selection in *Drosophila*. Nature. 2015;520(7549):633–9.

29. Berck ME, Khandelwal A, Claus L, Hernandez-Nunez L, Si G, Tabone CJ, et al. The wiring diagram of a glomerular olfactory system. bioRxiv. 2016 jan;.

30. Fushiki A, Zwart MF, Kohsaka H, Fetter RD, Cardona A, Nose A. A circuit mechanism for the propagation of waves of muscle contraction in *Drosophila*. eLife. 2016 feb;5:e13253.

31. Schneider-Mizell CM, Gerhard S, Longair M, Kazimiers T, Li F, Zwart MF, et al. Quantitative neuroanatomy for connectomics in *Drosophila*. bioRxiv. 2015;.

32. Wren aM, Small CJ, Abbott CR, Jethwa PH, Kennedy aR, Murphy KG, et al. Hypothalamic actions of neuromedin U. Endocrinology. 2002 nov;143(11):4227–34.

33. Malendowicz LK, Ziolkowska A, Rucinski M. Neuromedins U and S involvement in the regulation of the hypothalamo-pituitary-adrenal axis. Frontiers in endocrinology. 2012;3(DEC):156.

34. Swanson LW. Cerebral hemisphere regulation of motivated behavior. Brain Research. 2000;886(1-2):113–164.

35. Yoon H, Enquist LW, Dulac C. Olfactory inputs to hypothalamic neurons controlling reproduction and fertility. Cell. 2005;123(4):669–682.

36. Tessmar-Raible K, Raible F, Christodoulou F, Guy K, Rembold M, Hausen H, et al. Conserved Sensory-Neurosecretory Cell Types in Annelid and Fish Forebrain: Insights into Hypothalamus Evolution. Cell. 2007;129(7):1389–1400.

37. Strausfeld NJ. Arthropod brains : evolution, functional elegance, and historical significance. Cambridge, Mass. : Harvard University Press; 2012.

38. Abitua PB, Gainous TB, Kaczmarczyk AN, Winchell CJ, Hudson C, Kamata K, et al. The pre-vertebrate origins of neurogenic placodes. Nature. 2015 aug;524(7566):462–5.

39. Saalfeld S, Cardona A, Hartenstein V, Tomancak P. CATMAID: collaborative annotation toolkit for massive amounts of image data. Bioinformatics (Oxford, England). 2009 aug;25(15):1984–6.

40. Bader R, Wegener C, Pankratz MJ. Comparative neuroanatomy and genomics of hugin and pheromone biosynthesis activating neuropeptide (PBAN). Fly. 2007;1(4):228–31.

41. Bader R, Colomb J, Pankratz B, Schröck A, Stocker RF, Pankratz MJ. Genetic dissection of neural circuit anatomy underlying feeding behavior in *Drosophila*: distinct classes of hugin-expressing neurons. The Journal of Comparative Neurology. 2007 jun;502(5):848–56.

42. Prokop A, Meinertzhagen IA. Development and structure of synaptic contacts in *Drosophila*. Seminars in Cell and Developmental Biology. 2006;17(1):20–30.

43. Jarrell TA, Wang Y, Bloniarz AE, Brittin CA, Xu M, Thomson JN, et al. The connectome of a decision-making neural network. Science (New York, NY). 2012 jul;337(6093):437–44.

44. Warming S, Costantino N, Court DL, Jenkins NA, Copeland NG. Simple and highly efficient BAC recombineering using *galK* selection. Nucleic Acids Research. 2005;33(4):1–12.

45. Venken KJT, Carlson JW, Schulze KL, Pan H, He Y, Spokony R, et al. Versatile P[acman] BAC libraries for transgenesis studies in *Drosophila melanogaster*. Nature methods. 2009;6(6):431–434.

46. Wang S, Zhao Y, Leiby M, Zhu J. A new positive/negative selection scheme for precise BAC recombineering. Molecular Biotechnology. 2009;42(1):110–116.

47. Pfeiffer BD, Jenett A, Hammonds AS, Ngo TTB, Misra S, Murphy C, et al. Tools for neuroanatomy and neurogenetics in *Drosophila*. Proceedings of the National Academy of Sciences of the United States of America. 2008 jul;105(28):9715–20.

48. Pfeiffer BD, Ngo TTB, Hibbard KL, Murphy C, Jenett A, Truman JW, et al. Refinement of tools for targeted gene expression in *Drosophila*. Genetics. 2010 oct;186(2):735–55.

49. Venken KJT, He Y, Hoskins RA, Bellen HJ. P[acman]: a BAC transgenic platform for targeted insertion of large DNA fragments in *D. melanogaster*. Science (New York, NY). 2006;314(5806):1747–1751.

50. Vosshall LB, Wong AM, Axel R. An olfactory sensory map in the fly brain. Cell. 2000;102(2):147–159.

51. Cabrero P, Radford JC, Broderick KE, Costes L, Veenstra Ja, Spana EP, et al. The Dh gene of *Drosophila melanogaster* encodes a diuretic peptide that acts through cyclic AMP. The Journal of experimental biology. 2002;205:3799–3807.

52. Veenstra JA, Agricola HJ, Sellami A. Regulatory peptides in fruit fly midgut. Cell and tissue research. 2008 dec;334(3):499–516.

53. Schoofs L, Holman GM, Paemen L, Veelaert D, Amelinckx M, De Loof a. Isolation, identification, and synthesis of PDVDHFLRFamide (SchistoFLRFamide) in *Locusta migratoria* and its association with the male accessory glands, the salivary glands, the heart, and the oviduct. Peptides. 1993;14(3):409–421.

54. Hückesfeld S, Schoofs A, Schlegel P, Miroschnikow A, Pankratz MJ. Localization of Motor Neurons and Central Pattern Generators for Motor Patterns Underlying Feeding Behavior in *Drosophila* Larvae. PloS one. 2015;10(8):e0135011.

55. Schoofs A, Niederegger S, van Ooyen A, Heinzel HG, Spiess R. The brain can eat: establishing the existence of a central pattern generator for feeding in third instar larvae of Drosophila virilis and *Drosophila melanogaster*. Journal of insect physiology. 2010 jul;56(7):695–705.

56. Hwang RY, Zhong L, Xu Y, Johnson T, Zhang F, Deisseroth K, et al. Nociceptive neurons protect *Drosophila* larvae from parasitoid wasps. Current biology : CB. 2007 dec;17(24):2105–16.

57. Ghysen A, Dambly-Chaudière C, Aceves E, Jan LY, Jan YN. Sensory neurons and peripheral pathways in *Drosophila* embryos. Roux's Archives of Developmental Biology. 1986;195(5):281–289.

58. Bodmer R, Jan YN. Morphological differentiation of the embryonic peripheral neurons in *Drosophila*. Rouxs Archives Of Developmental Biology. 1987;196:69–77.

59. Colomb J, Grillenzoni N, Ramaekers A, Stocker RF. Architecture of the primary taste center of *Drosophila melanogaster* larvae. The Journal of comparative neurology. 2007 jun;502(5):834–47.

60. Vosshall LB, Stocker RF. Molecular architecture of smell and taste in *Drosophila*. Annual review of neuroscience. 2007 jan;30:505–33.

61. Miyazaki T, Ito K. Neural architecture of the primary gustatory center of *Drosophila melanogaster* visualized with GAL4 and LexA enhancer-trap systems. The Journal of comparative neurology. 2010 oct;518(20):4147–81.

62. Kwon JY, Dahanukar A, Weiss LA, Carlson JR. Molecular and Cellular Organization of the Taste System in the *Drosophila* Larva. Journal of Neuroscience. 2011 oct;31(43):15300–15309.

63. Park D, Veenstra JA, Park JH, Taghert PH. Mapping Peptidergic Cells in *Drosophila*: Where DIMM Fits In. PLoS ONE. 2008 mar;3(3):e1896.

64. de Velasco B, Erclik T, Shy D, Sclafani J, Lipshitz H, McInnes R, et al. Specification and development of the pars intercerebralis and pars lateralis, neuroendocrine command centers in the *Drosophila* brain. Developmental Biology. 2007;302(1):309–323.

65. van den Pol AN. Neuropeptide transmission in brain circuits. Neuron. 2012 oct;76(1):98–115.

66. Meng X, Wahlström G, Immonen T, Kolmer M, Tirronen M, Predel R, et al. The *Drosophila* hugin gene codes for myostimulatory and ecdysis-modifying neuropeptides. Mechanisms of development. 2002 sep;117(1-2):5–13.

67. Rosenkilde C, Cazzamali G, Williamson M, Hauser F, Søndergaard L, DeLotto R, et al. Molecular cloning, functional expression, and gene silencing of two *Drosophila* receptors for the *Drosophila* neuropeptide pyrokinin-2. Biochemical and Biophysical Research Communications. 2003;309(2):485–494.

68. Nusbaum MP, Blitz DM, Swensen AM, Wood D, Marder E. The roles of co-transmission in neural network modulation. Trends in Neurosciences. 2001;24(3):146–154.

69. Morris JF, Pow DV. Widespread release of peptides in the central nervous system: quantitation of tannic acid-captured exocytoses. The Anatomical record. 1991 dec;231(4):437–45.

70. Maley BE. Ultrastructural identification of neuropeptides in the central nervous system. Journal of electron microscopy technique. 1990 may;15(1):67–80.

71. Vogelstein JT, Park Y, Ohyama T, Kerr RA, Truman JW, Priebe CE, et al. Discovery of Brainwide Neural-Behavioral Maps via Multiscale Unsupervised Structure Learning. Science. 2014;344(6182):386–392.

72. Manning L, Heckscher ES, Purice MD, Roberts J, Bennett AL, Kroll JR, et al. A Resource for Manipulating Gene Expression and Analyzing cis-Regulatory Modules in the *Drosophila* CNS. Cell Reports. 2012 oct;2(4):1002–1013.

73. Karsai G, Pollák E, Wacker M, Vömel M, Selcho M, Berta G, et al. Diverse in- and output polarities and high complexity of local synaptic and non-synaptic signaling within a chemically defined class of peptidergic *Drosophila* neurons. Frontiers in neural circuits. 2013 jan;7(August):127.

74. Wang Y, Markram H, Goodman PH, Berger TK, Ma J, Goldman-Rakic PS. Heterogeneity in the pyramidal network of the medial prefrontal cortex. Nature Neuroscience. 2006;9(4):534–542.

75. Campbell RE, Gaidamaka G, Han Sk, Herbison AE. Dendro-dendritic bundling and shared synapses between gonadotropin-releasing hormone neurons. Proceedings of the National Academy of Sciences of the United States of America. 2009 jun;106(26):10835–40.

76. Theodosis DT. Oxytocin-Secreting Neurons: A Physiological Model of Morphological Neuronal and Glial Plasticity in the Adult Hypothalamus. Frontiers in Neuroendocrinology. 2002;23:101–135.

77. Getting PA. Emerging principles governing the operation of neural networks. Annual review of neuroscience. 1989;12:185–204.

78. Alfa RW, Park S, Skelly Kr, Poffenberger G, Jain N, Gu X, et al. Suppression of Insulin Production and Secretion by a Decretin Hormone. Cell metabolism. 2015;21(2):323–333.

79. Cazzamali G, Torp M, Hauser F, Williamson M, Grimmelikhuijzen CJP. The *Drosophila* gene CG9918 codes for a pyrokinin-1 receptor. Biochemical and Biophysical Research Communications. 2005;335(1):14–19.

80. Park Y, Kim YJ, Adams ME. Identification of G protein-coupled receptors for *Drosophila* PRXamide peptides, CCAP, corazonin, and AKH supports a theory of ligand-receptor coevolution. Proceedings of the National Academy of Sciences of the United States of America. 2002 aug;99(17):11423–8.

81. Burnstock G. Cotransmission. Current opinion in pharmacology. 2004 feb;4(1):47–52.

82. Merighi A. Costorage and coexistence of neuropeptides in the mammalian CNS. Progress in neurobiology. 2002 feb;66(3):161–90.

83. Brezina V. Beyond the wiring diagram: signalling through complex neuromodulator networks. Philosophical transactions of the Royal Society of London Series B, Biological sciences. 2010 aug;365(1551):2363–74.

84. Li C, Kim K. Neuropeptides. WormBook : the online review of *C elegans* biology. 2008;(212):1–36.

85. Jan YN, Jan LY. Coexistence and corelease of cholinergic and peptidergic transmitters in frog sympathetic ganglia. Federation Proceedings. 1983;42(12):2929–2933.

86. Weiss KR, Brezina V, Cropper EC, Heierhorst J, Hooper SL, Probst WC, et al. Physiology and biochemistry of peptidergic cotransmission in Aplysia. Journal of physiology, Paris. 1993;87(3):141–51.

87. Vilim FS, Cropper EC, Price Da, Kupfermann I, Weiss KR. Release of peptide cotransmitters in Aplysia: regulation and functional implications. The Journal of neuroscience : the official journal of the Society for Neuroscience. 1996;16(24):8105–8114.

88. Mitchell JD, Maguire JJ, Davenport AP. Emerging pharmacology and physiology of neuromedin U and the structurally related peptide neuromedin S. British journal of pharmacology. 2009 sep;158(1):87–103.

89. Peier A, Kosinski J, Cox-York K, Qian Y, Desai K, Feng Y, et al. The antiobesity effects of centrally administered neuromedin U and neuromedin S are mediated predominantly by the neuromedin U receptor 2 (NMUR2). Endocrinology. 2009 jul;150(7):3101–9.

90. Hanada T, Date Y, Shimbara T, Sakihara S, Murakami N, Hayashi Y, et al. Central actions of neuromedin U via corticotropin-releasing hormone. Biochemical and Biophysical Research Communications. 2003;311:954–958.