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Translational profiling of hypocretin neurons identifies candidate molecules for sleep regulation

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Hypocretin (orexin; Hcrt)-containing neurons of the hypothalamus are essential for the normal regulation of sleep and wake behaviors and have been implicated in feeding, anxiety, depression, and reward. The absence of these neurons causes narcolepsy in humans and model organisms. However, little is known about the molecular phenotype of these cells; previous attempts at comprehensive profiling had only limited sensitivity or were inaccurate. We generated a Hcrt translating ribosome affinity purification (bacTRAP) line for comprehensive translational profiling of all ribosome-bound transcripts in these neurons in vivo. From this profile, we identified >6000 transcripts detectably expressed above background and 188 transcripts that are highly enriched in these neurons, including all known markers of the cells. Blinded analysis of in situ hybridization databases suggests that ~60% of these are expressed in a Hcrt marker-like pattern. Fifteen of these were confirmed with double labeling and microscopy, including the transcription factor \textit{Lhx9}. Ablation of this gene results in a >30% loss specifically of Hcrt neurons, without a general disruption of hypothalamic development. Polysomnography and activity monitoring revealed a profound hypersomnolence in these mice. These data provide an in-depth and accurate profile of Hcrt neuron gene expression and suggest that \textit{Lhx9} may be important for specification or survival of a subset of these cells.

\textbf{Keywords:} translational profiling; hypocretin; orexin; bacTRAP; \textit{Lhx9}; narcolepsy

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There is an interest in identifying a comprehensive profile of proteins specifically found in Hcrt neurons for three reasons. First, there is a long-standing hypothesis that epitopes found specifically in Hcrt neurons may serve to direct the autoimmune-mediated destruction of these cells [Lim and Scammell 2010]. Previous work suggests that Trib2 may be one such epitope [Cvetkovic-Lopes et al. 2010; Kawashima et al. 2010; Toyoda et al. 2010], although this did not replicate in more recent patients with narcolepsy following H1N1 [Dauvilliers et al. 2010]. Second, there is an interest in understanding the suit of receptors and channels specifically expressed by these neurons, as these may serve as drug targets for modulating sleep even in healthy individuals. Third, there is an interest in understanding the transcription factors that may serve to specify these neurons as both candidates for rare variant analyses in humans with early onset narcolepsy or NwoC and tools to direct the differentiation of Hcrt neurons from patient cells. In the present study, we used translating ribosome affinity purification (TRAP) [Doyle et al. 2008; Heiman et al. 2008; Dougherty et al. 2010] to generate a comprehensive translational profile of Hcrt neurons. We then confirmed these results with independent methods and pursued functional studies of one transcription factor, Lhx9, that may be important for the normal development of a subset of Hcrt neurons and normal sleep behavior.

**Results**

*Translational profiling of Hcrt neurons*

To apply the TRAP methodology to Hcrt neurons, we generated mouse lines targeting Hcrt-producing cells [Hcrt::eGFP-RpL10a] [Fig. 1A]. Successful targeting was confirmed using confocal immunofluorescent microscopy for eGFP and Hcrt antibodies [Fig. 1B] as well as in situ hybridization [ISH] for Hcrt transcript and GFP [data not shown]. Both methods revealed GFP expression in >85% of neurons with detectable Hcrt expression and no instances of eGFP-RpL10a expression in Hcrt-negative cells. There was no eGFP-RpL10a expression elsewhere in the adult brain.

We then conducted replicate TRAP assays on four independent pools of adult mice. Biological replicates showed good reproducibility, with the minimum Pearson's correlation >0.96 across all comparisons [Fig. 2A]. Compared with total RNA from the diencephalon, mRNA purified from Hcrt neurons showed a substantial enrichment of many transcripts, including known markers of Hcrt neurons (Fig. 2B).

**Identification of transcripts enriched in the Hcrt neuron translational profile**

To systematically identify a set of RNAs specifically enriched in Hcrt neurons compared with cell types across the nervous system, we combined the results of three statistical filters: We removed probe sets with low expression, selected for those with more than twofold enrichment in Hcrt neurons compared with total diencephalic RNA, and selected those significantly specific to Hcrt neurons (pSI < 0.01) when compared with a previously collected set of 26 neural samples [Doyle et al. 2008] as described [Dougherty et al. 2010]. This identified 220 probe sets, representing products from 188 genes [Table 1, Supplemental Table S1], and included a significant overlap with the few known Hcrt cell markers Hcrt.

Comparison with previous studies and validation of microarray results

Previously, others have used different techniques to profile Hcrt neurons: using affinity purification of RNAs bound to a tagged polyA-binding protein [Pabp] expressed in Hcrt neurons [Cvetkovic-Lopes et al. 2010] or screening for transcripts lost from hypothalamic RNA when Hcrt neurons were ablated [Honda et al. 2009]. Careful comparison with these studies using statistical criteria matched to each publication indicates that our data are more accurate than Pabp [Fig. 2C–E] and are consistent with Honda et al. [2009] but with an order of magnitude more sensitivity.

As Hcrt neurons are relatively rare and thus contribute little RNA to a total RNA sample analyzed from whole hypothalamus, the strategy taken by Honda et al. [2009] would only be predicted to detect only very abundant and specific transcripts from these cells as well as changes in other cells responding to the loss of the Hcrt neurons. They discovered 53 probe sets depleted more than threefold, which overlapped with the known markers of these cells (P < 10 × 10^{-100}, χ^2 test). Thus, the approach was accurate although likely not comprehensive. Matching statistical criteria to the previous studies, TRAP would detect 534 probe sets more than threefold enriched. TRAP probe sets significantly overlap with that of Honda et al. [2009] (P < 7 × 10^{-7}, χ^2 test) and the known markers of these cells (P < 10 × 10^{-100}, χ^2 test). In contrast, the Pabp microarrays detected 1709 probe sets as enriched in Hcrt neurons more than threefold, although there was no significant overlap with either our analysis, that of Honda et al. [2009], or the known markers of these cells (all P > 0.1, χ^2 test) [see also Fig. 2C].

For a systematic and independent confirmation of our data, we also examined the Allen Brain Atlas database of mouse ISH patterns [Lein et al. 2007] for our 188 most enriched transcripts [Table 1; Supplemental Table S1]. Blinded scorers simultaneously examined the top 188 transcripts from Pabp and 188 transcripts randomly selected from the microarray. Due to the scattered nature of Hcrt neuron expression [Fig. 1B], it is impossible to
Table 1. Transcripts enriched in Hcrt neurons

<table>
<thead>
<tr>
<th>Probe set</th>
<th>Expression</th>
<th>Hcrt/total</th>
<th>pSI</th>
<th>Symbol</th>
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<tr>
<td>143360_at</td>
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<tr>
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<tr>
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unambiguously identify Hcrt neurons from single-label ISH. However, all Hcrt neuron-enriched genes should show a pattern of enrichment in scattered cells of the lateral hypothalamus. Therefore, we scored for this “Hcrt-like pattern,” [HLP] the fold change compared with whole diencephalon RNA. [pSI] the significance of enrichment compared with all published cell types; [symbol] official gene symbol (Doyele et al. 2008; Dougherty et al. 2010). This table includes only named genes. For a complete list, see Supplemental Table S1.

Of the 188 TRAP transcripts, 65 had coronal ISH patterns with some detectable signal. Of these, 37 (59%) had an expression pattern clearly consistent with a robust enrichment in Hcrt neurons, analogous to positive controls Pdyn and Ptx2. Compared with the frequency of HLPs from the 188 randomly selected transcripts, the odds of this enrichment occurring by chance are slim (P < 3 \times 10^{-10}, \chi^2 test). Seven seemed to nearly match the exact pattern of Hcrt expression [Fam46a, Creb3311, Gng2, Lhx9, Tm63, Rfx4, and Pcbd1] in the hypothalamus (Supplemental Fig. S1). Of the 65 scored, only two (Agrp and Benda5) had patterns of expression that would seem to exclude them from Hcrt neurons entirely. The remaining genes were more broadly expressed in hypothalamic cells. These would not necessarily be considered to contradict the microarray results: A difference of twofold may not be readily discernible by ISH. Also ISH and TRAP may differ because of differences between transcription and translation, and occasionally ISH from the Allen Brain Atlas are simply inaccurate. For example, Lhx9 shows strong ubiquitous brain expression in the Allen Brain Atlas at most ages, in contrast to other reports (Bertuzzi et al. 1999; Retaux et al. 1999; Nakagawa and O’Leary 2001; Gray et al. 2004). Nonetheless, even using only the 188 transcripts derived from our most
stringent criteria, TRAP increased by an order of magnitude the number of known Hcrt neuron-enriched genes. The Honda et al. (2009) data did not have a comparable number of transcripts to score, but of their scorable ISH patterns, they showed nearly the same pattern of enrichment as the TRAP data (57% with scores of 1–3). In contrast, the transcripts from the PaB pulldown were no more likely than chance to be expressed in a HLP ($P > 0.15$, $\chi^2$ test) [Fig. 2E].

We further confirmed colocalization with Hcrt peptide for 15 of our 188 genes by confocal immunofluorescence and ISH [Fig. 3, Table 2]. This suggests that the microarray results are predicting expression correctly in a substantial portion of the cases. Calb1 and Nnat labeled nearly all Hcrt neurons, but the Hcrt neurons were clearly only a subset of the hypothalamic cells expressing these proteins. This is similar to what has been seen with traditional markers of these cells, Pdyn and Nptx2. From these results, however, we also identified a previously unreported molecular diversity within these neurons. For example, both Pcsk1 and Ngb only labeled subsets of the Hcrt neurons at the protein level, in addition to labeling adjacent nuclei. Finally, probes of two genes, Stat5b and especially Rfx4, had nearly perfect overlap with Hcrt neurons, with the latter having expression only within these neurons.

Finally, to determine whether the data continued to be informative even beyond the top 188 genes, we also stained with two robust antibodies: Calb1 and Calb2. These were also predicted to have expression in Hcrt neurons, although only very modest enrichment (1.4-fold and 1.2-fold). We detected robust labeling in most Hcrt neurons, although again there was an interesting and previously unreported molecular diversity [Fig. 3C].

**Correlating the Hcrt neuron profile with function**

An unbiased examination of our transcripts [Supplemental Table S1] using two gene categorization tools [DAVID [Database for Annotation, Visualization, and Integrated Discovery] and BiNGO [Biological Network for Gene Ontology]] highlights several features that make these cells distinct. There is a substantial enrichment for genes containing signal peptides, such as peptide neurotransmitters, suggesting that these cells have an unusually robust repertoire of secreted molecules (UniprotKB term “Signal,” $P < 1.6 \times 10^{-5}$, as calculated by DAVID with Benjamini-Hochberg [B-H] correction). More surprisingly, there seem to be intact pathways enriched in these neurons related to cytokine signaling (for example, gene ontology [GO] terms “regulation of immune effector process,” and “regulation of cytokine production,” both $P < 5 \times 10^{-5}$, BiNGO hypergeometric test with B-H correction), driven by the genes H2-M3, Cd59A, Stat5b, Tlr2, Cd40, Il13ra1, Panx1, and Apoa2, and an unusually high level of Caspase1. It is possible that something about these transcripts renders Hcrt neurons particularly vulnerable to destruction in NC. For example, the presence of Caspase1, which perhaps normally serves some role in protein secretion in these cells [Keller et al. 2008], could render them vulnerable to pyroptosis [Miao et al. 2011] after infection.

Our analysis also identifies a set of receptors that makes clear predictions about what type of neurotransmitters or pharmacological agents these cells should be especially responsive to, including serotonin (Htr1a and Htr1f) and other monoamines [Adra2a], neurotensin [Ntsr1], arginine vassopressin [Avpr1a], growth hormone [Ghr], thyrotropin-releasing hormone [Thtr], parathyroid hormone [Pth2r], cholecystokinin [Cckar], and an orphan receptor and potentially novel drug target, Gpr45. The predictions about the monoamines, Avp, Ntsr, Trh, and Cck are supported by the literature [Bayer et al. 2005; Tsujino et al. 2005; Kumar et al. 2007; Harakat et al. 2009], while the others are novel. Finally, we identify a novel set of transcription factors—including Elk3, Hmx2, Fosil1, Creb3l1, Rfx4, Stat5b, and Lhx9—that may be important for the specification of these cells.

**Lhx9 is necessary for a subset of Hcrt neurons in vivo**

To determine whether any of the Hcrt neuron transcripts that we discovered here may have some functional significance for these cells, we examined Lhx9 knockout mice. Previously, two groups have generated deletions of Lhx9 in mice. One group identified an essential role of this transcription factor in formation of the gonads [Birk et al. 2000], while the other focused on the role of Lhx9 in conjunction with Lhx2 in commissural relay neuron axonal guidance in the embryonic development of the spinal cord [Wilson et al. 2008]. To our knowledge, no one has studied the functional consequences of Lhx9 deletion on hypothalamic development.

To determine whether Lhx9 may contribute to development or axonogenesis of Hcrt neurons, we quantified the distribution and density of Hcrt axons by immunohistochemistry from serial sections of adult brains in Lhx9 knockout mice [Wilson et al. 2008] and wild-type littermate controls ($n = 4$). In the absence of Lhx9, Hcrt fibers continued to project to all of their targets with a normal pattern of innervation [Peyron et al. 1998] but a somewhat decreased amount of fiber density. Throughout the brain, we found that targets had lost 20%–40% of Hcrt cell number in the Lhx9 knockout (Fig. 3D). This loss of Hcrt neurons could be due to a broad failure of brain development, as has been previously described for Ebf2 knockouts [De La Herran-Arita et al. 2011]. However, careful characterization of our Lhx9 knockout and wild-type mice demonstrated no consistent differences in brain size, weight, or structure. To determine whether this loss of neurons is due to a general decrease in the number of cells in the hypothalamus, we also examined two other populations of neurons in the hypo-
Figure 3. TRAP accurately predicts gene expression in Hcrt neurons. (A) Confocal immunofluorescence for positive control anti-Nptx2 (green) and anti-Hcrt (red) antibodies shows Hcrt is expressed in a subset of Npt2x cells, consistent with their known expression patterns. Colocalization of nine novel Hcrt neuron gene products identified as enriched in Hcrt neurons (Table 1) shows substantial overlap (Table 2). Lhx9 protein was expressed in a subset of Hcrt neurons, and a subset of Lhx9 cells were positive for Hcrt. (B) In situ hybridization for potential novel markers of Hcrt neurons (scored as a 1 or 2 in Supplemental Table S1), identifies six genes highly enriched in Hcrt neurons. (C) Genes identified as expressed but not substantially enriched by TRAP (Supplemental Table S2) also show robust expression in Hcrt neurons. Note the molecular diversity of Hcrt neurons in their expression of calcium-binding proteins Calb1 and Calb2 (white arrows point to triple expression of Calb1, Calb2, and Hcrt; yellow arrows point to double expression of Calb1 or Calb2 and Hcrt; cyan arrows point to single expression of Calb1). All of the images are captured at 40× magnification.
observed a 33% decrease of Hcrt cells in the hypothalamus containing Hcrt neurons. We again counted all Hcrt-, Mch-, or Th-positive cells in any sections for Hcrt and Mch or Hcrt and Th expression: dopaminergic neurons, labeled by anti-Lhx9 to determine whether this absence of Hcrt neurons may demonstrate a profound hypersomnolence, with a 20% decrease in time spent awake across a 24-h recording period and a corresponding increase in NREM [non-REM] sleep [Fig. 4B,C]. REM sleep was not affected. Circadian rhythm appears intact in these animals, with the normal increase in wakefulness seen during the dark period [Fig. 4C]. Thus, these mice that have a loss of a subset of Hcrt neurons also recapitulate a portion of the narcolepsy phenotype, hypersomnolence, in the absence of REM abnormalities or cataplexy. Submaximal doses of Hcrt receptor antagonists [Morairty et al. 2012] or partial ablations of the Hcrt neuron population [Gerashchenko et al. 2001] can produce a hypersomnolence similar to what we observed here. Thus, the most parsimonious explanation of our data is that Lhx9 is important for a subset of Hcrt neurons and that this subset is essential for normal sleep behavior.

However, this is but one of two alternative hypotheses regarding the mechanism of Hcrt loss in Lhx9 knockout mice. Either Lhx9 is essential in early fate specification or survival of a subset of Hcrt neurons or Lhx9 simply promotes expression of the Hcrt gene. We next conducted a set of experiments to address these alternative mechanisms.

**Lhx9 does not regulate Hcrt promoter activity in vitro**

To determine whether Lhx9 is a direct regulator of the known Hcrt promoter [pHcrt], we cloned a fragment of the Hcrt promoter, including the conserved regions previously reported to provide Hcrt neuron-specific activity in vivo and in vitro [Moriguchi et al. 2002; Adamantidis et al. 2007; Silva et al. 2009], and conducted luciferase assays in a neuroblastoma cell line overexpressing Lhx9 [Supplemental Fig. S2A]. Lhx9 did not induce activity from this promoter and indeed led to a very modest suppression of luciferase activity, providing strong evidence that Lhx9 is not a direct positive regulator of this genomic region. However, this experiment does not preclude the possibility that Lhx9 positively regulates Hcrt expression through a different genomic region, regulates Hcrt expression indirectly through a second transcription factor, or requires a cofactor not expressed in the neuroblastoma cell line. Finally, although it has been used experimentally in this cell line before [Silva et al. 2009], pHcrt has very little activity in vitro in any reported cell line, precluding analyses of the ability of Lhx9 to robustly suppress Hcrt expression. To test these possibilities, we generated a high-titer Lhx9 lentivirus and injected it stereotactically into the lateral hypothalamus in a set of two experiments.

**Lhx9 does not positively or negatively regulate Hcrt expression in vivo**

We first injected wild-type mice unilaterally in the hypothalamus with either Lhx9-producing [n = 3] or GFP-producing [n = 4] viruses and, 8 d later, processed them for immunofluorescence for Lhx9, GFP, and Hcrt.
peptide. Confocal fluorescence microscopy confirmed expression of exogenous Lhx9 and GFP in the injected sides and accurate targeting to the region of Hcrt neurons in six of seven injected animals. Excluding the one off-target GFP animal, we counted all Hcrt neurons in all animals on both injected and uninjected sides. There was no significant difference between injected and uninjected sides for either Lhx9 or GFP or between Lhx9- and GFP-injected animals (Supplemental Fig. S2B). These data demonstrate that Lhx9 is not a direct or indirect transcriptional regulator of Hcrt expression in adult animals in vivo, at least in wild-type animals. However, the possibility remained that Lhx9 could rescue the Hcrt neuron number and/or behavioral disruptions seen in adult Lhx9 knockout mice. Therefore, in our second experiment, we first validated a more high-throughput method for phenotyping the behavior of our animals and then attempted to rescue the knockout phenotype with bilateral Lhx9 injection into the lateral hypothalamus.

Figure 4. Genetic ablation of Lhx9 results in hypersomnolence. (A) Representative hypnograms for a single Lhx9 knockout (KO) and wild-type (WT) mouse over a 12-h active period show a lack of sleep-onset REM periods but an apparent increase in NREM sleep in the knockout mouse. (B, top panel) Quantification of minutes per hour spent in REM and NREM sleep and wakefulness for Lhx9 knockout and wild-type mice reveals a significant increase in NREM sleep at the expense of wakefulness (n = 5 per group, two-tailed t-test). (Bottom panel) There was no difference in bout duration of wakefulness and NREM sleep between Lhx9 knockout and wild-type mice (n = 5 per group, two-tailed t-test). (C) Both Lhx9 knockout and wild-type mice show normal circadian differences in activity between night and day (n = 5 per group, two-tailed t-test) with no significant difference between genotypes. (*) P < 0.05; (**) P < 0.01. Values represent mean ± SEM.
Replacement of Lhx9 in the lateral hypothalamus does not rescue disruption of behavior or Hcrt neuron number

Quantification of time at rest and horizontal ambulations using 24-h activity monitoring has previously been shown to provide reliable estimates of sleep and wakefulness [Pack et al. 2007]. The rest and activity patterns of Lhx9 knockout (n = 9) and wild-type (n = 6) mice were evaluated over a 48-h period in automated chambers using photobeam breaks. The hypersomnolence demonstrated by the Lhx9 knockout mice during EEG recording was replicated during activity monitoring. Lhx9 knockout mice exhibited a 20% increase in time at rest (minutes per hour) compared with wild-type mice (P < 0.05, ANOVA) (Fig. 5A) as well as normal increases in time at rest during the light period relative to the dark period, indicating intact circadian rhythms (P < 0.05, paired t-test) (Fig. 5B). Complementary to the sleep behavior results, a 57% decrease in average activity per hour was displayed by the Lhx9 knockout mice compared with wild-type mice (P < 0.01, ANOVA) (Fig. 5C). The decreases in activity were observed across both the light and dark periods (P < 0.05, repeated measures ANOVA) (Fig. 5D). These results support the EEG data and confirm that Lhx9-null mice with a loss of Hcrt neurons demonstrate a profound hypersomnolence.

Following the first 48-h activity monitoring session, a lentiviral vector was bilaterally injected into the Hcrt neurons of Lhx9 knockout mice to produce expression of either Lhx9 (n = 5) or GFP (n = 4). Sixteen days following injection, successful targeting was confirmed through confocal microscopy of immunofluorescence-labeled sections, showing GFP and Lhx9 expression within the Hcrt neuron-containing lateral hypothalamus [Fig. 5E] with successful Lhx9 expression in the targeted areas in four of five mice [Fig. 5F] and GFP in four of four mice. Immediately prior to these neuroanatomical studies, the behavior of these mice was evaluated again over a 48-h period to determine whether reinstatement of Lhx9 expression in adult lateral hypothalamus could rescue the perturbations observed in sleep and wakefulness behaviors. While the Lhx9 expression was successfully rescued within the lateral hypothalamus, the behavioral phenotype was not. During post-injection activity monitoring, the Lhx9-injected Lhx9 knockout mice did not demonstrate a change in rest or ambulatory activity levels from those observed during preinjection activity monitoring (P > 0.05, repeated measures ANOVAs) [Fig. 5G,H]. The Lhx9-injected Lhx9 knockout mice also demonstrated levels of rest and activity comparable with that of the GFP-injected Lhx9 knockout controls during both pre- and post-injection activity monitoring. In addition, staining and quantification indicated that Lhx9-injected Lhx9 knockout animals showed no rescue of Hcrt neuron number (P > 0.05, two-tailed t-test) [Fig. 5I].

Overall, we could not rescue either Hcrt neuron number or Lhx9 knockout sleep behavior, which suggests that these are related phenomena and that the perturbations in sleep and wakefulness behavior are due to a loss of cells during development rather than simple dysregulation of Hcrt promoter activity. Our current data do not address whether the cell loss is due to a cell-autonomous failure of specification or a secondary consequence of either pathfinding defects or loss of a distally acting signal. These hypotheses will need to be tested in the future with direct genetic approaches, including cell-specific deletion of Lhx9.

Regardless of the outcome of those studies, we discovered a genetic manipulation that results in a profound perturbation of sleep behavior. It is also of interest that a genome-wide association study of human narcoleptics [Hallmayer et al. 2009] identified a SNP on chromosome 1 with a suggestive association to narcolepsy (P < 10^{-4}) that is 96 kb upstream of Lhx9 (HG19 assembly, as accessed December 2012, University of California at Santa Cruz Genome Browser, http://www.genome.ucsc.edu). Thus, there remains the possibility that Lhx9 may be an important regulator of sleep in humans as well.

Discussion

We described here a mouse line permitting the in vivo profiling of Hcrt neurons and identified a set of 188 transcripts robustly enriched in these neurons (Supplemental Table S1) in addition to thousands more moderately enriched or nominally expressed (Supplemental Table S2), including many additional channels and receptors. Our validation studies suggest that our methods have a high true positive rate [at least 59%] and low false positive rate [~5%]. There are a small number of genes previously reported in Hcrt neurons (such as Foxa2) for which the arrays simply showed no signal in any sample. This suggests that there are some false negatives in our data, which may be ameliorated in future studies using RNA sequencing (RNA-seq). Also, TRAP does have some low level of nonspecific background, as indicated by the presence of signal from some glial genes [Fig. 2B, red circles]. We used the fold change from these glial genes to establish a fold change threshold (0.47) below which we cannot be certain whether a gene is expressed in Hcrt neurons or not. The proposed narcolepsy autoantigen Trib2 [Lim and Scammell 2010] falls below this threshold. This suggests that if it is expressed in healthy Hcrt neurons, it is at a much lower level in these cells than surrounding tissue.

Our anatomical analysis of these molecular results largely supported the array data but also discovered a surprising molecular heterogeneity in these neurons, with several gene products expressed only in a subset of these neurons [Dlk1, Gpx3, Pesk1, Lgals3, and Ngb]. It remains to be determined whether these represent truly functionally distinct subsets of the Hcrt population or are merely transiently expressed and reflect the state of particular neurons at the time of perfusion, analogous to the classically activity-induced protein cFos. Among those assayed, Stat5b and Rfx4 showed the highest concordance rate while remaining largely specific to Hcrt neurons and thus could potentially serve as alternate markers for the population in future studies. These would...
be of great interest to examine in human post-mortem tissue from narcoleptic patients.

Additionally, we noted an unusual concordance between the expression of our candidate genes in Hcrt neurons and in the axonal targets of Hcrt neurons: For example, both Ngb and Lhx9 proteins were dimly expressed in Hcrt neurons but more robustly expressed in their targets in the laterodorsal tegmentum and paraventricular thalamus, respectively. This hints that target-mediated signals may in some way be contributing to the gene expression of Hcrt neurons and will be an interesting direction for future investigation.

Finally, while we emphasized here the clear significance of the Hcrt system to narcolepsy, it is essential to mark the accumulating evidence that these neurons may also play a role in anxiety, depression, and reward in

Figure 5. Disturbances in behavior and Hcrt expression of Lhx9 knockout (KO) mice are not rescued by adult reinstatement of Lhx9 expression. During 48-h activity monitoring, Lhx9 knockout mice exhibited a 20% increase in time at rest, an estimate of sleep, compared with wild-type (WT) mice ($P < 0.05$, ANOVA) [A], while both groups demonstrated intact circadian differences in time at rest between the light and dark periods ($P < 0.05$, paired t-test) [B]. [C] Lhx9 knockout mice also demonstrated a 57% decrease in ambulatory activity, an estimate of wakefulness, relative to wild-type mice ($P < 0.01$, ANOVA). [D] The ambulatory differences were maintained across the light and dark periods ($P < 0.05$, repeated measures ANOVA). [E] Confocal microscopy revealed double-immunofluorescent labeling of GFP with orexin within Hcrt neurons, confirming successful targeting of hypocretinergic regions. [F] Representative example of Lhx9 expression in the targeted region of the hypothalamus in Lhx9 knockout mice. The white asterisk represents a labeling artifact at injection sites. [G,H] No differences were observed in time at rest or ambulatory activity between pre- and post-injection activity monitoring for Lhx9-injected Lhx9 knockout mice. In addition, time at rest and ambulatory activity was comparable during post-injection activity monitoring for both the Lhx9-injected Lhx9 knockout mice and the GFP-injected Lhx9 knockout mice (repeated measures ANOVA). [I] No difference was noted in the number of Hcrt neurons between Lhx9-injected and GFP-injected animals. (*) $P < 0.05$; (**) $P < 0.01$. Values represent mean ± SEM.
addition to their roles in sleep and feeding (Borgland and Labouebe 2010, Sakurai and Mieda 2011). Thus the data we provide here may serve to both better inform these studies and provide an important tool to profile Hcrt neurons under a variety of conditions.

Materials and methods

Animal research committees

All procedures involving animals were approved by the appropriate institutional animal care and use committees.

Generation of mice

A bacterial artificial chromosome (BAC), RP23-258L05, was modified as described (Doyle et al. 2008) to insert the eGFP-RPL10a transgene at the translation start site of the Hcrt gene. Successful modification was confirmed with Southern blot, and lack of gross rearrangement of the BAC was checked by BAC fingerprinting. Modified BAC DNA was purified with CsCl gradient centrifugation, dialyzed into injection buffer, and injected into FVB mouse eggs. Eggs were transplanted into pseudopregnant Swiss Webster dams, and the resultant pups were screened with tail tip PCR for eGFP to identify founders. Each founder was crossed to C57/bl6j wild-type mice, and F1 progeny were genotyped and then processed for anatomy as described below.

Immunofluorescence microscopy

Mice were killed and then perfused with phosphate-buffered saline (PBS) followed by 4% paraformaldehyde in PBS. Brains were dissected, cryoprotected in 30% sucrose PBS solution, and then frozen and sectioned serially on a Leica cryostat into PBS and 0.1% sodium azide for storage at 4°C. Floating sections were blocked in 5% normal donkey serum, 0.25% Triton, and PBS for 30 min and then incubated overnight with primary antibodies in the same buffer. All primary antibodies are detailed in Supplemental Table S4. Sections were then washed three times with PBS and then incubated for 60–90 min with the appropriate Alexa fluorophore-conjugated secondary antibodies and nuclear dyes (DAPI and or TOPO-3-Iodide, Life Technologies). Images were acquired on a LSM 510 Zeiss confocal microscope (Fig. 1) or a Perkin Elmer UltraView Vox spinning-disk confocal on a Zeiss Axiovert microscope (all other confocal figures).

Immunohistochemistry

Mice were processed as above. For anti-Orx-A DAB immunohistochemistry, brains were processed using multibrain technology by Neuroscience Associates as described (Doyle et al. 2008) using orexin A antibody [1:10,000, Calbiochem] and a nickel-enhanced DAB substrate for HRP. Sections were digitized with a Zeiss Axioskop2 and customized macros.

Anatomical analysis

All cell number quantification was done on a series of coronal sections spaced 200–210 μm apart through the hypothalamus in a minimum of three Lhx9 knockout and three wild-type mice, typically littermates. Counts from two independent investigators, blinded to condition, were averaged for each mouse. For Hcrt, Mch, and Th staining, all neuron labeling with any antibody was counted in any section showing any Hcrt neuronal labeling. Statistical comparisons were with unpaired two-tailed t-tests, as calculated in Microsoft Excel. For Dlk1, Celn6, Nnat, Ngb, Gpx3, Psck1, Stat5b, and Lhx9, cells were counted from confocal images of all available Hcrt-expressing regions from three wild-type mice. Antibodies used are detailed in Supplemental Table S4.

For Allen Brain Atlas analysis, the 188 TRAP transcripts were mixed with the top 188 transcripts from the Pabp study “Supplemental Excel File 1” from Cvetkovic-Lopes et al. (2011) and 188 transcripts selected at random from the genes present on the microarray and evaluated by two blinded reviewers using the following criteria to identify a HLP. First, transcripts without coronal sections were excluded, as were any ISH with no detectable signal anywhere in tissue. Then, if there was broad labeling of cells in the hypothalamus (or indeed, the entire brain), then they were scored as a 4: broadly expressed, including HLP (e.g., Snap25). If there was strong labeling in some population somewhere in the brain and absolutely no labeling in the region of an HLP, then they were scored as a 5: not expressed in HLP (e.g., Agrp). Looking at the entire brain, if the only signal was in a HLP, then they were scored as a 1: unique to Hcrt neurons (e.g., Hcrt). Looking just within the hypothalamus and ignoring the rest of the brain, if the only signal was in a HLP, then they were scored as a 2: unique within hypothalamus (e.g., Igfbp3, which showed an HLP plus labeling of choroid). Finally, looking just within the hypothalamus, if the labeling overlapped with HLP but also showed labeling in just a few other populations in hypothalamus, then it was scored as a 3: enriched in Hcrt neurons (e.g., Pdyn and Nptx2). Generally, markers from the literature for Hcrt neurons received scores between 1 and 3. For the purpose of statistical analysis, scores of 1–3 were pooled, and χ² tests were calculated in Microsoft Excel, comparing observed distributions [TRAP or Pabp] with those expected by chance (random).

ISH

ISH was performed as described previously (VanDunk et al. 2011) on coronal sections of P28 wild-type mouse brains that were immersion-fixed in 4% paraformaldehyde for 20 min and cryoprotected in sucrose before sectioning. Digoxigenin-labeled riboprobe was transcribed with T7 RNA polymerase using the templates described [Supplemental Table S3]. Hybridization was performed with 1–2 μg/mL probe for 12–16 h at 65°C. Slides were then washed with 2× SSC for 15 min at 62°C followed by two washes in 0.2× SSC for 30 min each at 62°C. After blocking in PBS, Triton [PBT], and 10% normal horse serum, slides were incubated in alkaline phosphatase-conjugated anti-DIG antibody [1:2000] overnight at 4°C. The following day, slides were washed twice in PBT for 30 min each, and color development proceeded in the dark using NBT and BCIP as a substrate. Color was allowed to develop for 2–20 h, depending on the abundance of the message. After three washes in PBS, slides were fixed in 4% paraformaldehyde for 15 min and stained for Hcrt following standard immunofluorescence protocol, and data were acquired as above. NBT and BCIP signal was inverted, pseudocolored green, and overlayed on Hcrt staining in ImageJ.

TRAP assays and analysis

Four replicate pools of four to six mixed-sex 6- to 12-wk-old mice from the brightest transgenic line were killed, and brains were removed and transferred to ice-cold dissection buffer containing cycloheximide; diencephalon was harvested with the aid of a dissecting microscope. TRAP was conducted as described (Heiman et al. 2008). Briefly, each pool was homogenized for 12 strokes in a glass Teflon homogenizer on ice in buffer (10 mM HEPES at pH 7.4, 150 mM KCl, 5 mM MgCl₂, 0.5 mM dithiothreitol, 100 μg/mL cycloheximide, protease inhibitors,
was run to identify those GO biological processes enriched (Cytoscape 2.8.2 with the BiNGO plugin (2.4) (Maere et al. 2005) at the mean plus two standard deviations of the glial gene fold change greater than the background threshold of 0.5 (demarked "Supplemental Excel File 1" from Cvetkovic-Lopes et al. (2010). Excel using the data from Table 3 of Honda et al. (2009) and (Dennis et al. 2003). functional annotation clustering tool of the DAVID interface test with B-H correction. The same list was analyzed using the 0.005) in the 188 Hcrt neuron transcripts using a hypergeometric rates, and scatter plots comparing replicate experiments. Data were normalized as described but using Affymetrix chip defini- tions. Briefly, GC robust multiarray average (GCRMA) was used to normalize within replicates and to biotinylated spike in probes between conditions. In Supplemental Table S2, fold change (FC), specificity index (SI), and pS1 are reported for all genes with expression >50 arbitrary fluorescent units and a fold change greater than the background threshold of 0.5 (demar ked at the mean plus two standard deviations of the glial gene fold changes) (Dougherty et al. 2010).

Gene list analysis was conducted using two tools in parallel. Cytoscape 2.8.2 with the BiNGO plugin (2.4) (Maere et al. 2005) was run to identify those GO biological processes enriched (P < 0.005) in the 188 Hcrt neuron transcripts using a hypergeometric test with B-H correction. The same list was analyzed using the functional annotation clustering tool of the DAVID interface (Dennis et al. 2003).

List-wise comparison with previous studies was conducted in Excel using the data from Table 3 of Honda et al. (2009) and “Supplemental Excel File 1” from Cvetkovic-Lopes et al. (2010). Markers considered for χ² were Gal, Hct, Pdyn, Igfbp3, and Cattpt.

Sleep physiology
Polysomnographic sleep–wake cycle analysis of mice was performed as described previously (Bero et al. 2011; Roh et al. 2012). Briefly, EEG and electromyogram (EMG) electrodes were implanted simultaneously 10 d prior to recording. For EEG recording, two stainless steel screws attached to wire electrodes were placed over the right frontal and parietal bone. EMG was recorded by two wire electrodes directly inserted into the neck muscles. The ground electrode was placed on the skull over the cerebellum. Insulated leads from the EEG and EMG electrodes were soldered to a miniconnector. After 10 d of habituation after surgery, mice were transferred to recording cages maintained in 12-h light/12-h dark conditions (light on at 6:00 a.m.), and the miniconnector was connected to flexible recording cables. Mice were habituated to the recording cages for three more days. At the end of the habituation period, EEG and EMG recordings began. EEG and EMG recordings were assessed using a P511K A.C. Preamplifier (Grass-Telefactor Instruments), digitized with a DigiData 1440A data acquisition system (Molecular Devices), and recorded digitally using pClamp 10.2 (Molecular Devices). Using sleep scoring software (SleepSign, Kissei Comtec Co. Ltd.), EEG and EMG signals were binned into 10-sec epochs as wakefulness, REM sleep, and NREM sleep based on the standard criteria of rodent sleep. Semiautomatic sleep scoring was visually inspected and corrected when appropriate. The automatic analy sis and visual inspection were performed in a blinded state to the genotypes of mice. Episodes of cataplexy, defined as described (Scammell et al. 2009), were not seen in Lhx9−/− knockout mice.

Generation of plasmids
Lhx9 (Open Biosystems, clone 40117467, BC131622.1) was cloned with Gateway technology into a custom Gateway-compat ible lentiviral vector derived from the previously published FCIV [Li et al. 2010] by replacing the IRES-Venus sequence with a Gateway acceptor cassette. This plasmid was validated with antibody staining for Lhx9 expression following both transient transfection and lentiviral transduction. For the luciferase as say, a fragment of the mouse promoter corresponding to the 3 kb upstream of the translation start site was cloned by PCR into the pGL3 basic vector (Invitrogen).

Overexpression of Lhx9 in the unilateral lateral hypothalamus
To investigate whether the overexpression of Lhx9 augments Hcrt signaling in the brain, Lhx9 lentiviral vector under the control of a ubiquitin promoter (1.5 μL, 1.9 × 10⁷ IU/mL) was unilaterally injected right above the left side lateral hypothalami s [anterioposterior [AP] −1.82, mediolateral [ML] −0.3, dor soventral [DV] 5.1 mm, directed vertically] in C57Bl/6J female mice. For a control group, GFP lentiviral vector (1.5 μL, 5 × 10⁷ IU/mL) was infused in the same way in C57Bl/6J female mice. After 8 d of viral vector infusion, mice were perfused, and brain tissue was obtained and stained as described. Immunofluorescence for either GFP or Lhx9 was used to confirm accurate targeting of viral injections. Two independent researchers blinded to the treatment manually counted the total number of cells stained with Hcrt.

Forty-eight-hour activity monitoring
The activity monitoring procedure was adapted from previously published methods (Dougherty et al. 2013). Briefly, Lhx9 knock-out and wild-type mice were placed in transparent polystyrene chambers (47.6 × 25.4 × 20.6 cm) containing food and clean home cage bedding spread on the floor and a water bottle attached to one wall. A metal grid containing a 4 × 8 matrix of photobeam pairs surrounded each chamber and was connected to a computer equipped with software (MotorMonitor, Kinder Scientific) that used an algorithm to quantify photobeam breaks as horizontal ambulations (an estimate of wakefulness) and the lack of photobeam breaks as time at rest (an estimate of sleep). A rest threshold of 40 sec was used based on previous findings that this threshold is optimal for photobeam assessment of inactivity.
as an estimate of sleep [Pack et al. 2007]. Activity monitoring began halfway through the light cycle and continued for 48 h. The testing room lighting was a 12-light:12-h dark cycle [light on at 6:00 a.m.]. Activity monitoring was conducted in two sessions separated by 1 mo, during which the Lhx9 knockout mice received Lhx9 or GFP lentiviral vector injections. SPSS statistics software was used for data analyses. To determine differences between genotypes during session 1, one-way ANOVAs were conducted on average time at rest and ambulations per hour, a repeated measures ANOVA was conducted on 6-h blocks of total ambulations across the light/dark cycle, and paired t-tests were conducted on time at rest within genotypes to assess circadian rhythms. One wild-type mouse was excluded from ambulation analyses as an outlier [z-score > 2.0].

For analysis of the influence of Lhx9 lentiviral vector injections on time at rest and ambulations of Lhx9 knockout mice, repeated measure ANOVAs were conducted on pre- and post-injection performance. One Lhx9-injected mouse was excluded because the injection was off-target.

**Viral rescue of Lhx9 in Lhx9 knockout mice**

To investigate whether the rescue of Lhx9 affects behavioral phenotype as well as Hcrt signaling in Lhx9 knockout mice, SPSS statistics software was used for data analyses. To determine differences in total ambulations across the light/dark cycle, and paired t-tests were conducted on time at rest within genotypes to assess circadian rhythms. One wild-type mouse was excluded from ambulation analyses as an outlier [z-score > 2.0]. For analysis of the influence of Lhx9 lentiviral vector injections on time at rest and ambulations of Lhx9 knockout mice, repeated measure ANOVAs were conducted on pre- and post-injection performance. One Lhx9-injected mouse was excluded because the injection was off-target.

**References**


