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Immunohistochemical assessment of cyclic guanosine monophosphate (cGMP) and soluble guanylate cyclase (sGC) within the rostral ventrolateral medulla

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Abstract

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ORIGINAL PAPER

Immunohistochemical assessment of cyclic guanosine monophosphate (cGMP) and soluble guanylate cyclase (sGC) within the rostral ventrolateral medulla

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Abstract Functional evidence suggests that nitric oxide (NO) signalling in the rostral ventrolateral medulla (RVLM) is cGMP-dependent and that this pathway is impaired in hypertension. We examined cGMP expression as a marker of active NO signalling in the C1 region of the RVLM, comparing adult (>18 weeks) Wistar-Kyoto (WKY, n = 4) and spontaneously hypertensive rats (SHR, n = 4). Double label immunohistochemistry for cGMPimmunoreactivity (IR) and C1 neurons [as identified by phenylethanolamine N-methyltransferase (PNMT-IR) or tyrosine hydroxylase TH-IR)], or neuronal NO synthase (nNOS) neurones, failed to reveal cGMP-IR neurons in the RVLM of either strain, despite consistent detection of cGMP-IR in the nucleus ambiguus (NA). This was unchanged in the presence of isobutylmethylxanthine (IBMX; 0.5 mM, WKY, n = 4, SHR n = 2) and in young animals (WKY, 10-weeks, n = 3). Incubation of RVLMslices (WKY, 10-weeks, n = 9) in DETA-NO (100 µm; 10 min) or NMDA (10 µM; 2 min) did not uncover cGMP-

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Cardiology Research, Royal Perth Hospital, School of Medicine and Pharmacology, The University of Western Australia, Perth, WA, Australia IR. In all studies, cGMP was prominent within the vasculature. Soluble guanylate cyclase (sGC)-IR was found throughout neurones of the RVLM, but did not co-localise with PNMT, TH or nNOS-IR neurons (WKY, 10-weeks, n = 6). Results indicate that within the RVLM, cGMP is not detectable using immunohistochemistry in the basal state and cannot be elicited by phosphodiesterase inhibition, NMDA receptor stimulation or NO donor application.

Keywords RVLM · Immunohistochemistry · Slice preparation · Nitric oxide · NMDA · C1 cell group

Introduction

The rostral ventrolateral medulla (RVLM) contributes significant excitatory drive to sympathetic preganglionic neurons and therefore also to vascular tone via two well characterised subpopulations of bulbospinal neurons: the C1 (adrenergic) and non-C1 cell groups [1–3]. Glutamate is the major neurotransmitter driving the activity of these neurons [3, 4], but the gaseous neurotransmitter nitric oxide (NO) is thought to play a key role in regulating glutamate induced pressor responses, and therefore modulating homeostatic blood pressure mechanisms [5–7]. Altered NO signalling in the RVLM is associated with increased sympathetic outflow in animal models of hypertension [8], however the mechanism of action is unclear, with a range of effects consistent with NO-mediated pressor, depressor or neutral effects being reported [9–11].

One of the most widely studied and best-understood NO second messenger systems is the activation of soluble guanylate cyclase (sGC) and the subsequent generation of intracellular 3',5'-cyclic guanosine monophosphate (cGMP) [12, 13]. Soluble GC is a heme-containing

heterodimer of α and β subunits, with the β 1 subunit being the major subunit, as there is no catalytic activity in its' absence [14, 15]. Activation of NMDA receptors can drive this pathway, with increased intracellular Ca²⁺ stimulating the Ca²⁺/calmodulin NO system, promoting conversion of L-Arginine to NO. Intracellular cGMP levels can also be regulated by membrane bound, or particulate guanylyl cyclases, incorporating the receptors for atrial (ANP), brain (BNP) and C-type (CNP) natriuretic peptides [13]. As a second messenger, cGMP can target various protein kinases and ion channels, and its activity is limited through degradation by phosphodiesterases (PDE) [13].

Nitric oxide has alternative neuromodulatory mechanisms. This includes the *S*-nitrosylation of proteins and in particular that of NMDA receptors [12], and interactions with superoxide, with the resultant peroxynitrite having potent oxidising properties that convey a variety of physiological and pathophysiological effects [16].

Within the RVLM, all three NO synthase (NOS) isoforms are present [17] and we have shown recently that neuronal (n)NOS is increased in the RVLM of spontaneously hypertensive rats (SHR) [18]. Work by Chan et al. [19] suggests that the relative balance of functional nNOS versus inducible (i)NOS activity determines RVLM output, and further, that the different NOS isoforms activate different downstream signals, with nNOS driving sGC/cGMPdependent sympathoexcitatory responses, and NO produced by iNOS driving peroxynitrite formation and sympathoinhibitory responses [20]. Glutamate-induced pressor responses in the RVLM are in general proposed to be modulated by NO-sGC/cGMP [5, 6, 21] and this is supported by electrophysiological studies showing cGMPdependent potentiation of glutamate currents in RVLM slice preparations [7].

To date, no studies have described the immunohistochemical localisation of neurons capable of expressing cGMP within the C1 region [22]. Given the strong evidence that NO signalling plays a functional role in the RVLM, we sought to identify the cellular targets for NO in the RVLM, visualising cGMP and its neuroanatomical relationship with the C1 cell group, as identified by the presence of tyrosine hydroxylase (TH) or phenylethanolamine N-methyltransferase (PNMT), and the more medially located nNOS expressing cell population [18, 23]. Given that studies in SHR show augmented pressor responses to microinjection of glutamate in the RVLM [24, 25], we considered the hypothesis that the NO downstream signalling sGC/cGMP pathway may be altered. We therefore also sought to examine if altered cGMP expression, as determined using fluorescence immunohistochemistry, was demonstrable in the RVLM of the SHR when compared its genetic control, the Wistar Kyoto (WKY). An inability to detect cGMP-immunoreactivity (-IR) in the RVLM of either strain led to additional studies that sought to increase synthesis of cGMP in fresh RVLM brain slices, and examine sGC-IR throughout the region.

Materials and methods

Animals

Animals were obtained from the Animal Resources Centre, Murdoch, Western Australia and all procedures conformed to the guidelines approved by the Murdoch University Animal Ethics Committee. Rats were housed on a 12 h light-dark cycle with access to standard rat chow and water ad libitum. Male rats were used in all experiments. Wistar– Kyoto (n = 26 in total) and SHR (n = 8 total) animals were used in the different age groups as detailed in each experimental protocol.

Animal tissue preparation for immunohistochemistry

Rats were anaesthetised with sodium pentobarbitone (Thiobarb, Jurox, Rutherford, Australia; 100 mg/kg) administered intraperitoneally. A pre-fixation solution of ice-cold heparinised saline (30 ml, 0.9% NaCl containing 2,000 I.U. of heparin [Jurox, Rutherford, Australia]) was perfused via the ascending aorta (6 ml per minute), followed by 180 ml of ice-cold 3.7% formalin diluted in 0.9% saline at the same rate. In one set of experiments, the phosphodiesterase inhibitor isobutylmethylxanthine (IBMX; 0.5 mM Sigma, St. Louis, MO) was added to the pre-fixation saline solution. Brains were removed and post fixed in 4% formalin for 4 h at 4°C. Tissue was washed in 0.1 M phosphate buffered saline (PBS, pH 7.4) $(3 \times 10 \text{ min})$ and coronal hindbrain sections (50 µm) sections were cut using a vibrating microtome (Vibratome, St. Louis, MO). Sections were split into two alternate series, with each section therefore 100 µm apart. Sections were then incubated in 50% ethanol for 30 min and then washed in 0.01 M PBS containing 10 mM Tris (TPBS; 2×15 min).

Animal tissue preparation for brainstem slice in-vitro incubation

Animals were anaesthetised and perfused as for the immunohistochemical experiments. Perfusate consisted of ice-cold sucrose based cutting solution (2 mM KCl, 2 mM MgSO₄, 1.25 mM NaH₂PO₄, 1 mM MgCl₂, 26 mM NaHCO₃, 0.1 mM CaCl₂, 10 mM D-glucose, 248 mM sucrose, 95% O₂/ 5% CO₂, pH 7.4 [26] containing IBMX (0.5 mM) and heparin 1,000 U/ml (Jurox). The brains were removed immediately and coronal RVLM sections (400 µm) were cut on a vibrating microtome while immersed in the same ice-cold sucrose cutting solution.

After cutting, brain slices were warmed to 37°C over 20 min in an artificial cerebrospinal fluid (aCSF) solution (124 mM NaCl, 2 mM KCl, 2 mM MgSO₄ · 7H₂O, 1.25 mM NaH₂PO₄, 26 mM NaHCO₃, 2 mM CaCl₂, 10 mM D-glucose, 0.5 mM IBMX, 95% O₂/5% CO₂, pH 7.4) [26]. Once at 37°C, slices were incubated for a further 30 min, prior to incubation in either 100 µM NMDA (Sigma) plus 10 μ M glycine for 1 \times 5 min [27] or 100 μ M DETA-NO (Sigma) for $1 \times 15 \text{ min}$ [28] in aCSF solution. Twenty minutes prior to use, DETA-NO was prepared in aCSF buffer and warmed to 37°C to stabilise NO release. Submerging the slices in ice-cold 3.7% formalin terminated the reaction. Control slices were incubated in aCSF solution only. Slices were post-fixed for 2 h in 3.7% formalin at 4°C, followed by washing in 0.1 M PBS (1×30 min). Slices were then cryoprotected in 30% sucrose in 0.1 M PBS and sodium azide (NaN₃, 0.1%; overnight) prior to cutting 50 µm sections on a cryostat (Leica CM1510; Leica Microsystems GmbH, Wetzlar, Germany) at -17° C for subsequent immunohistochemistry using alternate sections as described above.

Immunohistochemistry

Sections were pre-treated for one hour at room temperature in blocking solution containing 10% donkey serum (Chemicon, Temecula, CA), diluted in TPBS with 0.3% Triton-X (Tx) and 0.1% NaN₃. They were then incubated free floating in different combinations of primary antibody [cGMP/nNOS, cGMP/PNMT or TH, sGC/nNOS, sGC/ PNMT, sGC/Protein Gene Product (PGP9.5) or sGC/glial fibrillary acidic protein (GFAP)] at pre-optimised concentrations (Table 1) for 24 h at room temperature, then 72– 96 h at 4°C. From each animal, the RVLM was split into two series of alternating sections, allowing two different antibody combinations per animal. Antibodies were diluted in blocking solution. Sections were then washed $(3 \times 30 \text{ min TPBS})$ and incubated with species specific secondary antibodies (Table 1) for 12-14 h at 4°C, diluted in TPBS with 0.3% Tx, 0.1% NaN₃ and 1% donkey serum. Finally, sections were washed $(3 \times 30 \text{ min TPBS})$, mounted on slides and cover slipped with ProLong Antifade (Molecular Probes, Eugene, OR USA).

The RVLM region examined was defined as that area extending caudally 600–800 μ m from the caudal pole of the facial nucleus. This corresponds to -12.5 to -11.7 mm from Bregma [29] bounded laterally by the spinal trigeminal tract, medially by the inferior olive and pyramids, and dorsally by the compact formation of the NA. Sections were arranged in a rostro-caudal orientation prior to mounting and all sections were examined bilaterally for

immunostaining. The NA from each series of sections was used as an internal control for cGMP-IR as it consistently demonstrated neuronal expression.

Control experiments

For negative controls, RVLM tissue sections were incubated in blocking solution alone (no antibody controls) and run in parallel to each of the experimental protocols.

Positive control experiments for the cGMP, sGC and PGP9.5 antibodies were performed using additional sections from animals used in the experiments described above. For sGC, sections of cerebellum were processed in parallel to RVLM sections. A TH/PGP9.5 double label combination was used as a positive control for the PGP9.5 antibody. To confirm that the cGMP antibody was detecting both neuronal and vascular elements, a cGMP/mouse anti alpha-smooth muscle actin (alpha-SMA) double label combination was used (Table 1).

Previous studies and manufacturers product information have documented the specificity of antibody reactions and/ or characteristic staining patterns for the cGMP [30, 31], nNOS [32], sGC [33], PNMT [34], TH [35], PGP-9.5 [36, 37], GFAP [38] and SMA [39] antibodies.

Imaging and analysis

A BioRad MRC-1024 confocal laser-scanning microscope (Carl Zeiss Pty. Ltd. North Ryde, NSW, Australia) was used to examine immunofluorescence with filter settings for identification of secondary antibody fluorophores (fluorescein isothiocyanate [FITC], cyanine [CY2] and indocarbocyanine [CY3]). Each fluorochrome was viewed separately in single channel mode and no "bleed through" was observed. To excite FITC labelled and CY2 secondary antibodies, excitation was set at 488 nm, while 568 nm excitation was used for CY3. Images were captured by taking 4-6 optical "slices" through the sections as a "z" series imaging 10-30 microns of tissue, and then reconstructed as a single two-dimensional image using Confocal Assistant Software (BioRad). Figures were assembled and labelled using Photo Shop software (version 6, Adobe Systems, Mountain View, CA). Overall colour balance and contrast were adjusted, but no other modifications were made.

Results

Detection of cGMP-IR in the RVLM

Cells expressing either the adrenergic markers PNMT/TH, or nNOS, were used to delineate the neuronal populations

Antigen and host species	Dilution	Product code and source
Primary detection antibodies		
Anti cGMP: Rabbit polyclonal	1:500	AB303: Chemicon (Temecula CA, USA)
Anti nNOS: Mouse monoclonal	1:400	N2280: Sigma (St. Louis, MO, USA)
Anti PNMT: Sheep polyclonal	1:500	AB146: Chemicon
Anti TH: Mouse monoclonal	1:300	22941: Clone LNC1, Immunostar (Hudson, Wisconsin, USA)
Anti sGC (β1-subunit): Rabbit polyclonal	1:500	160897: Cayman Chemicals (Ann Arbour, MI USA)
Anti PGP9.5: Guinea pig polyclonal	1:750	AB5898: Chemicon
Anti GFAP: Mouse monoclonal	1:750	G3893, clone G-A 5: Sigma
Anti alpha-SMA: Mouse monoclonal	1:500	A5228, clone 1A4: Sigma
Secondary detection antibodies		
FITC: Donkey anti-mouse IgG	1:500	Jackson (West Grove, PA)
CY2: Donkey anti-sheep IgG	1:500	Jackson
CY3: Donkey anti-rabbit IgG	1:500	Jackson
CY3: Donkey anti-guinea pig IgG	1:750	Jackson
CY3: Donkey anti-mouse IgG	1:750	Jackson

Table 1 Primary and secondary antibodies: dilutions and source

Cyclic guanosine monophosphate (cGMP); neuronal nitric oxide synthase (nNOS), phenylethanolamine *N*-methyltransferase (PNMT), tyrosine hydroxylase (TH), soluble guanylate cyclase (sGC), Protein Gene Product-9.5 (PGP9.5), Glial fibrillary acidic protein (GFAP), alpha-Smooth Muscle Actin (alpha-SMA), fluorescein isothiocyanate (FITC), cyanine (CY2), indocarbocyanine (CY3)

of interest within the RVLM. PNMT/TH neurons defined the rostro-caudal axis of the C1 adrenergic cell group while nNOS cell bodies bounded the medial RVLM region [29]. In the first series of experiments, sections from mature WKY (n = 4) and SHR (n = 4) (>18 weeks) were examined for double labelling for cGMP/PNMT-IR and cGMP/nNOS-IR. Results showed very few cGMP immunoreactive neurons in the RVLM in association with either the C1 adrenergic or the nNOS cells groups in either strain of mature animal and no cells were double labelled for either cGMP:PNMT or cGMP:nNOS (Fig. 1a–f). There was strong cGMP-IR in the NA (Fig. 1b, f) and in these cells, staining was punctate in appearance, and localised to the cytoplasm and extending neurites. Cyclic GMP-IR was visible in the vasculature throughout the sections.

To control for rapid degradation of cGMP, in the second series of experiments, additional adult WKY (n = 4) and SHR (n = 2) were assessed after perfusion with IBMX (0.5 mM) in the pre-perfusate solution. Double labelling was performed for cGMP and either PNMT/TH or nNOS. The presence of IBMX did not reveal any increase in the number of cGMP-IR neurons in the RVLM and did not alter the PNMT, TH or nNOS-IR (data not shown). There was a visible increase in the intensity of staining for cGMP in cells of the NA and within blood vessels of the RVLM region in both the WKY and SHR (Fig. 2). To assess the influence of animal age, in the third series of experiments, immunohistochemistry for cGMP/PNMT was performed in young male WKY animals (10 weeks; n = 3). The pattern

of immunoreactivity was the same as that seen in the adult WKY, with very few cells outside of the NA showing cGMP-IR above the level of background in the RVLM region (data not shown).

Detection of cGMP-IR in brainstem slices after incubation in-vitro

In the fourth series of experiments, cGMP-IR in the RVLM was examined in brainstem slices that were treated in-vitro using experimental paradigms designed to increase cGMP synthesis. Due to the extended time frame of the experimental protocol, all experiments were performed in the presence of IBMX (0.5 mM). Sections were examined after incubation of brainstem slices in-vitro in aCSF (control), with 100 µM NMDA or the NO donor DETA-NO (100 μ M; n = 3 for each experiment, total n = 9 WKY 10 week-old animals). In the aCSF control experiments, the location of neuronal cGMP staining was comparable with that from the fixation perfused experiments (Fig. 3a, b). However, tissue integrity and overall fluorescence was reduced in this series of experiments due to the incubation protocol and the requirement for cryoprotection prior to sectioning. In those brainstem slice preparations incubated with NMDA (Fig. 3c, d) or DETA-NO (Fig. 3e, f), the cGMP staining in the vasculature and NA was brighter when compared to control (aCSF) preparations (inset panels b', d' and f'), but no additional neuronal staining in RVLM neurons was uncovered (Fig. 3).

Fig. 1 Confocal images depicting double labelling for PNMT/cGMP (a, b) and nNOS/ cGMP (c, d) in the RVLM of adult WKY in the absence of IBMX, and PNMT/cGMP (e, f) in the RVLM of an adult SHR in the absence of IBMX. PNMTimmunoreactivity (a, e) indicates the location of the C1 adrenergic cell group. Panel (c) illustrates nNOS immunoreactive cells, located adjacent to the inferior olive (IO) in the ventromedial region of the RVLM. cGMP-IR in the neurons of the NA and in blood vessels (arrows) is evident (panels **b**, **d**, **f**) however there is no labelling of neurons with cGMP in association with either the PNMT or nNOS cell groups. A single cGMP-IR neuron is visible (arrow head, panel f) in the C1 region of the SHR animal. Scale bar in Panel $(\mathbf{b}) = 200 \ \mu m$ for panels (\mathbf{a}, \mathbf{b}) . Scale bars in panels (d) and (f) equal 100 μ m for panels (c, d) and (e, f), respectively



Detection of sGC-IR in the RVLM

In the fifth series of experiments, sections from WKY animals (10 weeks, n = 3) were examined for sGC/PNMT and sGC/nNOS-IR. Within the RVLM region, sGC-IR was widely distributed and unlike the PNMT and nNOS-IR neuronal populations, sGC cells did not localise to a distinct group or nuclei. Cells immunoreactive for sGC were

often in close proximity to PNMT (Fig. 4a) or nNOS immunoreactive cells (data not shown) but there was no co-localisation.

The sixth and final series of experiments were undertaken in order to confirm the neuronal expression of sGC. Sections from WKY animals (10 weeks, n = 3) were double labelled for sGC and PGP-9.5 (neuronal specific marker). Parallel control experiments double labelling for



Fig. 2 Confocal images illustrating cGMP in RVLM sections taken from adult WKY (a) and SHR (b) animals treated with IBMX in the pre-perfusate solution. Midline is located to the left and ventral surface of the medulla towards the base. Figures show the marked increase in detection of cGMP in the vasculature (arrows) and cells of

sGC and a non-neuronal cell (astroglia: marker GFAP) were also performed. The cellular staining pattern for GFAP was consistent with the morphology and distribution of astroglia [40], and showed no colocalisation or pattern similarity to the sGC staining (Fig. 4b). In contrast, all cells showing sGC-IR were consistently double labelled with PGP9.5, confirming that sGC was expressed in neurones in the RVLM (Fig. 4c). Additional experiments in adult SHR (n = 2) showed the same expression pattern of sGC in PGP9.5-IR cells (data not shown).

Control experiments

Sections processed in the absence of primary antibody did not show any staining (Fig. 5a). Control experiments for sGC in the cerebellum showed the typical sGC-IR staining (Fig. 5b) as previously described by Ding et al [41]. Positive controls for PGP9.5 using a TH double label showed that all TH-IR neurons from the RVLM region also expressed PGP9.5-IR, in addition to adjacent neurons that expressed PGP9.5 only (Fig. 5c). Double labelling with alpha-SMA, which labels smooth muscle cells of precapillary arterioles in the brain [42], showed co-localisation with cGMP (Fig. 5d). Furthermore, our overall pattern of vascular/microvascular cGMP staining in the brain is as described by [31].

Discussion

the NA when compared to Fig. 1, however very few neurons expressing cGMP were detected in the RVLM region. Individual neurons showing cGMP-IR above the level of background staining are shown (arrow heads). Scale bar in (**a**) equals 200 μ m, scale bar in panel (**b**) equals 100 μ m

control of blood pressure [43] and that endogenous NO is an important mediator in this regulatory process [9, 10, 21]. Functional studies provide strong evidence that NO acts through the sGC-cGMP signalling pathway in the RVLM to drive sympathoexcitatory responses [6, 20, 44, 45], however, we were unable to detect cGMP in the RVLM of either the SHR or WKY rat strains. This was despite the use of PDE inhibitors of the use of specific stimulators of cGMP synthesis in slice preparations. We were able to demonstrate abundant sGC-IR in neurones throughout the RVLM region.

Cyclic GMP in the RVLM

An inability to detect cGMP in the RVLM may have been associated with methodological issues, for example the adequacy of antigen recognition/penetration, or sensitivity of the technique. These concerns are alleviated somewhat by our detection of cGMP in the adjacent brainstem region of the NA. Alternative methodologies such as radioimmunoassay may have been more sensitive, however the ability to define specific neuronal populations is lost and in a study examining hippocampal slices, analysis of cGMP radioimmunoassay versus cGMP immunofluorescence intensity showed comparable sensitivities [46]. The lack of detectable cGMP expression in neurons of the RVLM is in accord with a detailed study by De Vente et al. [22], who similarly observed cGMP in the NA and nucleus tractus solitarii (NTS) in the brain stem region, but do not comment on its expression in the RVLM, despite the use of invitro stimulation paradigms as applied in this study. In the work by De Vente et al., the importance of IBMX to reveal

Fig. 3 Confocal images depicting cGMP $(\mathbf{b}, \mathbf{d}, \mathbf{e})$ and either PNMT (a, c) or nNOS-IR (e) in RVLM sections from WKY rats after treatment invitro to increase cGMP synthesis. Panels (a) and (b) show the PNMT/cGMP-IR, respectively under control incubation conditions. Panels (c) and (d) illustrate PNMT/ cGMP-IR respectively after invitro incubation in NMDA (100 µm 2 min). Panels (e and f) show nNOS/cGMP-IR, respectively after incubation in DETA-NO (100 um 15 min). Insets \mathbf{b}' , \mathbf{d}' and \mathbf{f}' illustrate cGMP expression in the NA under control, NMDA and DETA-NO experimental conditions, respectively. All experiments were performed in the presence of 0.5 mM IBMX. Despite cGMP-IR in blood vessels (arrows) and NA being enhanced by the in-vitro treatments, they failed to reveal the presence of additional cGMP-IR neurons in the RVLM regions in association with either the PNMT or nNOS cell groups. Scale bar in (f) equals 100 µm for panels (a-f). Scale bar in \mathbf{f}' equals 100 μ m for panels $(\mathbf{b}', \mathbf{d}' \text{ and } \mathbf{f}')$



otherwise non-detectable cGMP populations was stressed [22, 47] and this has also been noted by other authors [48]. For this reason, IBMX was used in a subset of studies in perfusion fixed rats and for the brainstem slice in-vitro incubation experiments. However, while we found that IBMX did increase the levels of cGMP in already visible cell populations and in the vasculature of the brainstem, it did not uncover cGMP-IR neurons in the RVLM,

suggesting IBMX-sensitive PDE activity did not limit detection. This concurs with our previous work examining cGMP levels in the spinal cord, where we were able to show that cGMP expressing sympathetic preganglionic neurons could be readily detected in the absence of IBMX [30]. The effects of anaesthetic on cGMP levels also require consideration. For this project, anaesthetic was an ethical requirement. Results from studies investigating the Fig. 4 Confocal images illustrating double labelling for PNMT/sGC (a), GFAP/sGC (b) and PGP9.5/sGC (c) immunoreactivity in the RVLM from a WKY animal (male, 10-weeks-old). Panel (a) shows PNMT (red—CY3 secondary antibody) and sGC (green—FITC secondary antibody) double labelling and illustrates numerous cells IR for sGC (arrows) but lack of co localisation with PNMT (#). Panel (b) shows GFAP (red—CY3 secondary antibody) and sGC (green—FITC secondary antibody) and serves to demonstrate that the cells immunoreactive for sGC (arrows) show none of the characteristic morphological features of astrocytes (*) and that there is no double labelling for the two markers. Panel (c) shows PGP9.5 (red—CY3 secondary antibody) and sGC (green—FITC secondary antibody) and sGC (green—FITC secondary antibody) and sGC (arrows; yellow), with adjacent neurons immunoreactive for PGP9.5 only (*). Scale bar in (a) equal 100 μ m, scale bar in panels (b) and (c) equals 50 μ m

effect of anaesthetic on cGMP in the central nervous system are conflicting, with some reports describing the effects of anaesthetics as inhibitory, while others suggest no effect or indeed an increase in cGMP levels [49]. Thiopentone was chosen for this study on the rationale that intravenous agents are less likely to depress cGMP levels than inhalation anaesthetics [50], and that pentobarbital drugs specifically do not depress cGMP levels in the brainstem [51]. Given the time period available for anaesthetic washout and the demonstration of an increase of detectable cGMP in surrounding tissues, it is likely the effects of anaesthetic were minimal in this study.

The use of NMDA and NO donors to increase detectable cGMP in brain slice in-vitro preparations has been demonstrated previously in various tissues including the paraventricular nucleus [52] cerebellum [22, 47] and hippocampus and thalamus [46]. The choice of DETA-NO as a donor was based on its ability to spontaneously liberate NO in aqueous solutions in a stable, time-controlled fashion [53]. It has been proposed that the type of NO donor can make a significant difference to the way in which cGMP is stimulated [54], however a recent study comparing the effects of NONOates to the classical NO donor sodium nitroprusside found limited difference in their ability to stimulate sGC or influence cGMP staining patterns in brain slice preparations [46]. The NO donor nitroglycerin has also been shown to increase cGMP-IR in both neuronal and vascular elements of the brain, but in agreement with our study, did not uncover any additional or previously undetected cGMP immunoreactive neuronal cell groups [31].

Soluble guanylate cyclase expression within the RVLM

The widespread detection of sGC within neurones of the RVLM is in accord with previous studies that have demonstrated both mRNA and protein for sGC within the medulla [55, 56]. It is likely to be a functional form of sGC, as the antibody we used was specific for the β 1 subunit, which is the obligatory subunit for functional sGC [15],





Fig. 5 Control experimental results. Panel (a) shows a negative control for PGP9.5 (red—CY3 secondary antibody) and sGC (green—FITC secondary antibody). Double labelling on a control RVLM section from a 10-week-old WKY shows no immunoreactivity for either series of labelling reactions. Panel (b) shows intense labelling for sGC (red—CY3 secondary antibody) in the cerebellum from a 10 week old WKY. Panel (c) shows positive control experiments for PGP9.5 from an adult SHR animal. All TH positive cells (green—FITC secondary antibody) were double labelled for PGP9.5 (red—CY3 secondary antibody) resulting in a yellow colour on the overlaid images (arrows). Immediately adjacent to the double-

and has been shown to co-localise extensively with the α subunit throughout the CNS of the adult rat brain [41].

While we did not demonstrate co-localisation of sGC with the nNOS cell population, they were often in close association. This pattern of expression is consistent with other brain regions, where NO responsive and NO producing structures are not found within the same neuronal profile [22, 41, 57]. An exception is the NTS, where nNOS and sGC have been shown to co-localise [58]. Similarly, we saw sGC in close association but not co-localised with the C1 cell group. Additional studies aimed at determining the cell population which expresses sGC should include retrograde labelling as a means of identification of the non-

labelled cells are PGP9.5 only labelled neurons (*). Panel (**d**) shows control experiments assessing the vascular expression of cGMP in a 10 week old WKY. Sections were double labelled for alpha-smooth muscle actin (alpha-SMA; green—FITC secondary antibody) and cGMP (red—CY3 antibody). All alpha-SMA-IR structures showed clear co-localisation with cGMP as illustrated. The cGMP expression can be seen to extend from the larger precapillary arteriole (arrows) to the microvasculature, where it is expressed in pericytes (the contractile elements of the brain microvasculature) that do not label for alpha-SMA [64, 65]. Scale bar in (**a**) equal 50 µm, scale bar in panels (**b**) and (**c**) equal 100 µm, scale bar in panel (**d**) equals 20 µm

C1 bulbospinal group [2], and double labelling for markers such as neuropeptide Y to identify neurons which project to the hypothalamus [59], or markers to enable identification of glutamatergic and gabaergic neurons [3]. This would then allow potential functional relevance to be attributed to sGC expression in the region.

Conclusion

A number of physiological studies indicate that NO can modulate pressor and reflex responses in the RVLM via an sGC/cGMP dependent mechanism [6, 7, 44, 45]. While we were unable to detect cGMP-IR in the neurons of the C1 region, either in the resting state, when stimulated by NMDA or NO donor, or after PDE inhibition, our sGC-IR results certainly indicate the capacity for cGMP synthesis. In an in-vivo study of the cat, nNOS-sGC co-localisation was present in the RVLM only after activation by brady-cardia (as identified by the presence of *c-fos*) [60]. This raises the hypothesis that functional network inputs, such as the sympathetic baroreflex pathway [45] are required to drive a sGC/cGMP cascade in the RVLM. This may be the mechanism by which functional differences in the SHR and WKY are delineated and future studies investigating this possibility are warranted.

Basal cGMP levels in neurons are the result of a dynamic equilibrium between synthesis, driven by NOsGC, and the rate of degradation by PDEs, [61]. The rate of synthesis can change with time due to desensitisation of sGC, and cGMP kinetics can vary between not only different cell types but also different regions of the brain [62]. The expression of IBMX-insensitive PDEs, such as PDE9, which is specific for cGMP [46, 63], may be another important factor limiting detection of cGMP accumulation in regions such as the RVLM. Of note is a recent study that has shown under similar conditions to ours, that the use of an NO donor in the presence of IBMX was not sufficient to maximise cGMP detection in the hippocampus, but instead required the further addition of the NO-independent activators of sGC: YC-1 or BAY 41-2272 [46]. This stimulated cGMP synthesis in cells not normally known to express cGMP and the authors suggest the presence of an endogenous sGC inhibitor as a possible explanation [46]. Examination of the role of functional stimulatory inputs, NO-independent activation of sGC and the activity of specific PDEs is therefore required before the definitive role of cGMP as a contributor to altered sympathetic tone in the SHR can be ascertained.

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