Vglut2-based glutamatergic signaling in central noradrenergic neurons is dispensable for normal

breathing and chemosensory reflexes

Author names and affiliations

Yuan Chang[1,2], Savannah Lusk[1], Andersen Chang[1], Christopher S Ward[2], Russell S Ray[1,2,3,4]

[1]Department of Neuroscience, Baylor College of Medicine, Houston, TX, USA

[2]Department of Integrative Physiology, Baylor College of Medicine, Houston, TX, USA

[3]McNair Medical Institute, Houston, TX, USA

[4]Corresponding author, russell.ray@bcm.edu

Abstract

Central noradrenergic (NA) neurons are key constituents of the respiratory homeostatic network.

NA dysfunction is implicated in several developmental respiratory disorders including Congenital

Central Hyperventilation Syndrome (CCHS), Sudden Infant Death Syndrome (SIDS) and Rett

Syndrome. The current unchallenged paradigm in the field, supported by multiple studies, is that

glutamate co-transmission in subsets of central NA neurons plays a role in breathing control. If

true, NA-glutamate co-transmission may also be mechanistically important in respiratory

disorders. However, the requirement of NA-derived glutamate in breathing has not been directly

tested and the extent of glutamate co-transmission in the central NA system remains

uncharacterized. Therefore, we fully characterized the cumulative fate maps and acute adult

expression patterns of all three Vesicular Glutamate Transporters (*Slc17a7* (Vglut1), *Slc17a6*

(Vglut2), and *Slc17a8* (Vglut3)) in NA neurons, identifying a novel, dynamic expression pattern

for Vglut2 and an undescribed co-expression domain for Vglut3 in the NA system. In contrast to

our initial hypothesis that NA derived glutamate is required to breathing, our functional studies

showed that loss of Vglut2 throughout the NA system failed to alter breathing or metabolism

under room air, hypercapnia, or hypoxia in unrestrained and unanesthetized mice. These data

demonstrate that Vglut2-based glutamatergic signaling within the central NA system is not

required for normal baseline breathing and hypercapnic, hypoxic chemosensory reflexes. These

outcomes challenge the current understanding of central NA neurons in the control of breathing

and suggests that glutamate may not be a critical target to understand NA neuron dysfunction in

respiratory diseases.

Introduction

Breathing is a vital and life-sustaining function supporting homeostatic processes, most critically

maintaining blood pH/CO_2 and O_2 levels within a narrow physiological range. Respiratory

homeostasis is mediated by neuron-modulated lung ventilation adjustments in response to

physiological deviations resulting in high pCO_2 or low pO_2 blood and tissue levels, known as the

hypercapnic and hypoxic reflexes respectively (Del Negro et al., 2018; Dick et al., 2018). These

reflexes are part of a complex brainstem neural network that integrates a multitude of

information streams across the central and peripheral nervous systems to regulate respiratory

output. Within this brainstem network, central noradrenergic (NA) neurons are known to be an

important component that plays a variety of roles in modulating breathing. Furthermore, various

perturbations across the central NA system have been implicated in several developmental

disorders with respiratory and chemosensory features such as Congenital Central

Hyperventilation Syndrome (CCHS), Sudden Infant Death Syndrome (SIDS) and Rett Syndrome

(Beltrán-Castillo et al., 2017; Feldman et al., 2013; Gauda et al., 2007; Viemari, 2008).   Thus,

understanding how central NA neurons modulate respiratory chemoreflexes or chemosensory

breathing is critically important for the development of new diagnostic and therapeutic

interventions to address respiratory pathophysiology.

Central noradrenergic neurons are commonly thought to exert their effect on breathing through

their primary neurotransmitter noradrenaline and adrenaline. However, in addition to

noradrenaline, several studies provide strong evidence that glutamate is co-transmitted in

subsets of central NA neurons. Vesicular glutamate transporter 2 (Vglut2), a gene marker of

glutamatergic signaling, has been shown to be co-expressed in subsets of central NA neurons

including, C1/A1, C2/A2, A5, and LC in adult rats and mice (DePuy et al., 2013; Souza et al.,

2022a; Stornetta et al., 2002a, 2002b; Yang et al., 2021), though NA specific expression of

related Vglut1 and Vglut3 transporters remains unknown. Additionally, it has been well

documented that central NA neurons co-expressing Vglut2 innervate key respiratory centers,

such as preBötzinger complex and parafacial region (pFRG). Additionally, central NA neurons co-

expressing Vglut2 project to many key autonomic brainstem, spinal cord, and forebrain centers,

such as the dorsal motor nucleus of the vagus, intermediolateral nucleus (IML) and sympathetic

system, and the hypothalamus, all of which could drive a change in breathing if perturbed, i.e.,

indirect effects from cardio-vascular and metabolic dysregulation (Supplemental table 1). Thus,

it has become a dominant paradigm in the field of respiratory physiology that NA-based

glutamate release is a critical form of neurotransmission in the control of breathing. Abbott et al.

(2014) showed that Vglut2 is required for an increase in respiratory rate when anterior C1

neurons are unilaterally opto-genetically stimulated. Malheiros-Lima et al. (2020) showed that

Vglut2-expressing C1 neurons project to the pFRG region, and hypoxic breathing was blunted

after blockade of ionotropic glutamatergic receptors at the pFRG site in anesthetized rats,

together supporting a role for anterior C1 neurons releasing glutamate at the pFRG site to

regulate breathing under hypoxia. Similarly, Malheiros-Lima et al. (2022) and Malheiros-Lima et

al. (2018) showed that Vglut2-expressing C1 neurons project to the NA A5 region and the

preBötzinger complex, and, again, the blockade of ionotropic glutamatergic receptors at the A5

region or preBötzinger complex reduced the increase in phrenic nerve activity and respiratory

frequency elicited by optogenetic stimulation of C1 cells in an anesthetized preparation. In

addition, Guyenet et al. (2013) and others speculated that the apparent lack of plasmalemmal

monoamine transporter in C1 fibers indicates reduced or absent noradrenergic or adrenergic

signaling due a lack of re-uptake and neurotransmitter pool depletion (Comer et al., 1998; Lorang

et al., 1994). Cumulatively, the studies argue for glutamate as the predominant functional

neurotransmitter for C1 NA neurons in the breathing neural network. To our knowledge, this

dominant perspective has not been otherwise previously challenged. Although these studies are

informative, the evidence supporting the role of NA-based Vglut2 signaling in respiratory control

are either indirect and circumstantial or cannot be seen as physiological given experimental

limitations, such as the focal nature of opto-genetic stimulation. Thus, it is not yet clear what the

requirement is for NA-based glutamatergic signaling in homeostatic breathing in the
unanesthetized and unrestrained animal and how that might inform upon disease.
89
To better understand the role of NA-based glutamatergic signaling in breathing, we sought to
both fully characterize the molecular profiles of the central noradrenergic system with respect to
glutamate co-expression and to test the hypothesis that Vglut2-based glutamatergic release is
required in respiratory control under physiological chemosensory challenges in unanesthetized
and unrestrained mice. We first fully characterized the recombinase-based cumulative fate maps
for Vglut1, Vglut2 and Vglut3 expression and compared those maps to their real time expression
profiles in central NA neurons by RNA *in situ* hybridization in adult mice. We found a novel
dynamic expression pattern for Vglut2 and an entirely undescribed co-expression domain for
Vglut3 in the central NA system. Secondly, to determine if Vglut2-based glutamatergic signaling
in NA neurons is required for respiratory homeostasis, we conditionally ablated Vglut2 in all NA
neurons and tested respiratory, chemosensory, and metabolic function in unrestrained and
unanesthetized mice. Using the same genetic model in prior studies (Abbott et al., 2014),
conditional deletion of Vglut2 in NA neurons did not significantly impact breathing under room
air, hypercapnic, or hypoxic conditions. These results demonstrate, for the first time, that NA
Vglut2-based glutamatergic signaling is dispensable for respiratory control, which challenges the
prevalent perspective on the role of C1 and other Vglut2 expressing NA neurons in respiratory
homeostasis and suggests that glutamate may not be a critical target to understand NA neuron
dysfunction in respiratory diseases.
108
Results
Cumulative fate maps of central noradrenergic neurons co-expressing Vglut1, Vglut2 and
Vglut3
To fully characterize the expression profiles of all three glutamate markers Vglut1, Vglut2 and
Vglut3 in central noradrenergic neurons, we first used an intersectional genetic strategy (Figure
1A). We bred three Cre drivers $Slc17a7^{Cre}$ (Vglut1-Cre), $Slc17a6^{Cre}$ (Vglut2-Cre) and $Slc17a8^{Cre}$
(Vglut3-Cre) to $Dbh^{p2a-Flpo}$ (DBH-p2a-Flpo) (targeting noradrenergic neurons) mice, respectively.

The three compound lines of *Slc17a7^{Cre}*; *Dbh$^{p2a\text{-}Flpo}$*, *Slc17a6^{Cre}*; *Dbh$^{p2a\text{-}Flpo}$*, and *Slc17a8^{Cre}*; *Dbh$^{p2a\text{-}}$*

^{Flpo} were then crossed with the *Rosa26$^{RC::FLTG}$* (RC::FLTG). RC::FLTG are intersectional reporter

mice that express tdTomato in cells expressing only flippase (Flpo) and express eGFP in cells co-

expressing both Flpo and Cre recombinases. Thus, in each of the three intersectional reporter

crosses [e.g. 1) *Slc17a7^{Cre}*; *Dbh$^{p2a\text{-}Flpo}$*; *Rosa26$^{RC::FLTG}$*, 2) *Slc17a6^{Cre}*; *Dbh$^{p2a\text{-}Flpo}$*; *Rosa26$^{RC::FLTG}$* and

3) *Slc17a8^{Cre}*; *Dbh$^{p2a\text{-}Flpo}$*; *Rosa26$^{RC::FLTG}$*], NA neurons without any Vglut1, 2, or 3 expression are

labelled by red fluorescent protein (tdTomato) while NA neurons co-expressing either Vglut1,

Vglut2, or Vglut3 are labeled by green fluorescent protein (eGFP). By using this method, we

characterized and quantified the expression profiles of all three vesicular glutamate transporters

Vglut1, Vglut2, and Vglut3 across every anatomically defined NA nucleus in adult mice including

A7, Locus Coeruleus (LC), dorsal/ ventral subcoeruleus nucleus (sub CD/CV), A5, and the anterior

- posterior dimensions of C1/A1, C2/A2 (Robertson et al., 2013), and C3 (Figure 1B-D and Figure

1 supplement 1A-B). Vglut1-Cre was not co-expressed in any central NA nuclei in adult mice.

However, Vglut2-Cre and Vglut3-Cre both showed co-expression in central NA neurons. Vglut3-

Cre-expressing NA neurons were restricted to posterior C2/A2 and posterior C1/A1, with greatest

expression in posterior C2/A2 where $26.9 \pm 3.16\%$ of NA neurons were Vglut3-Cre positive. In

posterior C1/A1, only $1.26 \pm 0.559\%$ of NA neurons were Vglut3-Cre positive. Surprisingly, $84.6 \pm$

3.75% of NA neurons in total showed Vglut2-Cre co-expression and each NA nucleus was

predominantly labelled by Vglut2-Cre expression. Over 50% of NA neurons in each NA nucleus

were Vglut2-Cre positive. The percentages of Vglut2-Cre positive NA neurons in each NA nucleus

were as follows: $69.8 \pm 8.29\%$ in A7, $80.5 \pm 3.78\%$ in LC, $84.8 \pm 11.3\%$ in A5, $51.5 \pm 2.61\%$ in sub

CD/CV, $99.0 \pm 0.681\%$ in anterior C1/A1, $95.7 \pm 2.40\%$ in posterior C1/A1, $96.1 \pm 1.98\%$ in anterior

C2/A2, $97.8 \pm 0.771\%$ in posterior C2/A2, and $100 \pm 0.00\%$ in C3 (Mean $\pm$ SEM). The presence of

Vglut2-Cre co-expression in anterior NA groups was unexpected as previous *in situ* data in adult

rats found *Slc17a6* (Vglut2) positive NA neurons only in the posterior C2/A2 and C1/A1 (Stornetta

et al., 2002a, 2002b). Notably, however, the Vglut2 co-expression in the LC region agrees with

Yang et al. (2021) which also showed that 89% of LC NA neurons are Vglut2 positive using a

different intersectional strategy in mice: *Th^{Flpo}; Slc17a6^{Cre}; Rosa26^{Ai65}* (TH-Flpo; Vglut2-Cre; Ai65).

The differences in our and other fate maps compared to *in situ* hybridization may either reflect

early gene expression that is down regulated in the adult or may reflect low levels of expression
not detectable by *in situ* hybridization but that are nonetheless sufficient to affect recombination
in the intersectional genetic strategy.
148
Real time mRNA expression patterns of Vglut1, Vglut2 and Vglut3 in central noradrenergic
neurons in adult mice
To verify if the real time NA-based Vglut2 expression pattern in adult mice is comparable to
previous reports in adult rats (DePuy et al., 2013; Stornetta et al., 2002b, 2002a), and to further
characterize the expression patterns of the other two vesicular glutamate transporters (Vglut1
and Vglut3) in adult mice, we performed fluorescent RNA *in situ* hybridization experiments. We
co-stained *Slc17a7* (Vglut1), *Slc17a6* (Vglut2), or *Slc17a8* (Vglut3) with *Dbh* respectively in brain
tissue of adult mice and characterized the colocalization of *Slc17a7, Slc17a6, Slc17a8* with *Dbh* in
brainstem NA nuclei A7, LC, A5, sub CD/CV, anterior C1/A1 and C2/A2, posterior C1/A1 and
C2/A2, and C3 (Figure 2A-C and Figure 2 supplement 2A-B). No *Slc17a7/Dbh* double positive
neurons were detected in any part of the central NA system, consistent with our fate map.
Slc17a8 mRNA colocalization with *Dbh* was only found in the posterior part of C2/A2 where 27.1
$\pm$ 1.86% of *Dbh* positive neurons demonstrated *Slc17a8* colocalization, again consistent with our
fate map. However, we only found detectable levels of *Slc17a6* mRNA in the C1/A1, C2/A2 and
C3 NA regions, but not in the A7, LC, A5, sub CD/CV. The percentages of *Slc17a6/Dbh* double
positive neurons for regions where detected were as follows: 84.7 $\pm$ 5.82% in anterior C1/A1,
66.3 $\pm$ 0.335% in anterior C2/A2, 35.7 $\pm$ 3.01% in posterior C1/A1, 90.1 $\pm$ 2.45% in posterior
C2/A2, and 79.7 $\pm$ 3.94% in C3. This result is consistent with the previous *in situ* data in adult rats
(Stornetta et al., 2002a, 2002b) suggesting that there is no obvious expression difference of
Slc17a6 in the central NA system between mouse and rat. However, the *Slc17a6 in situ* data did
not show expression in anterior NA populations. This difference between our *in situ* data and fate
map data supports our previous hypothesis that many NA neurons expressed *Slc17a6* (Vglut2) at
some point from early development toward adulthood but the expression of *Slc17a6* (Vglut2) is
diminished during adulthood. Interestingly, Yang et al. (2021) did show adult Vglut2 co-
expression in LC by a viral injection of both Cre and Flpo-dependent eYFP into the LC of a bi-

transgenic mouse with both Th^{Flpo} and $Slc17a6^{Cre}$. To verify this result, we injected an AAV virus

containing Cre-dependent tdTomato (pAAV-EF1a-DIO-tdTomato-WPRE) into the LC region of

adult $Slc17a6^{Cre}$ mice. Consistent with Yang et al. (2021), we observed sparse Vglut2-Cre and TH-

immunopositive double labelled neurons in the LC (Figure 2 supplement 1). Additionally, Souza

et al. (2022a) showed about 28.5% of A5 neurons are $Slc17a6$ mRNA positive in adult rats by RNA

scope, a method which is more sensitive than the traditional *in situ* hybridization we used here.

These data suggest that some adult NA neurons in LC and A5 have $Slc17a6$ (Vglut2) co-expression,

but the $Slc17a6$ mRNA level cannot be detected by traditional *in situ* hybridization.

Vglut2 expression is effectively knocked down in the whole central noradrenergic system in

Dbh-Cre; Vglut2 cKO mice

To investigate the requirement of Vglut2-based glutamatergic signaling in the central NA system

in breathing under physiological challenges, we used Dbh-Cre; $Slc17a6^{flox/flox}$ (Dbh-Cre; Vglut2

cKO) to remove Vglut2 expression from all noradrenergic neurons. This is the same model used

by Abbott et al. (2014) to show that Vglut2 expression in the NA system was required for an

increase in respiratory frequency following unilateral optogenetic stimulation of anterior C1. To

verify if Vglut2 expression was effectively removed from central NA neurons in Dbh-Cre; Vglut2

cKO mice, we used fluorescent mRNA *in situ* hybridization for $Slc17a6$ (Vglut2) and Dbh in the

mouse brainstems and compared the $Slc17a6$ (Vglut2) signal intensity in Dbh positive neurons in

Dbh-Cre; Vglut2 cKO mice to their littermate controls. We found that $Slc17a6$ mRNA expression

was $96.4 \pm 0.226\%$ decreased compared to controls, indicating that the $Slc17a6$ (Vglut2) was

effectively recombined to abrogate expression in NA neurons (Figure 3A-B and Figure 3

supplement 1).

Vglut2-based glutamatergic signaling in central NA neurons is not required for baseline

breathing nor for the hypercapnic ventilatory reflex under distinct CO_2 challenges

Multiple prior studies provide indirect evidence that NA glutamate transmission may play roles

in respiratory function, particularly that anterior C1 neurons mediate the hypoxic ventilatory

response through the pFRG/RTN and/or the NA A5 group (Malheiros-Lima et al., 2022, 2020).

Additionally, the A5 group has been implicated in the hypercapnic reflex (Haxhiu et al., 1996).

Thus, we sought to determine if Vglut2-based glutamatergic signaling in central NA neurons is

necessary to regulate baseline breathing and the hypercapnic chemoreflex in unanesthetized and

unrestrained animals. We used whole-body barometric plethysmography to measure the

breathing and metabolism of unanesthetized and unrestrained mice. After a five-day habituation

protocol, the respiratory responses of Dbh-Cre; Vglut2 cKO mice and their littermate controls,

including the overall respiratory output or ventilatory equivalent of oxygen (V_E/V_{O2}), respiratory

rate (V_f), tidal volume (V_T), minute ventilation (V_E), metabolic demand (V_{O2}), inspiratory duration

(T_I), expiratory duration (T_E), breath cycle duration (T_{TOT}), inspiratory flow rate (V_T/T_I), and

expiratory flow rate (V_T/T_E), were measured under room air and hypercapnia (5% CO_2) (Figure

4A). 5% CO_2 gas challenge produced a significant change in all the respiratory parameters

compared to room air in both Dbh-Cre; Vglut2 cKO and control mice. However, surprisingly, Dbh-

Cre; Vglut2 cKO mice did not show significant differences in any respiratory or metabolic

parameter mentioned above compared to their littermate controls under both room air and 5%

CO_2 challenges (Figure 4B and Table 1-2). In addition, to investigate if Vglut2-based NA derived

glutamate is required for regulating the dynamic patterns of breathing, such as the breathing

rhythms, we generated Poincaré plots for T_I, T_E, T_{TOT}, V_T/T_I, V_T/T_E, V_f, V_T, and V_E and we calculated

the SD1 and SD2 statistics for each parameter under room air and 5% CO_2. We found that Dbh-

Cre; Vglut2 cKO mice only showed a marginally statistically significant increase in the SD1 of

inspiratory duration (T_I) (p=0.0492). Outside of this single comparison, however, we found no

significant differences in the other parameters between the two groups (Figure 4 supplement

1A-H). Thus, we theorize that the statistically significant result for the SD1 of T_I seen here is likely

either a result of measurement noise or a consequence of a type 1 error. The overall pattern of

results suggested that Vglut2-based glutamatergic signaling is not required for regulating either

the steady state of or the dynamic patterns of baseline breathing and hypercapnic ventilatory

reflex under 5% CO_2.

To further investigate the role of Vglut2-based glutamatergic signaling in the hypercapnic

response, we interrogated the system further with more severe hypercapnic exposures and

measured the breathing of Dbh-Cre; Vglut2 cKO mice under 7% CO_2 and 10% CO_2. Both 7% and

10% CO_2 stimuli produced a significant respiratory response in both mutant and control mice.

Under the 7% CO_2 condition, Dbh-Cre; Vglut2 cKO mice showed a significantly decreased tidal

volume (V_T) (p=0.023) and a significantly reduced inspiratory flow rate (V_T/T_I) (p=0.0016), but the

overall respiratory output (V_E/V_{O2}), respiratory rate (V_f), minute ventilation (V_E), metabolic

demand (V_{O2}), inspiratory duration (T_I), expiratory duration (T_E), breath cycle duration (T_{TOT}), and

expiratory flow rate (V_T/T_E) did not show a significant difference between the mutant mice and

their sibling controls (Figure 5A-B and Table 3). Additionally, none of the dynamic patterns of any

respiratory parameter showed a significant difference between the mutant and control groups

(Figure 5 supplement 1A-H). This result suggests that Vglut2-based glutamatergic signaling in

central NA neurons is not required for regulating the hypercapnic ventilatory reflex and breathing

regularity under 7% CO_2.

Under 10% CO_2 challenge, none of the steady state breathing parameters including the overall

respiratory outputs (V_E/V_{O2}), respiratory rate (V_f), tidal volume (V_T), minute ventilation (V_E),

metabolic demand (V_{O2}), inspiratory duration (T_I), expiratory duration (T_E), breath cycle duration

(T_{TOT}), inspiratory flow rate (V_T/T_I), and expiratory flow rate (V_T/T_E) were significantly different

between Dbh-Cre; Vglut2 cKO mice and their littermate controls, suggesting that Vglut2-based

glutamatergic signaling in central NA neurons is not required for the hypercapnic ventilatory

reflex under 10% CO_2 (Figure 6A-B and Table 4). For the dynamic patterns of breathing, the SD1

of breath cycle duration (T_{TOT}) (p=0.028) and SD1 of respiratory rate (V_f) (p=0.038) showed a

significant increase in mutant mice compared to the controls (Figure 6 supplement 1A-H). This

suggests that removing Vglut2 from central NA neurons may increase the breathing irregularity

under high CO_2 challenges like 10% CO_2.

Vglut2-based glutamatergic signaling in central NA neurons is not required for the hypoxic

ventilatory reflex under 10% O_2

To determine if Vglut2-based glutamatergic signaling in central NA neurons is necessary to

regulate the hypoxic chemoreflex, we measured the ventilation response of Dbh-Cre; Vglut2 cKO

mice under 10% O_2. We analyzed the ten respiratory parameters in three 5-min epochs following

10% O_2 challenge onset. Similar to the hypercapnic challenges, the 10% O_2 challenge produced a

significant breathing response in every 5-min epoch compared to room air, but no significant

difference was found in the overall respiratory output (V_E/V_{O2}), respiratory rate (V_f), tidal volume

(V_T), minute ventilation (V_E), metabolism demand (V_{O2}), inspiratory duration (T_I), expiratory

duration (T_E), breath cycle duration (T_{TOT}), inspiratory flow rate (V_T/T_I), and expiratory flow rate

(V_T/T_E) between Dbh-Cre; Vglut2 cKO mice and controls in any of the three 5-min 10% O_2 epochs

(Figure 7A-B and Table 5). These data suggest that Vglut2-based glutamatergic signaling in central

NA neurons is not required for the hypoxic ventilatory reflex under 10% O_2. For the dynamic

patterns of breathing, the SD2 of inspiratory flow rate (V_T/T_I) (p=0.005) and the SD2 of minute

ventilation (V_E) (p=0.026) were significantly increased during the first epoch (first 5 minutes)

under the 10% O_2 challenge in mutant mice, suggesting that Vglut2-based glutamate may play a

role in maintaining breathing regularity during the initial, or reflexive, response to hypoxia (Figure

7 supplement 1A-H).

Discussion

Neuron co-transmission of two or more neurotransmitters across excitatory, inhibitory, and

neuro-modulatory facets is becoming an increasingly appreciated phenomenon in the central

nervous system. Functional interrogation of co-transmission is essential not only to understand

the distinct and cooperative roles that multiple signaling molecules may play at the synapse but

also to determine the most critical targets for potential therapeutics. To our knowledge, the

unopposed paradigm in the field until now has been that vesicular glutamate transporter 2

(Vglut2)-based glutamate transmission from central noradrenergic neurons is important in

respiratory homeostasis. Anatomically, it has long been appreciated that central NA neurons co-

express Vglut2, the major glutamate marker among three glutamate transporters (DePuy et al.,

2013; Souza et al., 2022a; Stornetta et al., 2002a, 2002b; Yang et al., 2021). Also, it has been well

documented that NA Vglut2 positive fibers innervate known central respiratory centers or other

autonomic centers, that, when perturbed, could potentially disrupt respiratory homeostasis

(Supplemental Table 1). Functionally, multiple reports have suggested that Vglut2-based

glutamate transmission plays a role in respiratory homeostasis (Abbott et al., 2014;
Malheiros-Lima et al., 2022, 2020, 2018). It has also been suggested that, at least for C1 neurons,
the apparent lack of a plasmalemmal monoamine transporter may attenuate or eliminate
noradrenergic or adrenergic release from these fibers (Guyenet et al., 2013). However, as
discussed below, much of the functional evidence supporting a role for Vglut2-based glutamate
transmission from central noradrenergic neurons in breathing is circumstantial or of a non-
physiological nature, and absent or attenuated release of adrenaline and noradrenaline has not
been demonstrated. Nonetheless, the dominant perspective that NA-Vglut2 glutamate
transmission plays a role in breathing has remained unchallenged. Our studies, in contrast to
prior work, show that loss of Vglut2 in NA neurons does not appreciably change baseline or
chemosensory breathing in unanesthetized and unrestrained mice. Additionally, our work
uncovers a novel dynamic expression pattern for Vglut2 and an entirely undescribed co-
expression domain for Vglut3 in central NA neurons.

Vglut2 has been shown to be co-expressed in subsets of central NA neurons, however, to our
knowledge, the potential for the central NA neurons to express the other glutamate transporters
Vglut1 or Vglut3 has not been reported at the anatomical level. To determine if central NA
neurons express either Vglut1 or Vglut3 and to confirm the Vglut2 expression, we carried out
cumulative intersectional fate mapping using $Slc17a7^{Cre}$; $Dbh^{p2a-Flpo}$; $Rosa26^{RC::FLTG}$, $Slc17a6^{Cre}$;
$Dbh^{p2a-Flpo}$; $Rosa26^{RC::FLTG}$ and $Slc17a8^{Cre}$; $Dbh^{p2a-Flpo}$; $Rosa26^{RC::FLTG}$ compound mouse lines. As this
approach maps the cumulative history of expression, we also examined acute adult expression
of $Slc17a7$ (Vglut1), $Slc17a6$ (Vglut2) and $Slc17a8$ (Vglut3) using fluorescent RNA in $situ$
hybridization. Our in $situ$ results for $Slc17a6$ (Vglut2) agreed with earlier published outcomes
(DePuy et al., 2013; Stornetta et al., 2002a, 2002b) showing as much as 80% expression in
posterior NA neurons. However, there was no appreciable signal in anterior groups (A7, LC, A5,
sub CD/CV). This lack of expression was in stark contrast to the cumulative fate map for Vglut2,
showing as much as 75% of the anterior central NA neurons were recombined by the Vglut2-Cre
over the lifetime of the animal. To further interrogate the acute activity of the Vglut2-Cre in the
Locus Coeruleus in the adult mouse, we injected a Cre responsive virus in LC of $Slc17a6^{Cre}$ mice

and found sparse Vglut2-Cre positive NA neurons in the LC. The outcomes from the cumulative

fate map and acute injections are in agreement with published results from Yang et al. (2021).

Notably, our use of the $Dbh^{p2a-Flpo}$ avoided expression in the parabrachial nucleus (PBN), which

was a confounding variable in the Th^{Flpo} mouse. In addition, 28.5% of A5 neurons were shown to

be *Slc17a6* (Vglut2) positive in adult rats by RNA scope (Souza et al., 2022b). It is notable that

both our lab and the work published by (Stornetta et al., 2002a, 2002b) failed to detect *Slc17a6*

(Vglut2) expression in anterior groups, but that apparently very low levels can be detected by

more sensitive recombinase and RNA scope methods. Additional electrophysiological evidence

suggests that this expression is functional (Yang et al., 2021). However, it is notable that we see

nearly 80% of the LC and 85% of A5 recombined in the intersectional strategy representing

lifetime expression, but our study and others find only 20% of the LC and 28.5% of A5 may be

expressing *Slc17a6* (Vglut2) at any given moment in adults. Thus, it suggests that Vglut2 co-

expression in anterior NA groups is time dependent, though the underlying temporal dynamics

of Vglut2 remain unknown. We hypothesize that this could be either a temporal restriction in

expression as the animal matures or may reflect dynamic change driven by behavioral or

physiological experiences, which could be tested with the use of inducible conditional strategies.

For *Slc17a7* (Vglut1), neither fate map nor *in situ* hybridization revealed any co-expression within

the central NA system. However, *Slc17a8* (Vglut3) expression was found in the posterior part of

NA neurons including C2/A2 and C1/A1. This study is the first to characterize this expression. The

majority of this Vglut3 co-expression is restricted to the posterior part of the C2/A2 NA

population. This NA region has not been heavily implicated in respiratory control nonetheless it

readily lends itself to interrogation by intersectional genetic methods and *in situ* hybridization.

Given its distal expression from anterior C1, it is less likely that Vglut3 would compensate for loss

of Vglut2 in anterior C1, though this has not been ruled out. Further, while Vglut3 is a marker of

glutamatergic neurons, its role in neurotransmission is not wholly defined as Vglut3 is typically

found in soma and dendrites (Fremeau et al., 2004).

The cumulative fate map and *in situ* hybridization experiments were performed in both females

and males and no obvious sex difference was observed in the expression pattern of Vglut1, Vglut2

or Vglut3. However, only three mice were characterized in each dataset, thus, larger sample sizes

may capture more subtle outcomes for potential sex differences.

Based on the Vglut2 co-expression in NA neurons and their projections to multiple brain regions

important in respiration, several studies suggest that glutamate in NA populations is important

in breathing control. However, the evidence those studies provided is circumstantial, indirect, or

limited due to experimental caveats or technical limitations. Abbott et al. (2014), using exactly

the same mouse model as this study, showed that conditionally knocking out Vglut2 in the whole

central NA system did not significantly change respiratory rate under room air, which is

consistent with our findings here. Our results differ in that they reported removing Vglut2 from

central NA neurons attenuated an increase in respiratory rate resulting from unilateral C1

optogenetic stimulation. However, while the optogenetic stimulation of C1 neurons did drive a

Vglut2 dependent increase in respiratory rate, it is not clear if the resulting change in breathing

reflects a native feature of the network that might be engaged in chemosensory responses or

other aspects of breathing. It remains possible that strong unilateral optogenetic stimulation (up

to 20Hz) of a small, isolated population drives a Vglut2 dependent, but ectopic, function that is

not typically engaged in the normal operation of the breathing network. Such ectopic outcomes

could come from several potential, non-exclusive mechanisms. First, unilateral stimulation could

drive a network hysteresis or dysregulation similar to a focal injury that is not a typical biological

feature (Ducros et al., 2003). This point is well made in Abbott et al. (2013) in their discussion of

C1 optogenetic stimulation where they state, "resulting cardiorespiratory response pattern

should not be considered strictly "physiological," because a physiological response is never

initiated by selective activation of a single cluster of CNS neurons and the various subsets of C1

neurons are presumably never recruited en bloc under any physiological condition". Second,

strong stimulation could result in overwhelming synaptic mechanisms (i.e., glial uptake) resulting

in glutamate spillover and unintended cross talk to affect extra-synaptic neurons proximal to

targeted NA fibers. Activity dependent spillover transmission has been documented elsewhere

in the nervous system (Henneberger et al., 2020; Hülsmann et al., 2000). Third, the outcomes

could be secondary to a different autonomic or behavioral function requiring NA-derived

glutamatergic signaling involving metabolism or circulation (DePuy et al., 2013; Yang et al.,

2021). Additionally, respiratory parameters except for respiratory rate (V_f), such as tidal volume

(V_T) and minute ventilation (V_E) were not reported, making comprehensive comparison difficult.

More circumstantially, Malheiros-Lima et al. (2020) suggested C1 neurons potentially release

glutamate at the pFRG site to regulate active expiration under hypoxia in anesthetized rats by

providing three indirect lines of evidence: 1) Vglut2-expressing C1 neurons project to the pFRG

region; 2) Increased abdominal expiratory nerve activity (Abd_{EMG}) was blunted after blockade of

ionotropic glutamatergic receptors at the pFRG site under anesthesia using cytotoxic KCN

mediated hypoxia; and 3) Depletion of C1 neurons eliminated the increased Abd_{EMG} elicited by

hypoxia. However, 1) the glutamatergic signaling targeting the pFRG region is not necessarily

from C1 NA neurons since glutamatergic neurons from other regions also project to the pFRG site

(Yang and Feldman, 2018). Thus, it is possible that the glutamatergic signaling that is required for

hypoxic response is derived from other glutamatergic neurons such as the preBötzinger complex

and the RTN itself. Furthermore, 2) C1 neuron depletion knocks out all the signaling modalities

in the C1 population including both noradrenaline and glutamate. It is not clear which signaling

drives the hypoxic response. Finally, 3) KCN injection mimics a hypoxic challenge by activating

peripheral chemoreceptors, but the physiological responses differ from those seen during

environmental hypoxia exposure. Thus, the abdominal activity changes due to KCN injection may

not be recaptured under physiological hypoxic challenge.

Similarly, Malheiros-Lima et al. (2022) and Malheiros-Lima et al. (2018) showed that Vglut2-

expressing C1 neurons project to both the NA A5 region and the preBötzinger complex. The

blockade of ionotropic glutamatergic receptors at the A5 region or preBötzinger complex reduced

the increase in phrenic nerve activity and the breathing frequency caused by optogenetic

stimulation of C1 cells in an anesthetized preparation. Together these results suggest that Vglut2-

expressing C1 neurons communicate with A5 or preBötzinger complex neurons by releasing

glutamate in turn to regulate phrenic nerve activity or breathing frequency. Again, these two

studies showed that C1 neurons are important to regulate phrenic nerve activity or breathing

frequency, however, it is not necessarily through a direct C1-A5 or C1-preBötzinger complex

glutamatergic pathway, whereas an indirect multi-synaptic pathway originating with C1

noradrenaline and ending with glutamate transmission from an intermediate to A5 or

preBötzinger complex cannot be ruled out. Importantly, in all four studies noted here, respiratory

measurements were limited or proxies of breathing under anesthesia were used. The role of NA-

Vglut2 signaling was not reported in the context of an unanesthetized, unrestrained animal under

normoxic, hypoxic, or hypercapnic breathing in these previous studies.

Thus, the limitations and indirect lines of the evidence in these studies raised the question as to

whether or not glutamatergic signaling in central NA neurons is required or necessary to

modulate respiratory homeostasis under more physiologically relevant circumstances and if NA-

derived glutamate is an important mechanism to understand the pathophysiology of NA neurons

in respiratory diseases. The goal of our study was to test the requirement of NA-based

glutamatergic signaling in breathing homeostasis in the unanesthetized and unrestrained animal

under conditions that would engage the whole respiratory control network rather than a singular

component that may drive hysteresis or artifactual outcomes. Our *in vivo* breathing data under

room air, hypoxic, and multiple hypercapnic conditions failed to show the requirement of NA-

derived Vglut2 in normal breathing and respiratory chemoreflexes directly. For the dynamic

patterns of breathing, we measured the SD1 and SD2 of eight parameters under each gas

condition. We found no consistent change across multiple hypercapnic challenges or hypoxia.

We did find that under severe hypercapnic challenge (10% CO_2), NA derived Vglut2 removal

resulted in an increase in the SD1 of breath cycle duration and respiratory rate, which was not

observed under 5% and 7% CO_2 conditions. Under hypoxia (10% O_2), Dbh-Cre; Vglut2 cKO mice

only showed an increase in the SD2 of inspiratory flow rate and minute ventilation during the

first 5-minute of 10% O_2 exposure. These findings may suggest that Vglut2-based glutamatergic

signaling in central NA neurons may play a role in modulating breathing regularity under high CO_2

challenge and hypoxia. However, the phenotypes were of a small magnitude and not consistent

across challenges, and not at all seen under homeostatic breathing.

To ensure a rigorous and robust conclusion, we included several extra precautions and additional

measures in our experimental design and analysis. First, we use exactly the same mouse model,

DBH-Cre; Vglut2 cKO, as Abbott et al. (2014) used, and confirmed, by a second method

(fluorescent RNA *in situ* hybridization) that Vglut2 expression was indeed abrogated in the whole

central NA system. Our results are in strong agreement with DePuy et al. (2013) that

recombination is efficient. Notably, we assayed for expression at the cell body, rather than the

fibers and see no singular cell body that is scored positive. Second, we measured the breathing

of unanesthetized, unrestrained, and habituated mice under physiological challenges including

normoxia, hypercapnia and hypoxia. Third, to visualize breathing function comprehensively, the

metabolic parameter and multiple respiratory parameters (both the steady state and the

dynamic patterns) were measured and reported in absolute values including oxygen

consumption, respiratory rate, tidal volume, minute ventilation, overall respiratory output

(minute ventilation normalized to oxygen consumption), inspiratory duration, expiratory

duration, breath cycle duration, inspiratory flow rate, and expiratory flow rate. Fourth, our

experimental design was overpowered (i.e., n=16-21 vs 5-13 needed for power based on power

analysis and n=7-8 reported in other manuscripts). Each respiratory/metabolic parameter for

each physiological condition including room air, hypercapnia, and hypoxia was derived by

quantifying the entire respiratory trace and analyzed between mutant and sibling controls by

using a linear mixed-effects regression model with animal type (experimental vs. control) as fixed

effects, animal ID as a random effect, and sex as an experimental covariate (for which we did not

find a significant effect) (Lusk et al., 2023).

Despite our experimental design and the extensive nature of our measurements, there remain

several possibilities or considerations in the interpretation of our data. The first possibility is

Vglut3 in posterior CA domain (first characterized in this study) compensates for the effect of the

loss of Vglut2 in NA neurons in breathing. However, we argue that this is unlikely because 1) Our

model is the same used in the other study where a Vglut2-dependent effect was seen with

optogenetic stimulation. 2) Vglut3 is expressed in the posterior C2/A2 NA neurons which are

anatomically distant from anterior C1 and the LC (the two most likely NA candidates with Vglut2

co-expression to impact breathing). Also, posterior C2/A2 hasn't been heavily implicated in

breathing regulation. Future work will need to further investigate the role of Vglut3 in posterior

CA in respiratory control in order to test this possibility. The second possibility is that pre- or post-

natal developmental compensation corrects for the loss of NA derived glutamate. Again, we

argue that is unlikely, as 1) we are using the same adult model that provided the most direct

evidence and first functionally demonstrated a potential role for C1-derived glutamate in

breathing; 2) Abbott et al. (2014) highlight that C1 NA neurons showed no obvious abnormalities

in number, morphology, and projection patterns after knocking out Vglut2; and 3) we have

examined the requirement of NA-expressed Vglut2 in P7 neonate mice in the autoresuscitation

reflex and saw no differences (data not shown). However, it is still possible that developmental

compensation occurs before P7, which is something that could be better tested by using the Dbh-

CreERT2 (Stubbusch et al., 2011) to more acutely remove Vglut2 expression (though this leaves

a window of 2-3 weeks for compensation to occur). Third, as we only address the loss of NA-

Vglut2 based signaling across the entire NA system, it remains a formal possibility that this

ultimately results in the removal of Vglut2 dependent signaling from two counter balancing

regions of the NA system and are therefore left with null results whereas removal from anterior

C1 alone would show a requirement. To test this possibility, it would require an intersectional

conditional knockout/loss of function approach, something that has not yet been shown to be

efficient and effective and would be beyond the scope of these studies. Fourth, it is possible that

another neurotransmitter/neuropeptide within NA neurons might be released in higher amounts

in Dbh-Cre; Vglut2 cKO mice to compensate for the deficiency of glutamate in breathing. Loss of

Vglut2 could reduce dopamine release in subsets of dopaminergic neurons (Alsiö et al., 2011;

Fortin et al., 2012; Hnasko et al., 2010). Thus, it remains possible that loss of Vglut2 affects

dopamine loading into the vesicles and in turn affecting noradrenaline release as Dopamine Beta

Hydroxylase (DBH) synthesizes noradrenaline from dopamine inside the vesicles (Weinshenker,

2007). Changes in noradrenaline release in Vglut2 negative NA neurons could be further

examined with fast-scan cyclic voltammetry (FSCV) or microdialysis. Neuropeptide Y (NPY) and

galanin have been shown to co-exist in LC NA neurons and are involved in regulating energy

metabolism, stress, or anxiety (Ruohonen et al., 2012; Tasan et al., 2010; Weinshenker and

Holmes, 2016). In our studies, we account for potential metabolic changes that may underlie or

be coordinate with changes in breathing. However, we did not test for potential changes in blood

pressure or other autonomic functions as well as affective state that may, in some obscure way,

compensate for changes in breathing. Further interrogation of NPY or galanin signaling across NA

neurons and potential compensatory effects in breathing through changes in metabolism or

other autonomic function under stress or anxiety may yield notable insights. Lastly, our results

are loss of function in nature. We do not test sufficiency or gain of function and cannot fully rule

out a role for NA-Vglut2 based glutamatergic signaling in the control of breathing.

From a translational perspective, our data question whether or not glutamatergic signaling in NA

neurons is likely to be a key mechanism and therefore a therapeutic target for breathing

disorders, such as Rett syndrome and SIDS. *Mecp2*-deficient mice (a mouse model of Rett

Syndrome that phenocopies many human symptoms) showed both a deficiency of NA

populations (reduced number of NA neurons in C2/A2 and C1/A1 group) and highly variable

respiratory rhythm at around 4-5 weeks of age (Roux et al., 2007; Viemari et al., 2005). 80% of

Rett Syndrome patients experience breathing issues, such as unstable breathing, episodes of

hyperventilation, and breath holds, throughout their lifespan (Ramirez et al., 2020). SIDS

decedents show NA abnormalities and are hypothesized to ultimately succumb from a failure in

cardiorespiratory autoresuscitation   (Chigr et al., 1989; Garcia et al., 2013; Kopp et al., 1993;

Mansouri et al., 2001; Ozawa et al., 2003; Takashima and Becker, 1991).   However, Dbh-Cre;

Vglut2 cKO mice, have normal baseline and chemosensory respiratory parameters as adults and

neonate mice show normal autoresuscitation indicating that perturbed NA based glutamatergic

signaling may not be a key driver in these or other related respiratory pathophysiologies.

In conclusion, our studies show that Vglut2 has a dynamic and extensive expression profile across

the central NA system. We were able to characterize a novel Vglut3-expressing NA population in

the posterior C2/A2 nuclei. Despite prior studies providing indirect and circumstantial evidence

that noradrenergic-based glutamatergic signaling may play a role in control of breathing, our

conditional loss of function studies in adult unanesthetized and unrestrained mice failed to

consistently and significantly change room air breathing, the hypercapnic ventilatory reflex, and

the hypoxic ventilatory reflex. These outcomes offer a contrasting perspective from the current

field view and provides further insight into the potential role of NA-glutamate transmission in the

control of breathing and NA neuron dysfunction in respiratory disorders.

Materials and methods

Ethical approval

Studies were approved by the Baylor College of Medicine Institutional Animal Care and Use

Committee (IACUC) under protocol AN-6171, and all experiments reported here were performed

in accordance with relevant guidelines and regulations.

Breeding, genetic background, and maintenance of mice

We maintained all our heterozygous mouse strains by backcrossing to wildtype C57BL/6J mice

and homozygous mouse strains by sibling crosses. For immunofluorescence experiments,

heterozygous B6;129S-*Slc17a7$^{tm1.1(cre)Hze}$*/J (*Slc17a7^{Cre}*, Vglut1-Cre) (Jax Stock No: 023527),

Slc17a6$^{tm2(cre)Lowl}$/J (*Slc17a6^{Cre}*, Vglut2-Cre) (Jax Stock No: 016963) *and* B6;129S-

Slc17a8$^{tm1.1(cre)Hze}$/J (*Slc17a8^{Cre}*, Vglut3-Cre) (Jax Stock No: 018147) were mated with

heterozygous *Dbh$^{em2.1(flpo)Rray}$* (*Dbh$^{p2a-Flpo}$*, DBH-p2a-Flpo) (MMRRC ID: 41575) (Sun and Ray,

2016) mice respectively to derive compound lines with both Cre and Flpo alleles (*Slc17a7^{Cre}*;

Dbh$^{p2a-Flpo}$, *Slc17a6^{Cre}*; *Dbh$^{p2a-Flpo}$*, and *Slc17a8^{Cre}*; *Dbh$^{p2a-Flpo}$*). Then these three compound lines

were each mated with homozygous B6.Cg-*Gt(ROSA)26Sor$^{tm1.3(CAG-tdTomato,-EGFP)Pjen}$*/J (*Rosa26$^{RC::FLTG}$*)

(Jax Stock No: 026932) to derive three different intersectional mouse lines *Slc17a7^{Cre}*; *Dbh$^{p2a-Flpo}$*;

Rosa26$^{RC::FLTG}$, *Slc17a6^{Cre}*; *Dbh$^{p2a-Flpo}$*; *Rosa26$^{RC::FLTG}$* and *Slc17a8^{Cre}*; *Dbh$^{p2a-Flpo}$*; *Rosa26$^{RC::FLTG}$*. For

in situ hybridization experiments, wildtype C57BL/6J mice were ordered from the Center of

Comparative Medicine (CCM), Baylor College of Medicine. For NA-Vglut2 conditional loss of

function *in situ* hybridization and plethysmography experiments, hemizygous transgene Tg(Dbh-

cre)KH212Gsat (Dbh-Cre) (MMRRC ID: 036778-UCD GENSAT) mice were mated with homozygous

Slc17a6^{tm1Lowl}/J *(Slc17a6^{flox/flox})* (Jax Stock No: 012898) to derive Dbh-Cre; *Slc17a6^{flox/+}*. Dbh-Cre;

Slc17a6^{flox/+} mice were mated with *Slc17a6^{flox/flox}* to derive Dbh-Cre; *Slc17a6^{flox/flox}* (Dbh-Cre;

Vglut2 cKO). Sibling mice that lacked the Cre allele or carried the Cre allele but lacked the floxed

Vglut2 alleles were used as controls. Rosa26 specific primers for the *Rosa26^{RC::FLTG}* mice were 5'-

GCACTTGCTCTCCCAAAGTC,   5'-GGGCGTACTTGGCATATGAT,   and   5'-CTTTAAGCCTGCCCAGAAGA

(Ray et al., 2011) and yield a 495 bp band (targeted) and 330 bp band (wt). Cre-specific primers

for   all   Cre   drivers   were   5'-ATCGCCATCTTCCAGCAGGCGCACCATTGCCC   and   5'-

GCATTTCTGGGGATTGCTTA and yielded a 550 bp band if positive. Flpo-specific primers for *Dbh^{p2a-}*

^{Flpo} are 5'- CACGCCCAGGTACTTGTTCT and 5'-CCACAGCAAGAAGATGCTGA (Sun and Ray, 2016)

and yielded a 226 bp band if positive. *Slc17a6^{flox}* specific primers for Vglut2-floxed mice are

available at The Jackson Laboratory website (https://www.jax.org/strain/012898).

Immunofluorescence staining

Slc17a7^{Cre}; *Dbh^{p2a-Flpo}*; *Rosa26^{RC::FLTG}*, *Slc17a6^{Cre}*; *Dbh^{p2a-Flpo}*; *Rosa26^{RC::FLTG}* and *Slc17a8^{Cre}*; *Dbh^{p2a-}*

^{Flpo}; *Rosa26^{RC::FLTG}* adult mice of both sexes were sacrificed and transcardially perfused with 0.1

M phosphate-buffered saline (PBS) then with 4% paraformaldehyde (PFA) in PBS. Mouse brains

were dissected out and fixed for 2h in 4% PFA before a PBS rinse and dehydration in 30% sucrose

in PBS. Brains were embedded in OCT blocks, sectioned at the thickness of 30µm, mounted on

slides, and stored at -80°C until they were ready for staining. The slides were hydrated in 0.1%

Triton-X in PBS (PBST) for 15 mins, blocked with 5% donkey serum in 0.1% PBST for 1h at room

temperature and then incubated with primary antibodies for 72 hours at 4°C in 0.1% PBST with

5% donkey serum. Tissues were washed in 0.1% PBST 3 times for 10 min each and then incubated

with secondary antibodies for 2hs at room temperature in 0.1% PBST with 5% donkey serum.

Slides were washed with 0.1% PBST for 10 min and washed in PBS twice for 10 min each, stained

for DAPI, washed 3 times for 10 min each with PBS and mounted in ProLong Glass (Invitrogen).

The following primary and secondary antibodies were used: chicken anti-GFP (1:1,000, Abcam

ab13970), rabbit anti-dsRed (1:1,000, Clontech 632496), donkey anti-chicken Cy2 (1:500, Jackson

703-225-155), donkey anti-rabbit Cy3 (1:500, Jackson 711-165-152).

In situ hybridization

Mouse brains were dissected out from adult mice of both sexes with 6-8 week of age, sectioned into 25μm brain sections and mounted on slides. We generated a digoxigenin (DIG)-labeled mRNA antisense probe against *Slc17a7* (Vglut1), *Slc17a6* (Vglut2), and *Slc17a8* (Vglut3) and fluorescein (FITC)-labeled mRNA against *Dbh* using reverse-transcribed mouse cDNA as a template and an RNA DIG or FITC-labeling kits from Roche (Sigma). Primer and probe sequences for the *Slc17a7* (Vglut1), *Slc17a6* (Vglut2), and *Slc17a8* (Vglut3) and *Dbh* probes are available in the Allen Brain Atlas (http://www.brain-map.org). For the *Slc17a6* (Vglut2) and *Dbh* double ISH in Dbh-Cre; Vglut2 cKO and their littermate controls, we generated a new *Slc17a6* (Vglut2) probe targeting exon 2 of *Slc17a6* specifically (Tong et al., 2007) and the probe sequence is 892-1144bp as Slc17a6 transcript variant 1 and the size is 253bp. ISH was performed by the RNA In Situ Hybridization Core at Baylor College of Medicine using an automated robotic platform as previously described (Yaylaoglu et al., 2005) with modifications of the protocol for double ISH. Modifications in brief [see Yaylaoglu et al. (2005) for buffer descriptions]: both probes were hybridized to the tissue simultaneously. After the described washes and blocking steps the DIG-labeled probes were visualized using tyramide-Cy3 Plus (1/75 dilution, 15-minute incubation, Akoya Biosciences). After washes in TNT, the remaining HRP-activity was quenched by a 10-minute incubation in 0.2M HCl. The sections were then washed in TNT, blocked in TNB for 15 minutes, and incubated at room temperature for 30 minutes with HRP-labeled sheep anti-FITC antibody (1/500 in TNB, Roche/Sigma). Following washes in TNT, the FITC-labeled probe was visualized using tyramide-FITC Plus (1/50 dilution, 15-minute incubation, Akoya Biosciences). Following washes in TNT, the slides were stained with DAPI (invitrogen), washed again, removed from the machine, and mounted in ProLong Diamond (Invitrogen).

Viral injection

To verify Vglut2 co-expression in LC in adult mice (Yang et al., 2021), 6-week-old *Slc17a7^Cre* mice were injected with pAAV-EF1a-DIO-tdTomato-WPRE virus (RRID:Addgene_133786, obtained from Joshua Ortiz at the Optogenetics and Viral Vectors Core at the Jan and Dan Duncan Neurological Research Institute, 1ul at 7.90E+10 Gc/mL) into the LC (coordinates from bregma

anteroposterior −5.4 mm, lateral + 0.8 mm and dorsoventral – 4.0 mm) and allowed to incubate

for 4 weeks.

Plethysmography

Plethysmography on unanesthetized and free-moving mice was carried out as described in (Ray

et al., 2011). 6–8-week-old adult mice of both sexes with minimum group sizes n=16 were used

in both the experimental and control group for each experiment. Animals were subjected to a

five-day habituation protocol with each day including several minutes of handling, temperature

taken by rectal probe and at least 30 min exposure in the plethysmography chamber (Martinez

et al., 2019). Plethysmography started to be performed on the sixth day and was finished for all

animals within a week of the last day of habituation (Maximum 6 mice can be assayed for

plethysmography per day due to the limited number of plethysmography rigs). On the day of

testing, mice were taken out from their home cage, weighed, and rectal temperature was taken.

Animals were then placed into a flow-through, temperature-controlled (about 32°C with real-

time temperature recording) plethysmography chamber and allowed to acclimate for 20-40 mins

in room air (21% O_2/79% N_2) conditions. After acclimation (indicated by a steady respiratory trace

free from movement artifact), a 20-min baseline breathing trace was taken under room air, then

the chamber gas was switched to a hypercapnic or hypoxic mixture of 5% CO_2/21% O_2/74% N_2,

7% CO_2/21% O_2/72% N_2, 10% CO_2/21% O_2/69% N_2, or 10% O_2/90% N_2, depending on the protocol,

for 20 min. Chamber gas was then switched back to room air for another 20 min. The animals

were removed from the chamber and rectal temperature was measured immediately after the

mice were taken out from the chamber. Each testing period for an individual mouse was

separated by 24hs to allow for a full recovery.

Plethysmography data analysis and statistics

Details were previously described in (Martinez et al., 2019; Ray et al., 2011). Plethysmography

pressure changes were measured using a Validyne DP45 differential pressure transducer, CD15

carrier demodulator and a reference chamber, and were recorded with LabChart Pro in real time.

Respiratory waveforms were analyzed by the SASSI module of the Breathe Easy software to

determine respiratory frequency (V_f), tidal volume (V_T), minute ventilation (V_E), oxygen

consumption (V_{O2}), ventilatory equivalents for oxygen (V_E/V_{O2}), inspiratory duration (T_I),

expiratory duration (T_E), breath cycle duration (T_{TOT}), inspiratory flow rate (V_T/T_I), and expiratory

flow rate (V_T/T_E) (Lusk et al., 2023). Poincaré plots for T_I, T_E, T_{TOT}, V_T/T_I, V_T/T_E, V_f, V_T, V_E and their

SD1 and SD2 properties were generated and characterized by the STAGG module of the Breathe

Easy software. Analysis windows of the respiratory parameters were as follows: for room air, the

entire experimental period was considered; for hypercapnia, only the last 5 min challenge for

each of 5/7/10% CO_2 conditions were analyzed; and for hypoxia, three separate 5-min time

periods, namely the 5th-10th min, 10th-15th min, and 15th-20th min intervals, were used due to the

stereotypical biphasic respiratory response under this condition. Only steady quiescent breathing

periods were included in the data analysis. A power analysis was performed using the reported

effect size in Abbott et al. (2014), which used the same mouse model as we used here; 5-13 mice

were necessary to observe a statistically significant result (Abbott et al. (2014) was able to see a

significant difference between two groups with n=7 mice). In our experiments, the sample size

for each group (Dbh-Cre; Vglut2 cKO and control) exceeded 13. Steady state results (V_f, V_E, V_T,

V_{O2}, V_E/V_{O2}, T_I, T_E, T_{TOT}, V_T/T_I, V_T/T_E) for room air and hypercapnic or hypoxic data were compared

between Dbh-Cre; Vglut2 cKO cohorts and sibling controls using a linear mixed-effects regression

model with animal type (experimental vs. control) as fixed effects and animal ID as a random

effect (Lusk et al., 2023). SD1 and SD2 results for room air and hypercapnic or hypoxic data were

compared between Dbh-Cre; Vglut2 cKO cohorts and sibling controls using a Mann-Whitney U

test (Ferreira et al., 2022). A p-value threshold of $p < 0.05$ was used to test for statistical

significance. Individual data points, means, and standard errors of the mean are shown on all

charts. The graphs were plotted by Prism 8.

Image quantification

Images were taken by using a Zeiss upright epifluorescent microscope and a Zeiss LSM 880 with

Airyscan FAST confocal microscope. Images were captured using Zen software with z-stack

function from top to bottom with 0.34μm intervals, exported, and then analyzed in Imaris using

the spots and surface functions. For quantification of immunofluorescence staining, each GFP

positive area coincident with DAPI (to denote nuclear localization) was defined as Vglut2 or

Vglut3 expressing NA neurons while each tdTomato positive area coincident with DAPI was

defined as NA neurons without any Vglut2 or Vglut3 co-expression. For quantification of *Slc17a6*

(Vglut2) or *Slc17a8* (Vglut3) with *Dbh* double *in situ* hybridization in adult WT mice, *Dbh* positive

areas coinciding with DAPI were identified as NA neurons and the *Dbh* positive areas overlapped

with *Slc17a6* (Vglut2) or *Slc17a8* (Vglut3) positive pixels and DAPI were defined as NA neurons

colocalized with *Slc17a6* (Vglut2) or *Slc17a8* (Vglut3). The number of *Slc17a6* (Vglut2) or *Slc17a8*

(Vglut3) positive NA neurons and *Slc17a6* (Vglut2) or *Slc17a8* (Vglut3) negative NA neurons was

counted in each image for both immunofluorescence and *in situ* experiments and the percentage

of *Slc17a6* (Vglut2) or *Slc17a8* (Vglut3) positive NA neurons among all NA neurons in each NA

nucleus in each mouse brainstem was calculated every other brain section unilaterally. For

quantification of *Slc17a6* (Vglut2) and *Dbh* double ISH in Dbh-Cre; Vglut2 cKO and their littermate

controls, *Slc17a6* (Vglut2) pixel intensities in *Dbh* positive areas coincident with DAPI (NA

neurons) were measured in mutant and control images separately. The *Slc17a6* (Vglut2) pixel

intensity in NA neurons of control brains was normalized as 1 and the relative *Slc17a6* (Vglut2)

pixel intensity of NA neurons in mutant brains compared to that in control brains was calculated.

At least three mouse brains were examined for each set of experiments in each group. All

quantitative results were graphed using Prism 8.

Data availability

All the data supporting this study is available from the corresponding author upon request.

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AAV virus used in viral injection.

Author contributions

YC designed and completed immunofluorescence staining, imaging, and plethysmography

experiments, analyzed data, wrote the initial manuscript, and revised the manuscript.

SL completed the viral injection experiments and revised the manuscript.

AC updated the Poincaré function of Breathe Easy software, helped analyze the data, and revised

the manuscript.

CSW updated SASSI within Breathe Easy software, helped analyze the data, and revised the

manuscript.

RSR conceptualized and designed the study, analyzed the data, and helped write and revised the

manuscript.

Competing interests

No competing interests are declared.

Figure 1. Cumulative fate maps of glutamate co-expressing NA neurons characterized by

intersectional genetics. (A) Breeding schematic to generate the three intersectional reporter

lines $Slc17a7^{Cre}$; $Dbh^{p2a-Flpo}$; $Rosa26^{RC::FLTG}$, $Slc17a6^{Cre}$; $Dbh^{p2a-Flpo}$; $Rosa26^{RC::FLTG}$, $Slc17a8^{Cre}$; Dbh^{p2a-}

^{Flpo}; $Rosa26^{RC::FLTG}$. In each of the three intersectional reporter crosses, NA neurons co-expressing

either Vglut1, Vglut2, or Vglut3 are labeled by green fluorescent protein (eGFP) while NA neurons

without any Vglut1,2, or 3 expressions are labelled by red fluorescent protein (tdTomato). Shown

as an example is the $Slc17a6^{Cre}$; $Dbh^{p2a-Flpo}$; $Rosa26^{RC::FLTG}$ (Vglut2-Cre/+; DBH-p2a-Flpo/+;

RC::FLTG/+) intersectional reporter line. (B) Quantification of the percentage of Vglut2-

coexpressing NA neurons among NA neurons in each brainstem NA nuclei including A7, LC, A5,

sub CD/CV, anterior C1/A1 and C2/A2, posterior C1/A1 and C2/A2. Pink data points represent

female data while blue data points represent male data. (C) Quantification of the percentage of

Vglut3-coexpressing NA neurons among NA neurons in each NA nuclei. Pink data points represent

female data while blue data points represent male data. (D) Fluorescent expression of tdTomato
(red) and eGFP (green) in coronal sections of Vglut1, Vglut2, or Vglut3 intersectional reporter
lines in brainstem NA nuclei. Nucleus is labeled by DAPI (blue). Scale bar 50μm.

Figure 2. Characterization of real time co-expression of Vglut1, Vglut2 and Vglut3 in brainstem
NA neurons in adult mice by fluorescent *in situ* hybridization. (A) Representative images of
Slc17a7 (Vglut1), *Slc17a6* (Vglut2), and *Slc17a8* (Vglut3) and *Dbh* (DBH) double ISH in coronal
sections of WT mice in all of brainstem NA nuclei in adult mice. DBH (green), Vglut1/2/3 (red),
DAPI (cyan). Scale bar 50μm. (B) Quantification of the percentage of *Slc17a6* (Vglut2) co-
expression in NA neurons in each NA nuclei. Female data (pink), male data (blue). (C)
Quantification of the percentage of *Slc17a8* (Vglut3) co-expression in NA neurons in each NA
nuclei. Female data (pink), male data (blue).

Figure 3. DBH with Vglut2 co-staining by fluorescent *in situ* hybridization confirms that Vglut2
expression is disrupted in the whole central NA system in Dbh-Cre; Vglut2 cKO mice. (A)
Representative images of *Slc17a6* (Vglut2) and *Dbh* (DBH) double ISH in anterior C1/A1, posterior
C1/A1, anterior C2/A2 and posterior C2/A2 in control and Dbh-Cre; Vglut2 cKO mice. DBH (green),
Vglut2 (red), DAPI (cyan). Scale bar 20μm.(B) Quantification of intensity of *Slc17a6* (Vglut2) signal
in control and Dbh-Cre; Vglut2 cKO mice.

Figure 4. Vglut2 conditional knockout in central noradrenergic neurons fails to alter baseline
breathing and the hypercapnic ventilatory reflex (5% CO$_2$). (A) Mouse model schematic and
experimental protocol including habituation and hypercapnia protocol (5% CO$_2$). (B) Under both
room air and hypercapnia (5% CO$_2$), Dbh-Cre; Vglut2 cKO mice didn't show significant changes in
respiratory output (V$_E$/V$_{O2}$), minute ventilation (V$_E$), respiratory rate (V$_f$), tidal volume (V$_T$),
metabolism demand (V$_{O2}$), inspiratory duration (T$_I$), expiratory duration (T$_E$), breath cycle
duration (T$_{TOT}$), inspiratory flow rate (V$_T$/T$_I$), and expiratory flow rate (V$_T$/T$_E$). Linear mixed-effects
regression model, ****$p<0.0001$, **$p<0.01$, *$p<0.05$, ns: $p \geq 0.05$.

Figure 5. Vglut2 conditional knockout in central noradrenergic neurons fails to alter the

majority of hypercapnic ventilation parameters and metabolism under 7% CO_2. (A) Mouse

model schematic and experimental protocol including habituation and hypercapnia protocol (7%

CO_2). (B) Knocking out Vglut2 in the whole NA system failed to alter V_E/V_{O2}, V_f, V_E, V_{O2}, T_I, T_E, T_{TOT},

V_T/T_E but only showed a significantly reduce in V_T and V_T/T_I under 7% CO_2 condition. Linear mixed-

effects regression model, ****$p<0.0001$, **$p<0.01$, *$p<0.05$, ns: $p\geq0.05$.

Figure 6. Vglut2 conditional knockout in central noradrenergic neurons fails to alter the

hypercapnic ventilatory reflex (10% CO_2). (A) Mouse model schematic and experimental

protocol including habituation and hypercapnia protocol (10% CO_2). (B) Knocking out Vglut2 in

the whole NA system didn't significantly alter V_E/V_{O2}, V_f, V_T, V_E, V_{O2}, T_I, T_E, T_{TOT}, V_T/T_I, and V_T/T_E

under 10% CO_2 condition. Linear mixed-effects regression model, ****$p<0.0001$, **$p<0.01$,

*$p<0.05$, ns: $p\geq0.05$.

Figure 7. Vglut2 conditional knockout in central noradrenergic neurons fails to alter the hypoxic

ventilatory reflex (10% O_2). (A) Mouse model schematic and experimental protocol including

habituation and hypoxia protocol (10% O_2). (B) Knocking out Vglut2 in the whole NA system did

not show significant breathing changes including V_E/V_{O2}, V_E, V_f, V_T, V_{O2}, T_I, T_E, T_{TOT}, V_T/T_I, and V_T/T_E

in either of the three five-minute time periods under hypoxia (10% O_2). Linear mixed-effects

regression model, ****$p<0.0001$, **$p<0.01$, *$p<0.05$, ns: $p\geq0.05$.

771
772   **Figure 1 Supplement 1. Cumulative fate maps of glutamate co-expressing NA neurons in C3 NA**

773   **nucleus.** (A) Fluorescent expression of tdTomato (red) and eGFP (green) in coronal sections of

774   Vglut1, Vglut2, or Vglut3 intersectional reporter lines in C3 NA nucleus. Nucleus is labeled by DAPI

775   (blue). Scale bar 50μm. (B) Quantification of the percentage of Vglut2 or Vglut3-coexpressing NA

776   neurons among NA neurons in C3 NA nucleus. Female data (pink), male data (blue).

777
Figure 2 Supplement 1. Virus injection of Cre-dependent tdTomato into LC of *Slc17a6^{Cre}* mice.

TH (green), tdTomato (red), nuclei (DAPI). Scale bar 50μm.

Figure 2 Supplement 2. Characterization of real time co-expression of Vglut1, Vglut2 and Vglut3

in C3 NA neurons in adult mice by fluorescent *in situ* hybridization. (A) Representative images

of *Slc17a7* (Vglut1), *Slc17a6* (Vglut2), and *Slc17a8* (Vglut3) and *Dbh* (DBH) double ISH in coronal

sections of WT mice in C3 NA nuclei in adult mice. DBH (green), Vglut1/2/3 (red), DAPI (cyan).

Scale bar 50μm. (B) Quantification of the percentage of *Slc17a6* (Vglut2)/*Slc17a8* (Vglut3) co-

expression in C3 NA nucleus. Female data (pink), male data (blue).

Figure 3 Supplement 1. DBH with Vglut2 co-staining by fluorescent *in situ* hybridization

confirms that Vglut2 expression is disrupted in C3 NA nucleus in Dbh-Cre; Vglut2 cKO mice. DBH

(green), Vglut2 (red), DAPI (cyan). Scale bar 20μm.

Figure 4 Supplement 1. Characterization of dynamic patterns of breathing in Dbh-Cre; Vglut2

cKO mice under room air and hypercapnia (5% CO_2). Poincaré plots and the measurement of

SD1 and SD2 of inspiratory duration (T_I) (A), expiratory duration (T_E) (B), breath cycle duration

(T_{TOT}) (C), inspiratory flow rate (V_T/T_I) (D), expiratory flow rate (V_T/T_E) (E), respiratory rate (V_f) (F),

tidal volume (V_T) (G), and minute ventilation (V_E) (H) in Dbh-Cre; Vglut2 cKO mice and their

littermate controls under room air and 5% CO_2 challenge. Mann-Whitney U test, ns: $p \geq 0.05$, p

value was shown if $p < 0.05$.

Figure 5 Supplement 1. Characterization of dynamic patterns of breathing in Dbh-Cre; Vglut2

cKO mice under room air and hypercapnia (7% CO_2). Poincaré plots and the measurement of

SD1 and SD2 of T_I (A), T_E (B), T_{TOT} (C), V_T/T_I (D), V_T/T_E (E), V_f (F), V_T (G), and V_E (H) in Dbh-Cre; Vglut2

cKO mice and their littermate controls under room air and 7% CO_2 challenge. Mann-Whitney U

test, ns: $p \geq 0.05$, p value was shown if $p < 0.05$.

Figure 6 Supplement 1. Characterization of dynamic patterns of breathing in Dbh-Cre; Vglut2

cKO mice under room air and hypercapnia (10% CO_2). Poincaré plots and the measurement of

SD1 and SD2 of T_I (A), T_E (B), T_{TOT} (C), V_T/T_I (D), V_T/T_E (E), V_f (F), V_T (G), and V_E (H) in Dbh-Cre; Vglut2

cKO mice and their littermate controls under room air and 10% CO_2 challenge. Mann-Whitney U

test, ns: $p \geq 0.05$, p value was shown if $p < 0.05$.

Figure 7 Supplement 1. Characterization of dynamic patterns of breathing in Dbh-Cre; Vglut2

cKO mice under room air and hypoxia (10% O$_2$). Poincaré plots and the measurement of SD1

and SD2 of T$_I$ (A), T$_E$ (B), T$_{TOT}$ (C), V$_T$/T$_I$ (D), V$_T$/T$_E$ (E), V$_f$ (F), V$_T$ (G), and V$_E$ (H) in Dbh-Cre; Vglut2

cKO mice and their littermate controls under room air and 10% O$_2$ challenge. Mann-Whitney U

test, ns: p≥0.05, p value was shown if p<0.05.

Table 1. Respiratory and metabolic values under room air conditions and the statistical tests.

Table 2. Respiratory and metabolic values under 5% CO$_2$ conditions and the statistical tests.

Table 3. Respiratory and metabolic values under 7% CO$_2$ conditions and the statistical tests.

Table 4. Respiratory and metabolic values under 10% CO$_2$ conditions and the statistical tests.

Table 5. Respiratory and metabolic values under 10% O$_2$ conditions and the statistical tests.

Supplemental table 1. Vglut2 positive innervations from central noradrenergic neurons to the

brain nuclei important in breathing control.

823
824 **References**
825

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Figure 1

A

Rosa26^{RC::FLTG} intersectional reporter

Slc17a7^{Cre}; Dbh^{p2a-Flpo}; Rosa26^{RC::FLTG}
or
Slc17a6^{Cre}; Dbh^{p2a-Flpo}; Rosa26^{RC::FLTG}
or
Slc17a8^{Cre}; Dbh^{p2a-Flpo}; Rosa26^{RC::FLTG}

B   **C**

Figure 1. cont.

D

Figure 2

Figure 3

A

Anterior C1/A1

	Dbh-Cre; Vglut2 cKO	Control

DBH | Vglut2 | DBH/Vglut2/DAPI

Posterior C1/A1

	Dbh-Cre; Vglut2 cKO	Control

DBH | Vglut2 | DBH/Vglut2/DAPI

Anterior C2/A2

	Dbh-Cre; Vglut2 cKO	Control

DBH | Vglut2 | DBH/Vglut2/DAPI

Posterior C2/A2

	Dbh-Cre; Vglut2 cKO	Control

DBH | Vglut2 | DBH/Vglut2/DAPI

B

Relative Intensity of Vglut2 in DBH+ neurons
(Normalized to Ctrl)

Control

Dbh-Cre; Vglut2 cKO

0.0　0.5　1.0　1.5　2.0

Figure 4

A

B

Figure 5

Figure 6

Figure 7

Figure 1 Supplement 1

A

Vglut1	Vglut2	Vglut3

C3

GFP
tdTomato
DAPI

B

C3

GFP⁺/GFP⁺ + tdTomato⁺ (%)

Vglut2 Vglut3

Figure 2 supplement 1

Locus Coeruleus

TH

tdTomato

TH/ tdTomato/ DAPI

Figure 2 Supplement 2

A

	Vglut1	Vglut2	Vglut3

C3

B

C3

Ratio of co-expressed DBH⁺ neurons (%)

Vglut2   Vglut3

Figure 3 Supplement 1

C3

Figure 4 Supplement 1

Figure 5 Supplement 1

Figure 7 Supplement 1

Table 1. Respiratory and metabolic values under room air conditions and the statistical tests

	Dbh-Cre; Vglut2 cKO Mean ± SEM	Control Mean ± SEM	Dbh-Cre; Vglut2 cKO vs Control linear mixed-effects regression model
V_E/V_{O2}	30.01 ± 2.58	33.22 ± 3.97	P = 0.98
V_f (Breaths/min)	204.08 ± 10.04	213.58 ± 15.36	P = 0.98
V_T (ml/Breath/g)	0.009 ± 0.0007	0.009 ± 0.0006	P = 0.88
V_E (ml/min/g)	1.93 ± 0.14	1.98 ± 0.22	P = 0.995
V_{O2} (ml/min/g)	0.067 ± 0.004	0.061 ± 0.004	P = 0.78
T_I (s)	0.117 ± 0.004	0.118 ± 0.005	P = 0.9999
T_E (s)	0.265 ± 0.020	0.255 ± 0.021	P = 0.996
T_{TOT} (s)	0.381 ± 0.022	0.373 ± 0.024	P = 0.99997
V_T/T_I (ml/Breath/g/s)	2.12 ± 0.16	2.33 ± 0.26	P = 0.996
V_T/T_E (ml/Breath/g/s)	1.43 ± 0.19	1.85 ± 0.39	P = 0.99

Table 2. Respiratory and metabolic values under 5% CO_2 conditions and the statistical tests

	Dbh-Cre; Vglut2 cKO Mean ± SEM	Control Mean ± SEM	Dbh-Cre; Vglut2 cKO vs Control linear mixed-effects regression model
V_E/V_{O2}	47.99 ± 3.28	58.60 ± 5.44	P = 0.33
V_f (Breaths/min)	246.72 ± 9.78	261.66 ± 14.00	P = 0.24
V_T (ml/Breath/g)	0.011 ± 0.0007	0.010 ± 0.0008	P = 0.81
V_E (ml/min/g)	2.67 ± 0.20	2.80 ± 0.32	P = 0.98
V_{O2} (ml/min/g)	0.057 ± 0.003	0.051 ± 0.005	P = 0.42
T_I (s)	0.119 ± 0.004	0.118 ± 0.007	P = 0.62
T_E (s)	0.135 ± 0.005	0.136 ± 0.007	P = 0.42
T_{TOT} (s)	0.255 ± 0.009	0.254 ± 0.013	P = 0.32
V_T/T_I (ml/Breath/g/s)	2.32 ± 0.21	2.45 ± 0.25	P = 0.99
V_T/T_E (ml/Breath/g/s)	2.17 ± 0.21	2.27 ± 0.25	P = 0.91

Table 3. Respiratory and metabolic values under 7% CO_2 conditions and the statistical tests

	Dbh-Cre; Vglut2 cKO Mean ± SEM	Control Mean ± SEM	Dbh-Cre; Vglut2 cKO vs Control linear mixed-effects regression model
V_E/V_{O2}	58.48 ± 4.29	74.70 ± 6.22	P = 0.23
V_f (Breaths/min)	262.69 ± 12.82	284.44 ± 10.59	P = 0.98
V_T (ml/Breath/g)	0.011 ± 0.0011	0.015 ± 0.0012	P = 0.023*
V_E (ml/min/g)	2.90 ± 0.32	4.23 ± 0.43	P = 0.16
V_{O2} (ml/min/g)	0.051 ± 0.004	0.059 ± 0.006	P = 0.64
T_I (s)	0.114 ± 0.005	0.112 ± 0.007	P = 0.90
T_E (s)	0.128 ± 0.008	0.111 ± 0.005	P = 0.69
T_{TOT} (s)	0.242 ± 0.012	0.223 ± 0.009	P = 0.81
V_T/T_I (ml/Breath/g/s)	1.93 ± 0.22	2.96 ± 0.33	P = 0.0016**
V_T/T_E (ml/Breath/g/s)	1.86 ± 0.25	3.18 ± 0.41	P = 0.075

Table 4. Respiratory and metabolic values under 10% CO_2 conditions and the statistical tests

	Dbh-Cre; Vglut2 cKO Mean ± SEM	Control Mean ± SEM	Dbh-Cre; Vglut2 cKO vs Control linear mixed-effects regression model
V_E/V_{O2}	105.77 ± 10.80	105.69 ± 11.51	P = 0.9996
V_f (Breaths/min)	336.31 ± 5.26	336.38 ± 8.52	P = 0.9997
V_T (ml/Breath/g)	0.018 ± 0.0015	0.016 ± 0.0012	P = 0.98
V_E (ml/min/g)	5.94 ± 0.48	5.54 ± 0.45	P = 0.9996
V_{O2} (ml/min/g)	0.059 ± 0.003	0.058 ± 0.005	P = 0.9999999
T_I (s)	0.099 ± 0.003	0.103 ± 0.004	P = 0.97
T_E (s)	0.085 ± 0.004	0.081 ± 0.006	P = 0.63
T_{TOT} (s)	0.184 ± 0.003	0.184 ± 0.005	P = 0.995
V_T/T_I (ml/Breath/g/s)	3.62 ± 0.25	3.61 ± 0.34	P = 0.9995
V_T/T_E (ml/Breath/g/s)	4.59 ± 0.39	5.06 ± 0.65	P = 0.86

Table 5. Respiratory and metabolic values under 10% O_2 conditions and the statistical tests

	Dbh-Cre; Vglut2 cKO Mean ± SEM	Control Mean ± SEM	Linear mixed-effects regression model	Dbh-Cre; Vglut2 cKO Mean ± SEM	Control Mean ± SEM	Linear mixed-effects regression model	Dbh-Cre; Vglut2 cKO Mean ± SEM	Control Mean ± SEM	Linear mixed-effects regression model
	10% O$_2$_1			10% O$_2$_2			10% O$_2$_3		
V_E/V_{O2}	43.79 ± 4.57	57.75 ± 10.88	P = 0.99	41.30 ± 3.85	49.36 ± 6.93	P = 0.99	42.82 ± 3.97	49.19 ± 6.02	P = 0.99
V_f (Breaths/min)	269.71 ± 8.49	243.89 ± 7.64	P = 0.67	268.38 ± 8.40	251.15 ± 8.67	P = 0.83	273.96 ± 9.31	255.84 ± 12.19	P = 0.80
V_T (ml/Breath/g)	0.009 ± 0.0009	0.010 ± 0.0009	P = 0.89	0.009 ± 0.0008	0.011 ± 0.0009	P = 0.85	0.009 ± 0.0009	0.011 ± 0.0013	P = 0.64
V_E (ml/min/g)	2.58 ± 0.25	2.40 ± 0.21	P = 0.999998	2.45 ± 0.24	2.65 ± 0.21	P = 0.9998	2.53 ± 0.24	2.92 ± 0.41	P = 0.998
V_{O2} (ml/min/g)	0.063 ± 0.008	0.055 ± 0.006	P = 0.995	0.063 ± 0.007	0.061 ± 0.005	P = 0.9998	0.064 ± 0.008	0.063 ± 0.006	P = 0.99999999
T_I (s)	0.111 ± 0.005	0.126 ± 0.010	P = 0.44	0.115 ± 0.006	0.131 ± 0.012	P = 0.51	0.116 ± 0.006	0.132 ± 0.011	P = 0.44
T_E (s)	0.123 ± 0.007	0.133 ± 0.009	P = 0.995	0.119 ± 0.006	0.121 ± 0.008	P = 0.9999	0.114 ± 0.007	0.117 ± 0.008	P = 0.9997
T_{TOT} (s)	0.234 ± 0.007	0.259 ± 0.009	P = 0.53	0.234 ± 0.007	0.252 ± 0.009	P = 0.75	0.230 ± 0.008	0.248 ± 0.011	P = 0.69
V_T/T_I (ml/Breath/g/s)	1.83 ± 0.23	1.83 ± 0.20	P = 0.9999	1.66 ± 0.19	1.91 ± 0.20	P = 0.998	1.67 ± 0.18	1.98 ± 0.26	P = 0.99
V_T/T_E (ml/Breath/g/s)	1.79 ± 0.24	2.00 ± 0.29	P = 0.9994	1.69 ± 0.21	2.32 ± 0.32	P =0.99	1.83 ± 0.21	2.67 ± 0.51	P = 0.98

Supplemental table 1. Vglut2 positive innervations from central noradrenergic neurons to the brain nuclei important in breathing control

Vglut2[+] noradrenergic nuclei	Downstream target of Vglut2^{+} NA neurons	The role of the downstream target in breathing control	Reference
C1	preBötzinger complex	Generate inspiratory rhythm	Malheiros-Lima et al. (2018)
	parafacial region (pFRG)	Regulate active expiration during chemosensory stimulation	Malheiros-Lima et al. (2020)
	Locus Coeruleus (LC)	Chemosensitive, regulate chemosensation	Abbott et al. (2013); Holloway et al. (2013)
	A5	Inhibitory drive for chemosensation and respiratory rhythm	Abbott et al. (2013); Malheiros-Lima et al. (2022)
	A1, A2	Modulate chemosensation, stabilize respiratory rhythm	Abbott et al. (2013); Holloway et al. (2013)
	Lateral parabrachial nucleus (PBN)	Regulate chemosensation and arousal	Abbott et al. (2013)
	Medullary raphe	Regulate chemosensation and expiration	Abbott et al. (2013)
	Nucleus of the solitary tract (NTS)	Receive input from the carotid bodies (a key center for O_2 chemosensation) and other cardiopulmonary afferents	Abbott et al. (2013)
	Dorsal motor nucleus of the vagus	Control respiration rate, regulate airway tone and defense	Abbott et al. (2013)
	Dorsomedial hypothalamus (DMH) lateral hypothalamic area (LHA)	Modulate baseline respiration, chemosensation, arousal	Abbott et al. (2013)
	Paraventricular thalamic nucleus (PVT)	Regulate arousal	Abbott et al. (2013)
	Paraventricular nucleus (PVN)	Modulate baseline respiration, respiratory response to hypoxia	Abbott et al. (2013)
Locus Coeruleus (LC)	Lateral parabrachial nucleus	Regulate chemosensation and arousal	Yang et al. (2021)