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

breathing and chemosensory reflexes

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Abstract

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

NA dysfunction is implicated in several developmental respiratory disorders including Central

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

Syndrome. Multiple prior studies provide indirect evidence that glutamate is co-transmitted in

subsets of NA neurons and may play a role in breathing control. If true, NA-glutamate co-

transmission may also be mechanistically important in respiratory disorders. However, the extent

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

requirement of NA derived glutamate in breathing has not been directly tested. Therefore, we

fully characterized the cumulative fate maps and acute adult expression patterns of all three

Vesicular Glutamate Transporters (Vglut1, Vglut2, and Vglut3) in NA neurons, identifying broad

expression of Vglut2 as the dominant transporter in the NA system. 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 conscious mice, which

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

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

suggests that glutamate may be not 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, NA abnormalities have been implicated in several developmental disorders with respiratory and chemosensory features such as Central Congenital 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. Many *in vitro* experiments suggested that noradrenaline is essential for development of normal respiratory rhythm of mice and for modulation of respiratory chemoreflexes. For example, the blockade of α2 adrenergic receptors and the activation of catecholamine biosynthesis significantly depresses and facilitates, respectively, the respiratory rhythm generator, pre-Bötzinger complex (Zanella et al., 2006). External noradrenaline application to RTN, a key central chemosensory center, altered activities of subsets of RTN neurons. The blockade of α1 and α2 adrenergic receptors depressed and enhanced noradrenaline-mediated RTN neuron activities respectively (Kuo et al., 2016). Additionally, several respiratory disorders mentioned above showed various perturbations across the noradrenergic system. The embryonic lethality of *Phox2b-/-* mice (a mouse model of CCHS) can be (partially) rescued by maternal treatment with an α1 noradrenergic agonist. *Mecp2*

male mice (a mouse model of Rett Syndrome) show a reduction in noradrenaline levels and

external application of noradrenaline can restore fictive eupneic breathing to control levels

(Pattyn et al., 2000). Postmortem studies found abnormalities in noradrenaline levels in cases of

SIDS in the locus coeruleus and medulla (Denoroy et al., 1987; Lavezzi et al., 2005; Obonai et al.,

1998; Ozand and Tildon, 1983; Ozawa et al., 1999; Perrin et al., 1984) as well as loss of

adrenergic receptors in the medulla (Chigr et al., 1989; Kopp et al., 1993; Mansouri et al., 2001;

Ozawa et al., 2003; Takashima and Becker, 1991).

However, in addition to noradrenaline, several studies suggest that glutamate is co-transmitted

in subsets of central NA neurons and therefore may also play a role in breathing control. 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. Functionally, Abbott et al. (2014) showed that Vglut2 is required for an increase in

respiratory rate when anterior C1 neurons are unilaterally opto-genetically stimulated. More

circumstantially, 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 in turn 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

respectively, and again the blockade of ionotropic glutamatergic receptors at the A5 region or

preBötzinger complex reduced the increase in phrenic nerve activities or in respiratory frequency

elicited by optogenetic stimulation of C1 cells in an anesthetized preparation. Although these

studies offer circumstantial evidence for NA-based Vglut2 signaling in respiratory control, it is not

yet clear what the requirement is for NA-based glutamatergic signaling in homeostatic breathing

in the awake and unrestrained animal and how that might inform upon disease.

To better understand the role of NA-based glutamatergic signaling in breathing, 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 that Vglut2 and Vglut3, previously

undescribed, both show co-expression in the adult 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 conscious mice. Using the same genetic model in prior

studies, conditional deletion of Vglut2 in NA neurons did not significantly impact breathing under

room air, hypercapnic, or hypoxic conditions. These results suggest that NA Vglut2-based

glutamatergic signaling is dispensable for respiratory control and that glutamate may not be a

critical target to understand NA neuron dysfunction in respiratory diseases.

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 *Vglut1-Cre/+, Vglut2-Cre/+ and Vglut3-Cre/+* to *DBH-p2a-Flpo/+*

(targeting noradrenergic neurons) mice respectively. The three compound lines of *Vglut1-Cre/+;*

DBH-p2a-Flpo/+, Vglut2-Cre/+; DBH-p2a-Flpo/+, and Vglut3-Cre/+; DBH-p2a-Flpo/+ were then

crossed with the *RC::F_TdTomato_P_GFP (RC::FLTG)* intersectional reporter mice which express

tdTomato in cells co-expressing flippase (Flpo) while expressing eGFP in cells co-expressing both

Flpo and Cre recombinases. Thus, in each of the three intersectional reporter crosses, *Vglut1-*

Cre/+; DBH-p2a-Flpo/+; RC::FLTG/+, Vglut2-Cre/+; DBH-p2a-Flpo/+; RC::FLTG/+ and Vglut3-Cre/+;

DBH-p2a-Flpo/+; RC::FLTG/+, NA neurons co-expressing either Vglut1, Vglut2, or Vglut3 are

labeled by green fluorescent protein (eGFP) while NA neurons without any Vglut1/2/3 expression

are labelled by red fluorescent protein (tdTomato). By using this method, we characterized and

quantified the expression profiles of all three vesicular glutamate transporters Vglut1, Vglut2 and

Vglut3 across every NA nucleus in adult mice including A7, Locus Coeruleus (LC), sub CD/CV, A5,

anterior and posterior part of C1/A1, anterior and posterior part of C2/A2 (Figure 1B-D). *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 are

restricted to posterior C2/A2 and posterior C1/A1, and the majority is in posterior C2/A2 where

$26.9 \pm 3.16\%$ NA neurons are *Vglut3-Cre*[+]. In posterior C1/A1, only $1.26 \pm 0.559\%$ NA neurons are

Vglut3-Cre[+]. Surprisingly, $84.6 \pm 3.75\%$ NA neurons in total have *Vglut2-Cre* co-expression and

each NA nucleus was predominantly labelled by *Vglut2-Cre* expression. The percentage of *Vglut2-*

Cre^{+} NA neurons in A7, LC, A5, sub CD/CV, anterior and posterior part of C1/A1, anterior and

posterior part of C2/A2 is $69.8 \pm 8.29\%$, $80.5 \pm 3.78\%$, $84.8 \pm 11.3\%$, $51.5 \pm 2.61\%$, $99.0 \pm 0.681\%$,

$95.7 \pm 2.40\%$, $96.1 \pm 1.98\%$, $97.8 \pm 0.771\%$, respectively (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 Vglut2^{+} NA neurons only in the posterior NA populations C2/A2 and C1/A1 (DePuy et al.,

2013; 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 a high percentage of LC NA neurons

are Vglut2^{+} by using another intersectional strategy in mice, *TH-Flp; 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 effect recombination in

the intersectional genetic strategy.

Real time mRNA expression patterns of Vglut1, Vglut2 and Vglut3 in central noradrenergic

neurons in adult mice

DePuy et al. (2013), Stornetta et al. (2002a) and Stornetta et al. (2002b) showed that Vglut2 co-

expression is only located in the C2/A2 and C1/A1 region in the adult rat without existing in

anterior NA nuclei in the brainstem by *in situ* hybridization. To verify if the real time NA-based

Vglut2 expression pattern in adult mice is the same as in adult rats 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

Vglut1, Vglut2, Vglut3 with DBH respectively in brain tissue of adult mice and characterized the

colocalization of Vglut1/2/3 with DBH in brainstem NA nuclei A7, LC, A5, sub CD/CV, anterior

C1/A1 and C2/A2, posterior C1/A1 and C2/A2 (Figure 2A-C). No Vglut1/DBH double positive

neurons were detected in any part of the central NA system, consistent with our fate map. Vglut3

mRNA colocalization with DBH is only found in the posterior part of C2/A2 and $27.1 \pm 1.86\%$ DBH$^+$

neurons have Vglut3 co-localization, again consistent with our fate map. For Vglut2, we only

found detectable levels of Vglut2 mRNA in C1/A1 and C2/A2 NA region, but not in A7, LC, A5, sub

CD/CV. Quantitatively, the percentage of Vglut2/DBH double positive neurons in anterior C1/A1,

anterior C2/A2, posterior C1/A1 and posterior C2/A2 is $84.7 \pm 5.82\%$, $66.3 \pm 0.335\%$, $35.7 \pm 3.01\%$

and $90.1 \pm 2.45\%$, respectively. This result is consistent with the previous *in situ* data in adult rats

(DePuy et al., 2013; Stornetta et al., 2002a, 2002b) suggesting that there is no obvious

expression difference of Vglut2 in the central NA system between mouse and rat. However, the

Vglut2 *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 Vglut2 at some point from early development toward adulthood but the expression of

Vglut2 is turned back down 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 Vglut2-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 *Vglut2-Cre* mice. With TH co-staining in LC, our result is consistent with Yang et

al. (2021) (Figure 2 supplement 1). Additionally, Souza et al. (2022a) showed about 28.5% A5

neurons are Vglut2 mRNA$^+$ 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 Vglut2 co-expression, but the Vglut2 mRNA level cannot be detected by

traditional *in situ* hybridization.

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

***TgDBH-Cre/+; Vglut2$^{flox/flox}$* mice**

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

in breathing under physiological challenges, we used *TgDBH-Cre/+; Vglut2$^{flox/flox}$* as the mouse

model which is the same model used by Abbott et al. (2014) to show that *Vglut2* expression in

the NA system was required for a modest increase in respiratory frequency following unilateral

optogenetic stimulation of anterior C1. To verify if Vglut2 expression is effectively removed from

central NA neurons in *TgDBH-Cre/+; Vglut2$^{flox/flox}$* mice, we carried out fluorescent RNA *in situ*

hybridization for Vglut2 and DBH in the mouse brainstems and compared the Vglut2 signal

intensity in DBH$^+$ neurons in *TgDBH-Cre/+; Vglut2$^{flox/flox}$* and its littermate controls. We found that

Vglut2 mRNA expression is $96.4 \pm 0.226\%$ decreased compared to controls, indicating that the

Vglut2 is effectively recombined to abrogate expression in NA neurons (Figure 3A-B).

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 awake and

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

breathing and metabolism of conscious and free-moving mice. After a five-day habituation

protocol, the ventilation response of *TgDBH-Cre/+; Vglut2$^{flox/flox}$* mice and their littermate

controls was measured under room air and hypercapnia (5% CO$_2$) (Figure 4A). Surprisingly,

TgDBH-Cre/+; Vglut2$^{flox/flox}$ mice didn't show significant differences in overall respiratory output

(V_E/V_{O_2}), respiratory rate (V_f), tidal volume (V_T), minute ventilation (V_E) and metabolism demand

(V_{O_2}) compared to their littermate controls under both room air and 5% CO$_2$ challenge (Figure 4B

and Table 1-2). These results suggested that Vglut2-based glutamatergic signaling is not required

for regulating baseline breathing and hypercapnic ventilatory reflex under 5% CO$_2$.

To further investigate if Vglut2-based glutamatergic signaling in central NA neurons is required

for ventilation response of higher CO_2 challenges, we also measured the breathing of *TgDBH-*

Cre/+; Vglut2$^{flox/flox}$ mice under 7% CO_2 and 10% CO_2. We found that under the 7% CO_2 condition,

TgDBH-Cre/+; Vglut2$^{flox/flox}$ mice showed only a significantly decreased tidal volume (V_T), but the

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

demand (V_{O2}) didn't show a significant difference between the mutant mice and their sibling

controls (Figure 5A-B and Table 3). This result suggests that Vglut2-based glutamatergic signaling

in central NA neurons is not required or at least is not as important as previously expected for

regulating the hypercapnic ventilatory reflex under 7% CO_2.

Under 10% CO_2 challenge, none of the overall respiratory outputs (V_E/V_{O2}), respiratory rate (V_f),

tidal volume (V_T), minute ventilation (V_E) and metabolism demand (V_{O2}) were significantly

different between *TgDBH-Cre/+; Vglut2$^{flox/flox}$* 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).

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 *TgDBH-Cre/+;*

Vglut2$^{flox/flox}$ mice under 10% O_2. We analyzed the five respiratory parameters in three 5-min time

periods under 10% O2 challenge. 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) and metabolism

demand (V_{O2}) between *TgDBH-Cre/+; Vglut2$^{flox/flox}$* mice and controls in either of the three 5-min

10% O_2 period (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.

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. It has long been appreciated
that central NA neurons co-express Vesicular glutamate transporter 2 (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). Given the expression of Vglut2, it has been
assumed that the central NA neurons co-produce, release, and functionally communicate with
post-synaptic neurons via glutamate (Abbott et al., 2014, 2012; DePuy et al., 2013; Guyenet and
Stornetta, 2021; Guyenet et al., 2013; Holloway et al., 2013; Malheiros-Lima et al., 2022, 2020,
2018; Yang et al., 2021). However, to our knowledge, the potential for the central NA neurons to
express other glutamate transporters Vglut1 or Vglut3 has not been reported. 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 *Vglut1-Cre/+; DBH-p2a-Flpo/+;*
RC::FLTG/+, Vglut2-Cre/+; DBH-p2a-Flpo/+; RC::FLTG/+ and Vglut3-Cre/+; DBH-p2a-Flpo/+;
RC::FLTG/+ compound mouse lines. As this approach maps the cumulative history of expression,
we also examined acute adult expression of Vglut1, Vglut2 and Vglut3 using fluorescent RNA *in*
situ hybridization. Our *in situ* results for 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 *Vglut2-Cre* mice. Here
we observed about 20% of the cells recombined. 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 PBN that was seen in the *TH-Flp* mouse. In
addition, 28.5% A5 neurons were shown to be Vglut2$^+$ in adult rats by RNA scope (Souza et al.,

2022b). It is notable that both our lab and work published by (DePuy et al., 2013; Stornetta et al.,

2002a, 2002b) failed to detect 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). Our

data suggests that Vglut2 co-expression in anterior NA groups is time dependent, though the

underlying temporal dynamics of Vglut2 remain unknown. 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 and other studies find only 20% of the LC and 28.5% of A5 may be expressing

Vglut2 at any given moment in adults. This suggests either a temporal restriction in expression

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

experiences.

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

central NA system. However, Vglut3 expression was found in the posterior part of NA neurons

including C2/A2 and C1/A1, which is first characterized by this study. 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 unlikely 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).

Based on the Vglut2 co-expression in NA neurons, several studies suggest that glutamate in NA

populations has a functional role in breathing control. Those studies provide a mix of

circumstantial, indirect, or limited evidence for the potential role of Vglut2-based glutamatergic

signaling in central NA neurons in breathing regulation. It has not yet been shown whether or not

NA-based Vglut2 signaling is required for respiratory control due to experimental caveats or

limitations.

Abbott et al. (2014) showed that conditionally knocking out Vglut2 in the whole central NA
system attenuated a modest increase in respiratory rate resulting from unilateral C1 optogenetic
stimulation. Absolute values and other respiratory parameters, including tidal volume (V_T) and
minute ventilation (V_E) were not reported, making direct comparison difficult. While the
optogenetic stimulation 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, exercise, or volitional control. Thus, it remains possible that strong
optogenetic stimulation 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 akin 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).

More circumstantially, Malheiros-Lima et al. (2020) suggested C1 neurons potentially release
glutamate at the pFRG site to regulate breathing under hypoxia by providing three indirect lines
of evidence: 1) Vglut2-expressing C1 neurons project to the pFRG region; 2) Increased breathing
was blunted after blockade of ionotropic glutamatergic receptors at the pFRG site under
anesthesia using chemical hypoxia; 3) Depletion of C1 neurons eliminated the increased

breathing 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 pre-Bötzinger complex and the RTN itself; 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.

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 respectively.

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

reduced the increase in phrenic nerve activities or the breathing frequency caused by

optogenetic stimulation of C1 cells in 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 activities or breathing frequency. Again,

these two studies showed that C1 neurons are important to regulate phrenic nerve activities 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 awake, unrestrained animal under

normoxic, hypoxic, or hypercapnic breathing.

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 awake 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. To ensure a rigorous

and robust conclusion, first we use exactly the same mouse model, *TgDBH-Cre/+; Vglut2^{flox/flox}*,

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 conscious, unrestrained, and

habituated mice under physiological challenges including normoxia, hypercapnia and hypoxia.

Third, multiple respiratory and metabolic parameters were measured and reported in absolute

values including respiratory rate, tidal volume, minute ventilation, oxygen consumption, overall

respiratory output (minute ventilation normalized to oxygen consumption) in order to visualize

breathing function comprehensively. 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 powerful linear mixed-effects

regression model with animal type (experimental vs. control) as fixed effects, animal ID as a

random effect and including sex as a variable (there was no sex specific effect) (Lusk et al., 2022)..

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

several considerations in the interpretation of our data. First, we uncovered a novel NA co-

expressed glutamate transporter, Vglut3. It remains a formal possibility that Vglut3 somehow

compensates for the loss of Vglut2, however we argue that this is unlikely for the following

reasons. First, our model is the same used in the other study where an effect was seen with

optogenetic stimulation. Second, focus has been on anterior C1 whereas Vglut3 is expressed in

the posterior CA domains. Another consideration is that pre- or post-natal developmental

compensation corrects for the loss of NA derived glutamate. Again, we argue that is not likely, as

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. Second, Abbott et al.

(2014) highlight that Vglut2 negative NA neurons showed no obvious abnormalities in number,

morphology, and projection patterns. Third, we have examined the requirement of NA-expressed

Vglut2 in P7 neonate mice in the auto-resuscitation reflex and saw no differences (data not

shown). However, this could be better tested by using the *TgDBH-CreER* (Stubbusch et al., 2011)

to more acutely remove Vglut2 expression (though this leaves a window of 2-3 weeks for

compensation to occur). Yet another consideration in interpreting our results is that we only

address the loss of NA-Vglut2 based signaling across the entire NA system. It remains a formal

possibility that we have removed 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 intersection conditional

approach, something that has not yet been shown to be efficient and effective and would be

beyond the scope of these studies. Additionally, in our studies, we account for potential

metabolic changes that may underlie or be coordinate with changes in breathing. However, in

this study 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.

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 questions 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% Rett

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

hyperventilation and breathing holds, during the whole lifespan including both childhood and

adulthood (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, *TgDBH-Cre/+; Vglut2^flox/flox* 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 demonstrated the extent of glutamate as a functional vesicular

glutamate transporter co-expression in central noradrenergic system. We were able to

characterize a novel Vglut3-expressing NA population in the posterior C2/A2 nuclei and found a

different Vglut2 co-expression pattern in anterior NA groups from a cumulative intersectional

fate map compared to a viral fate map and *in situ* hybridization in the adult, suggesting that

anterior NA populations may have a time-dependent or experience-dependent manner for

Vglut2 expression. Furthermore, despite prior studies providing indirect and circumstantial

evidence that noradrenergic-based glutamatergic signaling may play a role in control of

breathing, our studies that remove Vglut2 expression from noradrenergic neurons failed to

perturb room air breathing, the hypercapnic ventilatory reflex, and the hypoxic ventilatory reflex,

providing further insight into the potential role of NA-glutamate transmission in the control of

breathing. Based on our data, we suggest that noradrenergic-based glutamatergic signaling is not

required for regulating baseline breathing or the hypercapnic and hypoxic respiratory

chemoreflexes, and glutamate may not be a critical mechanistic component of 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 *Vglut1*-Cre *(Jax Stock No: 023527), Vglut2-Cre (Jax Stock No: 016963) and Vglut3-*

Cre (Jax Stock No: 018147) were mated with heterozygous *DBH-p2a-Flpo (MMRRC ID: 41575)*

(Sun and Ray, 2016) mice respectively to derive compound lines with both Cre and Flpo alleles

(*Vglut1-Cre/+; DBH-p2a-Flpo/+, Vglut2-Cre/+; DBH-p2a-Flpo/+, and Vglut3-Cre/+; DBH-p2a-*

Flpo/+). Then these three compound lines were each mated with homozygous

RC::F_TdTomato_P_GFP (RC::FLTG, Jax Stock No: 026932) to derive three different intersectional

mouse lines *Vglut1/Cre/+; DBH-p2a-Flpo/+; RC::FLTG/+, Vglut2/Cre/+; DBH-p2a-Flpo/+;*

RC::FLTG/+ and Vglut3/Cre/+; DBH-p2a-Flpo/+; 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 *TgDBH-Cre (MMRRC ID: 036778-UCD GENSAT)* mice

were mated with homozygous *Vglut2$^{flox/flox}$ (Jax Stock No: 012898)* to derive *TgDBH-Cre;*

Vglut2$^{flox/+}$. *TgDBH-Cre; Vglut2$^{flox/+}$* mice were mated with *Vglut2$^{flox/flox}$* to derive *TgDBH-Cre;*

Vglut2$^{flox/flox}$. 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 *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. Vglut2^{flox} specific primers for Vglut2-floxed mice are

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

Immunofluorescence staining

Vglut1, Vglut2, or Vglut3-Cre/+; DBH-p2a-Flpo/+; RC::FLTG/+ adult mice 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 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 *Vglut1, Vglut2, and 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 *Vglut1, Vglut2, Vglut3 and DBH* probes are available in the Allen Brain Atlas (http://www.brain-map.org). For the Vglut2 and DBH double ISH in *TgDBH-Cre/+; Vglut2^{flox/flox}* and their littermate controls, we generated a new Vglut2 probe targeting exon 2 of Vglut2 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 *Vglut2-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 conscious and free-moving mice was carried out as described in (Ray et al.,

2011) on 6-8-week-old adult animals with at least 16 animals 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

was then performed for each mouse within 1 week of the last day of habituation. 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 at least 45

min in room air (21% O_2/79% N_2) conditions. After acclimation and measurement under room

air, 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.

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 BASSPRO module of the Breathe Easy software to

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

consumption (V_{O2}) and ventilatory equivalents for oxygen (V_E/V_{O2}) (Lusk et al., 2022). 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 and 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 (*TgDBH-Cre/+; Vglut2$^{flox/flox}$* and

control) exceeded 13. Results (V_f, V_E, V_T, V_{O2}, V_E/V_{O2}) for room air and hypercapnic or hypoxic

data were compared between *TgDBH-Cre/+; Vglut2$^{flox/flox}$* 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., 2022). A $p < 0.05$ was used to indicate statistical

significance, and individual data points, mean, and standard error 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$^+$

area coincident with DAPI (to denote nuclear localization) was defined as Vglut2 or Vglut3-

expressing NA neurons while each tdTomato$^+$ area coincident with DAPI was defined as NA

neurons without any Vglut2 or Vglut3 co-expression. For quantification of Vglut2 or Vglut3 with

DBH double *in situ* hybridization in adult WT mice, DBH$^+$ areas coinciding with DAPI were

identified as NA neurons and the DBH$^+$ areas overlapped with Vglut2/3$^+$ pixels and DAPI were

defined as NA neurons colocalized with Vglut2/3. The number of Vglut2/3$^+$ NA neurons and

Vglut2/3$^-$ NA neurons was counted in each image for both immunofluorescence and in situ

experiments and the percentage of Vglut2/3$^+$ NA neurons among all NA neurons in each NA

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

quantification of Vglut2 and DBH double ISH in *TgDBH-Cre/+; Vglut2^{flox/flox}* and their littermate

controls, Vglut2 pixel intensities in DBH$^+$ areas coincident with DAPI (NA neurons) were measured

in mutant and control images separately. The Vglut2 pixel intensity in NA neurons of control

brains was normalized as 1 and the relative 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, and prepared the manuscript.

SL completed the viral injection experiments.

RR conceptualized and designed the study, analyzed the data, and prepared 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. *Vglut1-Cre/+*, *Vglut2-Cre/+* and *Vglut3-Cre/+* were each bred with *DBH-p2a-Flpo/+* mice respectively. These *Vglut1, Vglut2, or Vglut3-Cre/+; DBH-p2a-Flpo/+* compound lines were then crossed with the *RC::F_TdTomato_P_GFP* intersectional reporter mice (*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 expression are labelled by red fluorescent protein (tdTomato). Shown as an example is the *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. (C) Quantification of the percentage of Vglut3-coexpressing NA neurons among NA neurons in each NA nuclei. (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 Vglut1, Vglut2, or Vglut3 and 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 Vglut2 co-expression in NA neurons in each NA nuclei. (C)

Quantification of the percentage of Vglut3 co-expression in NA neurons in each NA nuclei.

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 *TgDBH-Cre/+; Vglut2$^{flox/flox}$* mice. (A)

Representative images of Vglut2 and DBH double ISH in anterior C1/A1, posterior C1/A1, anterior

C2/A2 and posterior C2/A2 in control and *TgDBH-Cre/+; Vglut2$^{flox/flox}$* mice. DBH (green), Vglut2

(red), DAPI (cyan). Scale bar 20μm.(B) Quantification of intensity of Vglut2 signal in control and

TgDBH-Cre/+; Vglut2$^{flox/flox}$ 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. (B) Under both room air

and hypercapnia (5% CO_2), *TgDBH-Cre/+; Vglut2$^{flox/flox}$* 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), and

metabolism demand (V_{O2}). Linear mixed-effects regression model, *$p<0.05$.

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. (B)

Knocking out Vglut2 in the whole NA system failed to alter ventilation (V_E/V_{O2}, V_f, V_E) and

metabolism (V_{O2}) but only showed a significantly reduce in V_T under 7% CO_2 condition. Linear

mixed-effects regression model, *$p<0.05$.

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. (B) Knocking out Vglut2 in the whole

NA system didn't significantly alter ventilation (V_E/V_{O2}, V_f, V_T, V_E) and metabolism (V_{O2}) under 10%

CO_2 condition. Linear mixed-effects regression model, *$p<0.05$.

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. (B) Knocking out Vglut2 in the whole NA system didn't show

significant breathing changes including V_E/V_{O_2}, V_E, V_f, V_T, and V_{O_2} in either of the three five-minute

time periods under hypoxia (10% O$_2$). Linear mixed-effects regression model, *p<0.05.

Figure 2 Supplement 1. Virus injection of Cre-dependent tdTomato into LC of *Vglut2-Cre* mice.

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.

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Figure 1

A

B *Vglut2-Cre/+; DBH-p2a-Flpo/+; RC::FLTG/+*

C *Vglut3-Cre/+; DBH-p2a-Flpo/+; RC::FLTG/+*

Figure 1. cont.

D

Figure 2

Figure 3

A

Anterior C1/A1

| Control | DBH | Vglut2 | DBH/Vglut2/DAPI |
| DBH-Cre; Vglut2flox/flox | | | |

Anterior C2/A2

| Control | DBH | Vglut2 | DBH/Vglut2/DAPI |
| DBH-Cre; Vglut2flox/flox | | | |

Posterior C1/A1

| Control | DBH | Vglut2 | DBH/Vglut2/DAPI |
| DBH-Cre; Vglut2flox/flox | | | |

Posterior C2/A2

| Control | DBH | Vglut2 | DBH/Vglut2/DAPI |
| DBH-Cre; Vglut2flox/flox | | | |

B

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

Control

TgDBH-Cre/+; Vglut2flox/flox

0.0   0.5   1.0   1.5   2.0

Figure 4

Figure 5

Figure 6

Figure 7

Locus Coeruleus

TH

tdTomato

TH/ tdTomato/ DAPI

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

	TgDBH-Cre/+; Vglut2^{flox/flox} Mean ± SEM	Control Mean ± SEM	*TgDBH-Cre/+; Vglut2^{flox/flox}* vs Control linear mixed-effects regression model
V_E/V_{O2}	30.01 ± 2.58	33.22 ± 3.97	P = 0.98
V_f	204.08 ± 10.04	213.58 ± 15.36	P = 0.98
V_T	0.009 ± 0.0007	0.009 ± 0.0006	P = 0.88
V_E	1.93 ± 0.14	1.98 ± 0.22	P = 0.995
V_{O2}	0.067 ± 0.004	0.061 ± 0.004	P = 0.78

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

	TgDBH-Cre/+; Vglut2^{flox/flox} Mean ± SEM	Control Mean ± SEM	*TgDBH-Cre/+; Vglut2^{flox/flox}* vs Control linear mixed-effects regression model
V_E/V_{O2}	47.99 ± 3.28	58.60 ± 5.44	P = 0.33
V_f	246.72 ± 9.78	261.66 ± 14.00	P = 0.24
V_T	0.011 ± 0.0007	0.010 ± 0.0008	P = 0.81
V_E	2.67 ± 0.20	2.80 ± 0.32	P = 0.98
V_{O2}	0.057 ± 0.003	0.051 ± 0.005	P = 0.42

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

	TgDBH-Cre/+; Vglut2^{flox/flox} Mean ± SEM	Control Mean ± SEM	*TgDBH-Cre/+; Vglut2^{flox/flox}* vs Control linear mixed-effects regression model
V_E/V_{O2}	58.48 ± 4.29	74.70 ± 6.22	P = 0.23
V_f	262.69 ± 12.82	284.44 ± 10.59	P = 0.98
V_T	0.011 ± 0.0011	0.015 ± 0.0012	P = 0.023*
V_E	2.90 ± 0.32	4.23 ± 0.43	P = 0.16
V_{O2}	0.051 ± 0.004	0.059 ± 0.006	P = 0.64

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

	TgDBH-Cre/+; Vglut2^{flox/flox} Mean ± SEM	Control Mean ± SEM	*TgDBH-Cre/+; Vglut2^{flox/flox}* vs Control linear mixed-effects regression model
V_E/V_{O2}	105.77 ± 10.80	105.69 ± 11.51	P = 0.9996
V_f	336.31 ± 5.26	336.38 ± 8.52	P = 0.9997
V_T	0.018 ± 0.0015	0.016 ± 0.0012	P = 0.98
V_E	5.94 ± 0.48	5.54 ± 0.45	P = 0.9996
V_{O2}	0.059 ± 0.003	0.058 ± 0.005	P = 0.9999999

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

	TgDBH-Cre/+; Vglut2$^{flox/flox}$ Mean ± SEM	Control Mean ± SEM	Linear mixed-effects regression model	TgDBH-Cre/+; Vglut2$^{flox/flox}$ Mean ± SEM	Control Mean ± SEM	Linear mixed-effects regression model	TgDBH-Cre/+; Vglut2$^{flox/flox}$ 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	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	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	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}	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