Cellular/Molecular

# Molecular Determinants for Modulation of Persistent Sodium Current by G-Protein $\beta\gamma$ Subunits

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Voltage-gated sodium channels are responsible for the upstroke of the action potential in most excitable cells, and their fast inactivation is essential for controlling electrical signaling. In addition, a noninactivating, persistent component of sodium current,  $I_{\text{NaP}}$ , has been implicated in integrative functions of neurons including threshold for firing, neuronal bursting, and signal integration. G-protein  $\beta\gamma$  subunits increase  $I_{\text{NaP}}$ , but the sodium channel subtypes that conduct  $I_{\text{NaP}}$  and the target site(s) on the sodium channel molecule required for modulation by  $G\beta\gamma$  are poorly defined. Here, we show that  $I_{\text{NaP}}$  conducted by  $\text{Na}_{\text{v}}1.1$  and  $\text{Na}_{\text{v}}1.2$  channels ( $\text{Na}_{\text{v}}1.1 > \text{Na}_{\text{v}}1.2$ ) is modulated by  $G\beta\gamma$ ;  $\text{Na}_{\text{v}}1.4$  and  $\text{Na}_{\text{v}}1.5$  channels produce smaller  $I_{\text{NaP}}$  that is not regulated by  $G\beta\gamma$ . These qualitative differences in modulation by  $G\beta\gamma$  are determined by the transmembrane body of the sodium channels rather than their cytoplasmic C-terminal domains, which have been implicated previously in modulation by  $G\beta\gamma$ . However, the C-terminal domains determine the quantitative extent of modulation of  $\text{Na}_{\text{v}}1.2$  channels by  $G\beta\gamma$ . Studies of chimeric and truncated  $\text{Na}_{\text{v}}1.2$  channels identify molecular determinants that affect modulation of  $I_{\text{NaP}}$  located between amino acid residue 1890 and the C terminus at residue 2005. The last 28 amino acid residues of the C terminus are sufficient to support modulation by  $G\beta\gamma$  when attached to the proximal C-terminal domain. Our results further define the sodium channel subtypes that generate  $I_{\text{NaP}}$  and identify crucial molecular determinants in the C-terminal domain required for modulation by  $G\beta\gamma$  when attached to the transmembrane body of a responsive sodium channel.

Key words: sodium; channels; G-proteins; inactivation; neuromodulation; excitability

#### Introduction

Voltage-gated Na  $^+$  channels are essential for neuronal excitability. They initiate fast action potentials and shape subthreshold electrical properties that contribute to important integrative functions. Voltage-gated Na  $^+$  channels are complexes of a poreforming  $\alpha$  subunit and auxiliary  $\beta$  subunits (Catterall, 2000). The primary sequence of the  $\alpha$  subunit contains four homologous domains (I–IV), each containing six predicted transmembrane  $\alpha$ -helices (S1–S6). Five different  $\alpha$  subunits are expressed in adult brain: Na<sub>v</sub>1.1, Na<sub>v</sub>1.2, Na<sub>v</sub>1.3, Na<sub>v</sub>1.5, and Na<sub>v</sub>1.6 (Goldin et al., 2000).

In addition to the transient rapidly inactivating sodium current ( $I_{\rm NaT}$ ) (Hodgkin and Huxley, 1952), voltage-gated Na <sup>+</sup> channels also generate a "persistent" current ( $I_{\rm NaP}$ ), which is maintained during long depolarizations, and whose importance in neurons has become increasingly apparent (Crill, 1996).  $I_{\rm NaP}$  has been observed in multiple neuron types. It contributes to

shaping repetitive firing (Azouz et al., 1997; Mantegazza et al., 1998; Parri and Crunelli, 1998; Brumberg et al., 2000), generating rhythmicity (Alonso and Llinas, 1989; Pennartz et al., 1997; Pape et al., 1998; Taddese and Bean, 2002) and amplifying both IPSPs and EPSPs (Schwindt and Crill, 1995; Stuart and Sakmann, 1995; Stuart, 1999).  $I_{\rm NaP}$  has also been implicated in the generation of epileptiform activities (Kearney et al., 2001), suggesting that its regulation plays a crucial role in controlling electrical excitability (Schwindt and Crill, 1995; Stuart and Sakmann, 1995; Segal and Douglas, 1997; Stuart, 1999).

Central neuronal  $I_{\rm NaP}$  is subject to modulation by intracellular signal transduction pathways. It is decreased in parallel with  $I_{\rm NaT}$  by activation of muscarinic acetylcholine receptors and consequent phosphorylation by protein kinase C in hippocampal neurons (Cantrell et al., 1996). It is increased by hypoxia and nitric oxide in hippocampal neurons (Hammarstrom and Gage, 1998, 1999, 2000). In addition,  $I_{\rm NaP}$  is increased when G-protein  $\beta\gamma$  subunits are coexpressed with Na<sub>v</sub>1.2 channels (Ma et al., 1997). This increase was prevented by a putative  $G\beta\gamma$ -binding peptide from the C terminus of the Na<sub>v</sub>1.2 channel, suggesting that G-protein  $\beta\gamma$  subunits interact with that C-terminal site during modulation (Ma et al., 1997). Consistent with this idea, G-protein  $\beta$  subunits immunoprecipitate with sodium channel  $\alpha$  subunits from cortical neuron preparations (Marin et al., 2001).

In the experiments presented here, we have compared modulation of  $I_{\text{NaP}}$  by G-protein  $\beta\gamma$  subunits for Na<sub>v</sub>1.1, Na<sub>v</sub>1.2,

Received Aug. 16, 2004; revised; accepted Jan. 27, 2005.

This work was supported by National Institutes of Health (NIH) Research Grant NS34801 to T.S., a Human Frontiers Science Program Fellowship to M.M., a grant from the Fondazione Pierfranco e Luisa Mariani to M.M., and NIH Research Grant NS25704 to W.A.C. We thank Dr. Mel Simon for the kind gift of plasmids encoding G-protein subunits.

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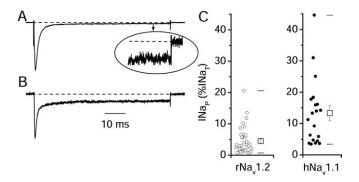
 $Na_v1.4$ , and  $Na_v1.5$  channels. We show that both  $Na_v1.1$  and  $Na_v1.2$  conduct  $I_{NaP}$  ( $Na_v1.1 > Na_v1.2$ ) that can be modulated by  $G\beta\gamma$ , but  $Na_v1.4$  and  $Na_v1.5$  do not. Analysis of channel chimeras reveals that the transmembrane bodies of  $Na_v1.4$  and  $Na_v1.5$  channels are responsible for their lack of G-protein modulation rather than their C-terminal domains. However, the quantitative extent of modulation of  $Na_v1.2$  channels is critically dependent on the C-terminal domain. Through analysis of deletion mutants, we identify new molecular determinants for modulation in the  $Na_v1.2$  channels in the C terminus and show that the final 28 amino acids are necessary for generation of  $I_{NaP}$  and can substitute for the entire distal half of the C terminus in supporting regulation by  $G\beta\gamma$ .

#### **Materials and Methods**

Isolation of cDNA for hNa $_v$ 1.1 and generation of cell lines CL1 and CL2. Six overlapping clones spanning the human Na $_v$ 1.1 coding region were isolated from human cerebellum and medulla cDNA libraries. A full-length cDNA was assembled from these partial clones using natively occurring restriction sites (BamHI, nucleotide 561; BamHI, nucleotide 2433; SphI, nucleotide 2694; NdeI, nucleotide 3786; SapI, nucleotide 5630). This was then inserted upstream of the internal ribosome entry site (IRES) element in the mammalian expression vector pCIN5 (Rees et al., 1996). Cell lines stably expressing hNa $_v$ 1.1 were isolated after transfection of human embryonic kidney (HEK) 293 cells with 2  $\mu$ g of pCIN5-hNa $_v$ 1.1 and selection for 3–4 weeks in 800  $\mu$ g/ml Geneticin-G418 (Burbidge et al., 2002). Clonal cell lines CL1 and CL2 were isolated after two rounds of single-cell dilution cloning.

Construction of Na<sub>v</sub>1.2 and Na<sub>v</sub>1.5 channel mutants. The mammalian expression plasmids, pCDM8-rH1 encoding the rat cardiac rNa<sub>a</sub>1.5 α subunit and pCDM8-rIIA encoding the rat brain rNa<sub>v</sub>1.2a α subunit, were described previously (Qu et al., 1994; Linford et al., 1998). cDNA encoding the full-length human brain type I Na + channel hNa, 1.1 was in pCIN5-hNa<sub>v</sub>1.1 (Clare et al., 2000). cDNA encoding the rat skeletal muscle Na + channel rNa, 1.4 (Trimmer et al., 1989) (kind gift from Dr. P. Ruben, Utah State University, Logan, UT) was subcloned into pCDM8. The chimeric Na<sup>+</sup> channel rNa<sub>v</sub>1.2/Na<sub>v</sub>1.5 C terminus (CT) was described previously (Mantegazza et al., 2001). Chimeric Na + channel Na<sub>v</sub>1.2/1.4 CT was comprised of the Na<sub>v</sub>1.4 C-terminal cytoplasmic domain (beginning at amino acid position E1592) appended to Na<sub>v</sub>1.2a cDNA after residue L1776. In mutant Na<sub>v</sub>1.2/1.4QxxER, the Na<sub>v</sub>1.2a sequence was changed from RIQMEER (R1876 to R1882) to KQTMEEK, the equivalent sequence in rat Na<sub>v</sub>1.4. In Na<sub>v</sub>1.2/AAMEAA mutant, the rNa<sub>v</sub>1.2a sequence IQMEER beginning at I1875 was converted to AAMEAA. The truncation mutants  $Na_v 1.2\Delta K1890$ ,  $Na_v 1.2\Delta A1909$ ,  $Na_v1.2\Delta S1929$ ,  $Na_v1.2\Delta T1951$ ,  $Na_v1.2\Delta S1977$ , and  $Na_v1.2\Delta K1998$ , which delete segments of C-terminal cytoplasmic region of rat Na<sub>v</sub>1.2a, have been described previously (Mantegazza et al., 2001). The Na<sub>v</sub>1.2a deletion mutant Na<sub>v</sub>1.2/ $\Delta$ 1891–1977 removed an internal segment bounded by amino acid residues V1891 and S1977. Full-length cDNA of bovine G-protein  $\beta_2$  subunit was cloned into a bicistronic mammalian expression plasmid, pIRES-enhanced yellow fluorescent protein (YFP) (Clontech, Palo Alto, CA), which encodes the yellow variant of the green fluorescent protein (GFP). This construct was called pG $\beta_2$ IRES-YFP. The G-protein  $\gamma_3$  subunit was cloned into a cyan variant of the same bicistronic vector and was named pGy<sub>3</sub>IRES-cyan fluorescent protein (CFP). All Na + channel mutations generated by PCR mutagenesis were sequenced in between the restriction sites used for subcloning to verify that they were free of unintended alteration of sequences.

Expression of sodium channels. The fluorescent proteins in the bicistronic vectors or the CD8 receptor in pCD8-neomycin were used as markers of transfected cells (Margolskee et al., 1993). Plasmids were cotransfected into tsA-201 cells by CaPO<sub>4</sub> precipitation. Cells were grown to 75% confluence in 35 mm tissue culture dishes (Corning, Acton, MA). After addition of DNA, they were incubated at 37°C in 3% CO<sub>2</sub>. Twelve hours after transfection, cells were removed from the dishes using 2 mm EDTA in PBS and replated at low density for electrophysio-



**Figure 1.** Normalized current traces elicited by a step stimulus to 0 mV from a holding potential of -70 mV from representative tsA-201 cells transfected with rNa $_{\rm v}$ 1.2a ( $\it A$ ) or with hNa $_{\rm v}$ 1.1 ( $\it B$ ). The inset in  $\it A$  (oval) shows the end of the pulse on a 15-fold expanded vertical axis.  $\it C$ , Individual data points (circles) and mean values  $\pm$  SEM (open squares) of  $\it I_{\rm NaP}$  as a percentage of  $\it I_{\rm NaT}$  in tsA-201 cells transiently transfected with rNa $_{\rm v}$ 1.2a ( $\it n=36$ ) or hNa $_{\rm v}$ 1.1 ( $\it n=20$ ;  $\it p<0.01$ ). The horizontal lines represent the first and 99th percentiles of the range.

logical recordings. HEK293 cell lines that expressed hNa $_{\rm v}$ 1.1, CL1 and CL2, were transfected using TransFast (Promega, Madison, WI). Positive transfectants were selected visually either by anti-CD8-coated beads (Dynal, Brown Deer, WI) or by their fluorescence using a Nikon (Tokyo, Japan) Eclipse TE300 microscope for epifluorescence. Cells transfected with plasmids encoding green fluorescent proteins were selected visually using excitation/emission cubes for YFP (Chroma 41028; Chroma Technology, Rockingham, VT) and CFP (Chroma 31044v2). The tsA-201 subclone of HEK293 cells and stably transfected HEK cell lines were maintained as described previously (Herlitze et al., 1996).

Electrophysiology and data analysis. Whole-cell patch-clamp recordings were performed at room temperature using an Axopatch 200B amplifier (Axon Instruments, Union City, CA). Capacitative currents were minimized by means of the amplifier circuitry. Seventy percent prediction and 90-95% series resistance compensation were used routinely. The remaining capacity transients and leakage currents were eliminated using P/4 subtraction. The intracellular solution contained the following (in mm): 120 Cs-aspartate, 5 NaCl, 2 MgCl<sub>2</sub>, 10 EGTA, 10 HEPES, pH 7.3 with CsOH. The extracellular solution contained the following (in mm): 140 NaCl, 2 CaCl<sub>2</sub>, 2 MgCl<sub>2</sub>, 10 HEPES, pH 7.4 with NaOH. pClamp 6.0.4 software and a Digidata 1200 interface (Axon Instruments) were used to generate the voltage stimuli and to acquire the current signals, which were filtered at 5 or 10 kHz. The data were analyzed using pClamp and Origin 6.0 (OriginLab, Northampton, MA) on a Pentium II-based personal computer (Intel, Santa Clara, CA). Unless indicated, the holding potential for voltage clamp recordings was -70 mV.

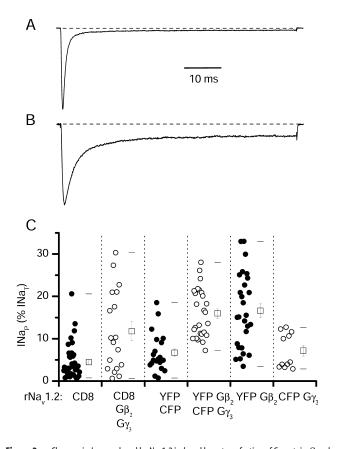
Conductance–voltage (G-V) relationships were calculated from the current–voltage (I-V) relationships according to extended Ohm's law  $G_{\rm Na}=I_{\rm Na}/(V-E_{\rm Na})$ , where  $I_{\rm Na}$  was the peak Na  $^+$  current measured at potential V,  $G_{\rm Na}$  was the sodium conductance, and  $E_{\rm Na}$  was the calculated Nernst equilibrium potential for Na  $^+$ . Curves were fit using the Levenberg-Marquardt algorithm. The voltage dependence of activation and voltage dependence of fast inactivation were fitted to Boltzmann relationships of the following form: normalized  $G_{\rm Na}=((1-C)/(1+\exp(V-V_{1/2})/k))+C$ , where V was the membrane potential,  $V_{1/2}$  was the voltage of half-maximal activation or inactivation, k was a slope factor, and C was the baseline noninactivating current. For cells with large  $I_{\rm NaP}$  a second Boltzmann component was included, as follows:  $((1-C-A2)/(1+\exp((V-V_{1/2})/k_1)))+(A2/(1+\exp((V-V_{1/2})/k_2)))+C$ . The statistical results are given as mean  $\pm$  SEM. The threshold p value for statistical significance was 0.05.

Sequence alignments were produced by ClustalW (Thompson et al., 1994) followed by manual editing to produce the alignments shown.

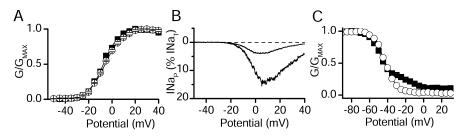
#### Results

### I<sub>NaP</sub> conducted by rNa<sub>v</sub>1.2a and hNa<sub>v</sub>1.1 channels

Sodium currents produced by expression of Na<sub>v</sub>1.2 channels in tsA-201 cells have two components: a large, rapidly inactivating



**Figure 2.** Changes in  $I_{\rm NaP}$  produced by Na<sub>v</sub>1.2 induced by cotransfection of G-protein  $\beta$  and  $\gamma$  subunits. **A**, **B**, Current traces from representative tsA-201 cells transfected with rNa<sub>v</sub>1.2a alone (**A**) or cotransfected with  $G\beta_2$  and  $G\gamma_3$  (**B**) elicited by a depolarization to 0 mV from a holding potential of -70 mV. **C**, Individual data points (circles) and mean values  $\pm$  SEM (open squares) of  $I_{\rm NaP}$  as a percentage of  $I_{\rm NaT}$  in tsA-201 cells transfected with rNa<sub>v</sub>1.2a and the indicated plasmids. The whiskers represent the first and 99th percentile values. Mean values were the following, for cells transfected with (from left to right): CD8 receptor as reporter gene  $(I_{\rm NaP}=4.5\pm0.7\%;n=36)$ ; rNa<sub>v</sub>1.2a,  $G\beta_2$ ,  $G\gamma_3$ , and CD8 receptor ( $I_{\rm NaP}=11.8\pm2.3\%;n=18$ ); rNa<sub>v</sub>1.2a with YFP and CFP as reporter genes ( $I_{\rm NaP}=6.8\pm1.0\%;n=20$ ); rNa<sub>v</sub>1.2a,  $G\beta_2$  expressed in a bicistronic vector with YFP ( $I_{\rm NaP}=16\pm1.0\%;n=26$ ); rNa<sub>v</sub>1.2a and  $I_{\rm NaP}=16\pm1.0\%;n=26$ ; rNa<sub></sub>



**Figure 3.** Properties of  $I_{\rm NaT}$  and  $I_{\rm NaP}$  in tsA-201 cells transfected with Na<sub>Q</sub>1.2 alone or cotransfected with  $G\beta_2\gamma_3$ . **A**, Mean voltage dependence of activation for cells transfected with rNa<sub>Q</sub>1.2a alone (open circles) and cells cotransfected with rNa<sub>Q</sub>1.2a and  $G\beta_2\gamma_3$  (filled squares). The solid lines are the Boltzmann fits that gave the following parameters (see Materials and Methods for definitions): Na<sub>Q</sub>1.2 alone, n=9,  $V_{1/2}=-5.9\pm0.2$  mV,  $k=-7.3\pm0.2$  mV; Na<sub>Q</sub>1.2a plus  $G\beta_2\gamma_3$ , n=13,  $V_{1/2}=-7.2\pm0.2$  mV,  $k=-6.6\pm0.2$  mV. **B**, Currents elicited by slow voltage ramps from a representative cell transfected with rNa<sub>Q</sub>1.2a alone (smaller current) or cotransfected with  $G\beta_2\gamma_3$  (larger current). **C**, Voltage dependence of inactivation from representative cells with the mean level of  $I_{\rm NaP}$  determined with 100 ms prepulses to a variable voltage followed by a test depolarization to 0 mV for Na<sub>Q</sub>1.2a alone (open circles) or cotransfected with  $G\beta_2\gamma_3$  (filled squares). Normalized test pulse current is plotted as a function of prepulse potential. Mean parameters derived from fits of Boltzmann functions to the data were: rNa<sub>Q</sub>1.2a alone, n=7,  $V_{1/2}=-44.1\pm0.2$ ,  $k=7.3\pm0.1$ ,  $C=0.023\pm0.002$ ; rNa<sub>Q</sub>1.2a plus  $G\beta_2\gamma_3$ , n=13 (fit with the sum of 2 Boltzmann components),  $V_{1/2,1}=-45.1\pm0.4$ ,  $V_{1}=8.3\pm0.4$ ,  $V_{2}=8.3\pm0.4$ ,  $V_{2}=8.4$ 

component followed by a persistent component that fails to inactivate by the end of 60 ms depolarizations (Fig. 1A).  $I_{\rm NaP}$  was quantitated as the mean current remaining between 45 and 55 ms after the beginning of the voltage step and expressed as a percentage of  $I_{\rm NaT}$ . The level of  $I_{\rm NaP}$  varied considerably from cell to cell with a mean of 4.5  $\pm$  0.7% of  $I_{\rm NaT}$  (n=36) (Fig. 1C). hNa<sub>v</sub>1.1 channels expressed similarly in tsA-201 cells conducted significantly larger  $I_{\rm NaP}$  than rNa<sub>v</sub>1.2a (mean  $I_{\rm NaP}=13\pm2\%$ ; n=20; p<0.01) (Fig. 1B, C), similar to the results of Smith and Goldin (1998) for expression of rNa<sub>v</sub>1.1 in *Xenopus* oocytes. The variability of the fraction of  $I_{\rm NaP}$  versus  $I_{\rm NaT}$  among single clonal tsA-201 cells transfected with identical cDNA for either rNa<sub>v</sub>1.2a and hNa<sub>v</sub>1.1 channels (Fig. 1C) suggests that cellular signaling processes that differ from cell to cell can control the level of  $I_{\rm NaP}$ .

#### Modulation of $I_{NaP}$ through rNa<sub>v</sub>1.2a channels by $G\beta\gamma$

 $I_{\text{NaP}}$  conducted by Na<sub>v</sub>1.2 channels is increased by coexpression of G-protein  $\beta \gamma$  subunits (Fig. 2 *B*, *C*) (Ma et al., 1997). Transfection of  $G\beta_2\gamma_3$  increased  $I_{NaP}$  from 4.5  $\pm$  0.7 to 11.8  $\pm$  2.3% (n=18) (Fig. 2C). The level of  $I_{\text{NaP}}$  obtained with cotransfection of plasmids encoding G-protein  $\beta_2$  and  $\gamma_3$  subunits was highly variable in different cells (Fig. 2C), and this variability complicated the study of  $I_{\text{NaP}}$  modulation. One possible source of variability was the requirement for cotransfection of cDNAs encoding three different proteins: the Na<sub>v</sub>1.2  $\alpha$  subunit, the G-protein  $\beta_2$  subunit, and the G-protein  $\gamma_3$  subunit. To ensure expression of both G-protein  $\beta$  and γ subunits in all cells studied, we cloned the cDNAs encoding these G-protein subunits into bicistronic vectors containing an IRES followed by cDNA encoding the yellow or cyan mutants of GFP as reporter genes (Trouet et al., 1997). Control cells transfected with the same fluorescent protein vectors lacking G-protein subunits (Fig. 2C, CFP, YFP) had  $I_{\text{NaP}}$  that was not significantly different from cells transfected with rNa<sub>v</sub>1.2 and CD8 (CD8, mean  $I_{\rm NaP} = 4.5 \pm 0.7\%$ , n = 36; CFP, YFP, mean  $I_{\text{NaP}} = 6.8 \pm 1.0\%$ , n = 20; p = 0.08) (Fig. 2C). When  $G\beta_2$ -YFP and  $G\gamma_3$ -CFP were cotransfected, and only cells clearly fluorescent for both markers were studied, the data were less variable than without use of bicistronic vectors (mean  $I_{\text{NaP}}$  =  $16 \pm 1.0\%$ ; n = 26) (Fig. 2C, YFP G $\beta_2$ /CFP G $\gamma_3$ ). Variance of the experimental groups decreased from 92 with CD8 as a reporter to 34 with bicistronic G $\beta\gamma$  as reporter ( $p = 2 \times 10^{-8}$ ). As a result of the reduced variability using GFP reporters to monitor expression,

smaller numbers of experiments were required to obtain meaningful results when  $G\beta\gamma$  coexpression was studied. The IRES vectors were used to verify expression in all additional studies.

## Modulation of $I_{\text{NaP}}$ through rNa<sub>v</sub>1.2a channels by $G\beta_2$ subunits alone

To better characterize  $G\beta\gamma$  modulation, we examined the ability of single G-protein  $\beta$  and  $\gamma$  subunits to increase  $I_{\text{NaP}}$ . Expression of only  $G\beta_2$  with rNa<sub>v</sub>1.2a was sufficient to increase  $I_{\text{NaP}}$  comparably to that caused by expression of  $G\beta\gamma$  (mean  $I_{\text{NaP}}=17\pm2\%; n=27; p=0.00005)$  (Fig. 2C, YFP,  $G\beta_2$ ). In contrast, expression of  $G\gamma_3$  alone did not modulate  $I_{\text{NaP}}$  (mean  $I_{\text{NaP}}=7\pm1\%; n=11; p=0.8)$  (Fig. 2C, CFP,  $G\gamma_3$ ). Expression of  $G\beta$  subunits is also sufficient for G-protein modulation of calcium channels (Herlitze et al., 1996).

### Effect of $G\beta_2\gamma_3$ on voltage-dependent gating of rNa<sub>v</sub>1.2

We compared the voltage-dependent gating of  $I_{NaT}$  and  $I_{NaP}$  before and after modulation by  $G\beta_2\gamma_3$ . As in previous work (Ma et al., 1997), the major effect of  $G\beta_2\gamma_3$  on the properties of rNa<sub>v</sub>1.2a was the increase in  $I_{\rm NaP}$ . Little change in the voltage dependence of activation of  $I_{\text{NaT}}$  was observed (control,  $V_{1/2} = -5.9 \pm 0.2$ mV;  $G\beta_2\gamma_3$ ,  $V_{1/2} = -7.2 \pm 0.2$  mV) (Fig. 3A). Coexpression of  $G\beta\gamma$  strikingly increased the amplitude of  $I_{NaP}$  as measured in response to slowly rising voltage ramps (Fig. 3B), during which  $I_{\text{NaT}}$  is inactivated by the slow ramp depolarization. This protocol gives the clearest visual illustration of the large effect of  $G\beta\gamma$ coexpression on  $I_{\text{NaP}}$ . The presence of  $I_{\text{NaP}}$  resulted in a biphasic inactivation curve, which was fit by the sum of two Boltzmann relationships (Fig. 3C). The component of current that had the more positive voltage dependence of inactivation also had slower inactivation kinetics and corresponded to  $I_{NaP}$  (data not shown) (Ma et al., 1997). GB $\gamma$  caused an increase in the fraction of current inactivating with the more positive voltage dependence with little change in the voltage dependence of the individual components (Fig. 3C).

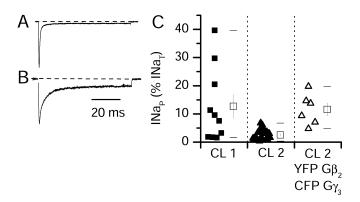
#### Modulation of $I_{\text{NaP}}$ conducted by hNa<sub>v</sub>1.1

We were concerned that the large variation in  $I_{\text{NaP}}$  among single tsA-201 cells expressing hNa<sub>v</sub>1.1 channels (Fig. 1) might impair measurements of  $G\beta\gamma$  modulation, even using our bicistronic vectors and imaging transfected  $G\beta\gamma$ . Therefore, we examined the level of  $I_{\text{NaP}}$  in two clonal cell lines, derived by stable transfection of hNa<sub>v</sub>1.1 into HEK293 cells (Clare et al., 2000). In the first cell line tested, CL1, the level of  $I_{\text{NaP}}$  was similar to that observed after transient transfection of hNa<sub>v</sub>1.1 into tsA-201 cells (mean  $I_{NaP} = 13 \pm 4\%$ ; n = 10) (Fig. 4C). In the second cell line, CL2, lower levels of  $I_{\text{NaP}}$  were observed (mean  $I_{\text{NaP}} = 2.5 \pm 0.4\%$ ; n = 25) (Fig. 4A, C, CL2). These results with two clonal cell lines are consistent with the striking variation of  $I_{NaP}$  among single cells transfected transiently (Fig. 1C).

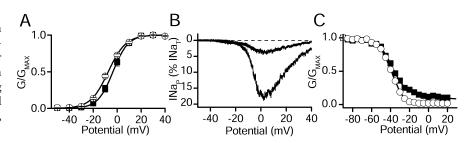
Because of its low level of intrinsic  $I_{\rm NaP}$  in control, we chose CL2 to study the effect of G $\beta_2\gamma_3$  on I $_{\rm NaP}$ . We cotransfected pG $\beta_2$ IRES-YFP and pG $\gamma_3$ IRES-CFP into CL2 cells stably expressing hNa $_{\rm v}$ 1.1. I $_{\rm NaP}$  with G $\beta_2\gamma_3$  was significantly higher than in untransfected CL2 cells (mean  $I_{\rm NaP}=11\pm2\%$ ; n=6;  $p=10^{-7}$  relative to untransfected CL2) (Fig. 4B, C, CL2, YFP G $\beta_2$ , CFP G $\gamma_3$ ). Thus, as for rNa $_{\rm v}$ 1.2a,  $I_{\rm NaP}$  conducted by hNa $_{\rm v}$ 1.1 is also increased by coexpression of G $\beta_2\gamma_3$ .

#### Effect of $G\beta_2\gamma_3$ on voltage-dependent gating of hNa<sub>v</sub>1.1

Cotransfection of hNa<sub>v</sub>1.1 with  $G\beta_2\gamma_3$  resulted in a small positive shift in the voltage dependence of activation of  $I_{\rm NaT}$  (Fig. 5A). Coexpression of  $G\beta_2\gamma_3$  also substantially increased  $I_{\rm NaP}$  measured using slowly rising voltage ramps (Fig. 5B). The increased persistent sodium current in cells expressing  $G\beta_2\gamma_3$  caused a positive shift in the overall inactivation curve, and the baseline of noninactivating current at positive potentials was significantly increased (Fig. 5C). However, as a result of the relatively small level of  $I_{\rm NaP}$  in this cell line, even in the presence of  $G\beta_2\gamma_3$ , the second Boltzmann component from these cells was not as clearly resolved as for Na<sub>v</sub>1.2. As described above, the relative size of  $I_{\rm NaP}$ 



**Figure 4.**  $I_{\text{NaP}}$  conducted by hNa<sub>v</sub>1.1 in two stable cell lines and its modulation by  $G\beta_2\gamma_3$ .  $I_{\text{NaP}}$  was measured in two cell lines, CL1 and CL2, stably expressing hNa<sub>v</sub>1.1 and in CL2 transiently transfected with G-protein  $\beta_2$  and  $\gamma_3$  subunits. **A**, Current traces from representative cells during depolarizations to 0 mV from a holding potential of -70 mV from CL2 alone (**A**) or CL2 cotransfected with  $G\beta_2$  and  $G\gamma_3$  subunits (**B**). **C**,  $I_{\text{NaP}}$  as a percentage of  $I_{\text{NaT}}$  in the indicated cells. Values for individual cells are plotted as small symbols; open squares indicate mean  $\pm$  SEM. Horizontal bars represent the first and 99th percentiles of the range.

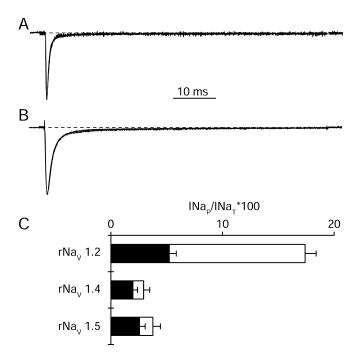


**Figure 5.** Properties of transient and persistent current in Na<sub>v</sub>1.1 alone and cotransfected with  $G\beta_2\gamma_3$  as expressed in CL2. **A**, Mean voltage dependence of activation for CL2 stably expressing hNa<sub>v</sub>1.1 (open circles) and CL2 cells transiently transfected with  $G\beta_2\gamma_3$  (filled squares). The solid lines are fits of a Boltzmann equation to the mean data. For CL2 cells expressing Na<sub>v</sub>1.1 (n=18),  $V_a=-7.5\pm0.5\,\text{mV}$  and  $k=-7.3\pm0.4\,\text{mV}$ ; for CL2 cells cotransfected with  $G\beta_2\gamma_3$  (n=6),  $V_a=-3.5\pm0.5\,\text{mV}$  and  $k=-6.4\pm0.4\,\text{mV}$ . **B**, Currents elicited by slow (70 mV/s) voltage ramps from a representative CL2 cell (smaller current) or a representative CL2 cell cotransfected with  $G\beta_2\gamma_3$  (larger current). The ramps shown are from cells with  $I_{\text{NaP}}$  that is somewhat larger than the means of the control and  $G\beta\gamma$ -transfected groups to more clearly demonstrate the voltage-dependent properties of  $I_{\text{NaP}}$ . **C**, Voltage dependence of inactivation from representative cells, selected to have approximately the mean level of  $I_{\text{NaP}}$ , determined with 100 ms prepulses to a variable voltage followed by a test depolarization to 0 mV for CL2 alone (open circles) or CL2 cotransfected with  $G\beta_2\gamma_3$  (filled squares). Normalized test pulse current is plotted as a function of prepulse potential. Mean parameters derived from fits of Boltzmann functions to the data were as follows: for CL2,  $V_{1/2}=-37.6\pm0.1\,\text{mV}$ ,  $V_{1/2}=0.029\pm0.003$ ,  $v_{1/2}=0.003$ ,  $v_{1/2}=0.0$ 

in tsA-201 cells transiently transfected with hNa<sub>v</sub>1.1 or in cell line CL1, in which hNa<sub>v</sub>1.1 had been stably expressed in HEK293 cells, was much larger than in CL2. However, the voltage-dependent properties of  $I_{\rm NaT}$  and  $I_{\rm NaP}$  in these cells were not different from those of CL2 except for the larger amplitude of  $I_{\rm NaP}$  (data not shown). Thus, for both hNa<sub>v</sub>1.1 and rNa<sub>v</sub>1.2a, coexpression of  $G\beta_2\gamma_3$  increases both the amount of  $I_{\rm NaP}$  relative to  $I_{\rm NaT}$  and the fraction of current with slowed and positive voltage-dependent inactivation without major effects on the voltage dependence of activation of  $I_{\rm NaT}$ .

#### Modulation of $I_{\rm NaP}$ through rNa, 1.4 and rNa, 1.5 channels by G $\beta_2\gamma_3$

We tested whether skeletal muscle  $\text{rNa}_v$ 1.4 and cardiac  $\text{rNa}_v$ 1.5 channel isoforms were modulated by  $G\beta_2\gamma_3$  when cotransfected in tsA-201 cells. When transfected alone,  $\text{rNa}_v$ 1.4 and  $\text{rNa}_v$ 1.5 give little  $I_{\text{NaP}}$  ( $I_{\text{NaP}}=1.9\pm0.4\%, n=7;$  and  $2.6\pm0.5\%, n=10,$  respectively) (Fig. 6). When  $G\beta_2\gamma_3$  was coexpressed with either Na $_v$ 1.4 or Na $_v$ 1.5 channels, no significant increase in  $I_{\text{NaP}}$  was observed (Na $_v$ 1.4 plus  $G\beta_2\gamma_3$ ,  $2.9\pm0.6\%, n=8;$  Na $_v$ 1.5 plus



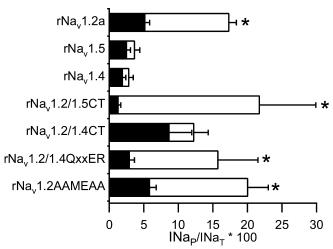
**Figure 6. A**, Normalized superimposed current traces from two representative tsA-201 cells transfected with rNa<sub>v</sub>1.4 alone or cotransfected with G $\beta_2$  and G $\gamma_3$ . Currents were elicited by a depolarization to 0 mV from a holding potential of -70 mV. **B**, Normalized superimposed current traces from two representative tsA-201 cells transfected with rNa<sub>v</sub>1.5 alone or cotransfected with G $\beta_2$  and G $\gamma_3$ . Currents were elicited by a depolarization to -10 mV from a holding potential of -70 mV. **C**, Bar graph showing  $I_{\text{NaP}}$  as percentage of  $I_{\text{NaT}}$  for cells transfected with the indicated sodium channel  $\alpha$  subunit alone (black bars) or in combination with G $\beta_2$  and G $\gamma_3$  (open bars). For rNa<sub>v</sub>1.2a: control (pooled data),  $I_{\text{NaP}} = 5.3 \pm 0.6\%$ , n = 56; plus G $\beta_2\gamma_3$ ,  $I_{\text{NaP}} = 16 \pm 1.0\%$ , n = 26. For rNa<sub>v</sub>1.4: control,  $I_{\text{NaP}} = 1.9 \pm 0.4\%$ , n = 7; plus G $\beta_2\gamma_3$ ,  $2.9 \pm 0.6\%$ , n = 8. For rNa<sub>v</sub>1.5: control,  $2.6 \pm 0.5\%$ , n = 10; plus G $\beta_2\gamma_3$ ,  $3.7 \pm 0.7\%$ , n = 5. Error bars represent SEM.

 $G\beta_2\gamma_3$ , 3.7  $\pm$  0.7%, n=5) (Fig. 6). Thus, little  $I_{\rm NaP}$  is produced by these two isoforms, and it is not increased by coexpression of  $G\beta_2\gamma_3$ .

# Modulation of $I_{\rm NaP}$ by the CT domains of rNa<sub>v</sub>1.4 and rNa<sub>v</sub>1.5 channels

We proposed previously that the CT of rNa<sub>v</sub>1.2a is a domain required to produce  $I_{\rm NaP}$  in that channel (Ma et al., 1997). To test this, we used the construct Na<sub>v</sub>1.2/1.5 CT (Mantegazza et al., 2001). In this construct, the rNa<sub>v</sub>1.5 CT beginning with E1755 replaced the CT of rNa<sub>v</sub>1.2a, which had been truncated before E1777. This chimeric mutation did not increase  $I_{\rm NaP}$  in the absence of modulation by G $\beta\gamma$  (Fig. 7). However, the chimera was strongly modulated by G $\beta_2\gamma_3$  (Fig. 7). Thus, although the CT of Na<sub>v</sub>1.5 does not produce modulation when attached to its native subunit, it produces strong modulation of rNa<sub>v</sub>1.2a.

This contrasts with the effects observed in chimeras of rNa<sub>v</sub>1.4 and rNa<sub>v</sub>1.2a, in which the CT of rNa<sub>v</sub>1.2a was completely or partially replaced by the analogous sequence from Na<sub>v</sub>1.4. In Na<sub>v</sub>1.2/1.4 CT, the rNa<sub>v</sub>1.4 CT beginning with E1592 replaced the CT of rNa<sub>v</sub>1.2a, which had been truncated before E1777. Substitution of the C terminus in Na<sub>v</sub>1.2/1.4 CT did not significantly change the level of  $I_{\rm NaP}$  under control conditions. In addition, there was no increase after coexpression of  $G\beta_2\gamma_3$  (Fig. 7). Thus, the Na<sub>v</sub>1.4 C terminus does not support modulation by  $G\beta\gamma$ . These findings are consistent with the CT domains of Na<sub>v</sub>1.2 and Na<sub>v</sub>1.5 containing molecular determinants required for modulation of  $I_{\rm NaP}$  by  $G\beta\gamma$  that are absent in the Na<sub>v</sub>1.4 CT.



**Figure 7.**  $I_{\rm NaP}$  in sodium channels containing mutations affecting the QXXER motif and their modulation by G-protein  $\beta\gamma$  subunits. Bar graph showing  $I_{\rm NaP}$  as percentage of  $I_{\rm NaT}$  for cells transfected with the indicated sodium channel  $\alpha$  subunit alone (black bars) or in combination with  $G\beta_2$  and  $G\gamma_3$  (open bars). For rNa<sub>v</sub>1.2a, rNa<sub>v</sub>1.4, and rNa<sub>v</sub>1.5, see Figures 2 and 6 for mean values and errors. For Na<sub>v</sub>1.2a/1.5CT: control,  $I_{\rm NaP}=1.4\pm0.3$ , n=7;  $G\beta_2\gamma_3$ ,  $I_{\rm NaP}=21.8\pm8.1$ , n=5. For Na<sub>v</sub>1.2a/1.4 CT: control,  $I_{\rm NaP}=8.7\pm3.2$ , n=8;  $G\beta_2\gamma_3$ ,  $I_{\rm NaP}=12\pm2$ , n=12. For rNa<sub>v</sub>1.2/1.4QxxER: control,  $I_{\rm NaP}=3.0\pm0.7$ , n=9;  $G\beta_2\gamma_3$ ,  $I_{\rm NaP}=16\pm6$ , n=5. For rNa<sub>v</sub>1.2a/AAMEAA: control,  $I_{\rm NaP}=5.9\pm0.9$ , n=10;  $G\beta_2\gamma_3$ ,  $I_{\rm NaP}=20\pm3$ , n=7. Error bars represent SEM. Asterisks indicate significant modulation by  $GB_2\gamma_3$  (p<0.05).

### Requirement for the rNa<sub>v</sub>1.2a CT and its QxxER motif for modulation by $G\beta\gamma$

A short sequence motif (QxxER) in the Na<sub>v</sub>1.2a CT was suggested initially to be an important molecular determinants of  $G\beta\gamma$  modulation based on our finding that a peptide containing this motif effectively inhibited G-protein modulation (Ma et al., 1997). A QxxER motif is conserved in hNa<sub>v</sub>1.1, partially conserved in rNa<sub>v</sub>1.5, but absent in the CT of rNa<sub>v</sub>1.4. To assess the role of the QxxER region of rNa<sub>v</sub>1.2a in modulation by  $G\beta_2\gamma_3$ , we constructed two mutant channels. For the first, we used the CT of Na<sub>v</sub>1.4 to replace the QxxER sequence in the CT of Na<sub>v</sub>1.2a, because Na<sub>v</sub>1.4 did not support modulation by G $\beta\gamma$ . In Na<sub>v</sub>1.2/ 1.4QxxER, the Na<sub>v</sub>1.4 CT from K1691 to K1697 replaced the QxxER region in rNa<sub>v</sub>1.2a CT from R1876 and R1882. In the second construct, Na<sub>v</sub>1.2/AAMEAA, I1875, Q1876, E1879, and R1880 in rNa<sub>v</sub>1.2a were replaced with alanines, thus removing the specific side chains of the critical amino acids in the QxxER motif. Both Na<sub>v</sub>1.2/1.4QxxER and Na<sub>v</sub>1.2/AAMEAA were modulated fully by  $G\beta_2\gamma_3$  (Fig. 7), indicating that this motif is not necessary for modulation of Na<sub>v</sub>1.2 by G $\beta\gamma$ . Molecular determinants for modulation of Na<sub>v</sub>1.2a sodium channel by G $\beta\gamma$  must reside in other regions of the Na<sub>v</sub>1.2 CT that have amino acid sequence differences from the Na<sub>v</sub>1.4 CT.

## Requirement for the last 28 amino acids of rNa<sub>v</sub>1.2a CT for modulation by G $\beta\gamma$

To localize the molecular determinants in the CT responsible for  $I_{\rm NaP}$  and its modulation by  $G\beta\gamma$ , we used a series of rNa<sub>v</sub>1.2a mutants in which the CT was truncated at different positions, as described previously (Mantegazza et al., 2001). Mutants that were truncated on the N-terminal side of K1890 did not express measurable sodium current or gave rise to currents that were too small to study (Mantegazza et al., 2001). Therefore, we only tested mutants in which the truncation was on the C-terminal side of K1890. Although the mean level of  $I_{\rm NaP}$  in the absence of transfected  $G\beta\gamma$  subunits varied among the truncation mutants, the

differences from wild type (WT) were not significant (p > 0.05) (Fig. 8). However, the effects of cotransfected  $G\beta\gamma$  on these mutant channels differed significantly. Coexpression of  $G\beta_2\gamma_3$  did not significantly increase  $I_{NaP}$  when the channel was shortened beyond T1951 in mutants  $\Delta$ K1890,  $\Delta$ K1909,  $\Delta$ K1929, and  $\Delta$ T1951 (Fig. 8, bars lacking asterisks). In constructs with longer C termini, including  $\Delta$ S1977 and  $\Delta$ K1998,  $I_{NaP}$  was increased significantly by  $G\beta_2\gamma_3$  coexpression (Fig. 8, bars with asterisks). However, the increase of  $I_{\text{NaP}}$  caused by  $G\beta_2\gamma_3$  coexpression with  $\Delta$ S1977 and  $\Delta$ K1998 was not as large as for WT rNa<sub>v</sub>1.2, as denoted by the bars labeled with #. The pattern of decreased modulation by  $G\beta\gamma$  in these deletion constructs suggests that the amino acid residues between positions 1951 and 1977 and between position 1977 and the C terminus of the protein at position 2005 are important for modulation by  $G\beta\gamma$ .

To test the functional role of the final 28 amino acid residues directly, we constructed the mutant  $Na_v1.2a/\Delta1891-1977$ , in which amino acid residues from V1891 to S1977 were deleted. This is equivalent to  $Na_v1.2a/\Delta K1890$  having the last 28 amino acids of the C terminal added directly to it.

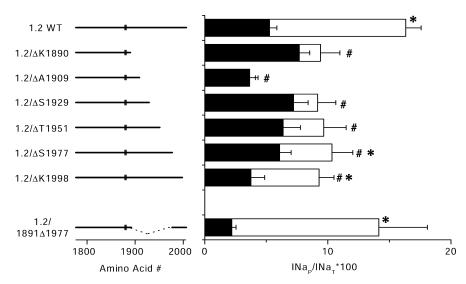
Modulation of this construct by Na<sub>v</sub>1.2a/ $\Delta$ 1891–1977 was similar to modulation of the WT Na<sub>v</sub>1.2a channel (Fig. 8). Thus, the last 28 amino acids of the CT are necessary for modulation by  $G\beta\gamma$  and are sufficient to replace the requirement for the remainder of the distal half of the C-terminal domain.

## Voltage-dependent gating and modulation of $Na_v 1.2\Delta 1891-1977$

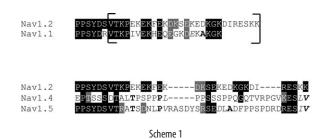
We analyzed the functional properties of Na<sub>v</sub>1.2 $\Delta$ 1891–1977 more completely and compared them with WT. Coexpression of  $G\beta_2\gamma_3$  increased  $I_{NaP}$  during single depolarizations (Fig. 9 A,B) or during slow voltage ramps (Fig. 9C,D). The voltage dependence of activation of  $I_{\text{NaT}}$  conducted by Na<sub>v</sub>1.2a/ $\Delta$ 1891–1977 was unchanged from that of wild-type Na<sub>v</sub>1.2a, and, as for WT, cotransfection of  $G\beta\gamma$  caused little change in the voltage dependence of activation (Fig. 9E). The voltage dependence of inactivation was shifted  $\sim$  10 mV more negative than for WT Na $_{\rm v}$ 1.2a. This is consistent with previous findings implicating the C-terminal region of the sodium channel in modulating inactivation (Deschenes et al., 2001; Mantegazza et al., 2001; Cormier et al., 2002; Motoike et al., 2004). Cotransfection of  $G\beta_2\gamma_3$  subunits with Na<sub>v</sub>1.2a/ $\Delta$ 1891–1977 did not appreciably change the negative component of the steady-state inactivation curve but increased the amplitude of a more positive component of inactivation (Fig. 9F, closed squares), similar to  $G\beta\gamma$ modulation of WT. Thus, although the deletion in Na<sub>v</sub>1.2a/ $\Delta$ 1891– 1977 causes a negative shift in the voltage dependence of inactivation of  $I_{\text{NaT}}$  under control conditions,  $I_{\text{NaP}}$  is modulated essentially normally by cotransfection of  $G\beta_2\gamma_3$ .

# Comparison of the amino acid sequences of the distal C-terminal domains of Na<sub>v</sub>1 channels

Because the distal CT of  $Na_v1.1$  and  $Na_v1.2$  can support modulation by  $G\beta\gamma$ , but the CT of  $Na_v1.4$  cannot, it is interesting to



**Figure 8.**  $I_{\text{NaP}}$  in truncated Na<sub>v</sub>1.2a channels and its modulation by G-protein  $\beta_2\gamma_3$  subunits. Left, Diagram of the CT of the truncated channel constructs. The rectangle indicates the position of the QXXER motif. Right, Bar graph showing  $I_{\text{NaP}}$  as percentage of  $I_{\text{NaT}}$  for cells transfected with the indicated sodium channel  $\alpha$  subunit construct alone (black bars) or in combination with  $G\beta_2$  and  $G\gamma_3$  (open bars). For rNa<sub>v</sub>1.2/K1890: control,  $I_{\text{NaP}} = 7.7 \pm 0.8\%$ , n = 9; plus  $G\beta_2\gamma_3$ ,  $I_{\text{NaP}} = 9 \pm 2\%$ , n = 6. For rNa<sub>v</sub>1.2/A1909: control,  $I_{\text{NaP}} = 3.6 \pm 0.7\%$ , n = 16; plus  $G\beta_2\gamma_3$ ,  $I_{\text{NaP}} = 3.5 \pm 0.6\%$ , n = 8. For rNa<sub>v</sub>1.2/S1929: control,  $I_{\text{NaP}} = 7 \pm 1\%$ , n = 8; plus  $G\beta_2\gamma_3$ ,  $I_{\text{NaP}} = 9 \pm 1\%$ , n = 10. For rNa<sub>v</sub>1.2/T1951: control,  $I_{\text{NaP}} = 6 \pm 1\%$ , n = 10; plus  $G\beta_2\gamma_3$ ,  $I_{\text{NaP}} = 10 \pm 2\%$ , n = 9. For rNa<sub>v</sub>1.2/S1977: control,  $I_{\text{NaP}} = 6.1 \pm 0.9\%$ , n = 21; plus  $G\beta_2\gamma_3$ ,  $I_{\text{NaP}} = 10 \pm 2\%$ , n = 10. For rNa<sub>v</sub>1.2/K1998: control,  $I_{\text{NaP}} = 4 \pm 1\%$ , n = 7; plus  $G\beta_2\gamma_3$ ,  $g \pm 1\%$ 



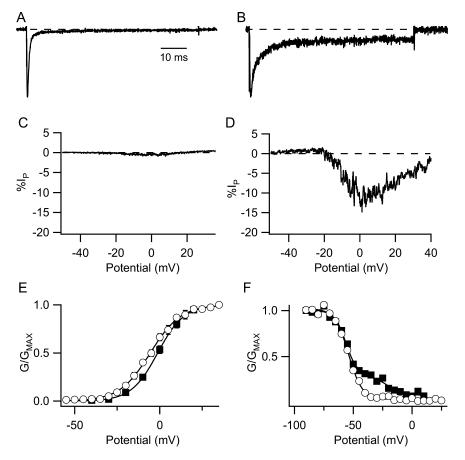
compare the amino acid sequences of the distal CT showing the identities (black blocks) and similarities (gray blocks) to  $\rm Na_v 1.2a$ , as follows:

 $\rm Na_v 1.1$  is quite similar to  $\rm Na_v 1.2$  but is seven amino acids shorter. Among the 21 aligned amino acid residues, 10 are identical, two are similar, and there are no gaps. In contrast,  $\rm Na_v 1.4$  has only five identical and one similar residues, and a four-residue gap in  $\rm Na_v 1.2$  is required for alignment.  $\rm Na_v 1.5$  has seven identical and three similar residues but requires gaps of four and five residues in  $\rm Na_v 1.2$  for alignment. Thus, the similarities of the  $\rm Na_v 1.1$  and  $\rm Na_v 1.2$  sequences support a common function for their distal C-terminal segments, whereas the differences in sequence of  $\rm Na_v 1.5$  and especially  $\rm Na_v 1.4$  C-terminal sequences suggest different functions. Additional experiments will be required to determine whether these segments play important roles in some aspect of G-protein modulation of cardiac and skeletal muscle sodium channels.

#### Discussion

### Persistent sodium current in neurons

 $I_{
m NaP}$  is implicated in many aspects of neuronal function, including shaping bursting behavior, controlling firing frequency, integrating synaptic input, and generating epileptiform hyperexcit-



**Figure 9.** Modulation of rNa<sub>v</sub>1.2a/1891 $\Delta$ 1977 channels by G-protein  $\beta\gamma$  subunits. **A, B,** Examples of representative current traces during depolarizations to 0 mV from a holding potential of -70 mV from a cell expressing rNa<sub>v</sub>1.2a/1891 $\Delta$ 1977 channels alone (**A**) and from a cell coexpressing rNa<sub>v</sub>1.2a/1891 $\Delta$ 1977 and G $\beta_2\gamma_3$  (**B**). **C, D,** Currents in response to voltage ramps at 70 mV/s from -60 to +40 mV from the same cells shown in **A** and **B,** respectively. **E,** Mean voltage dependence of activation for cells transfected with rNa<sub>v</sub>1.2a/1891 $\Delta$ 1977 channels alone (open circles) and cotransfected with G $\beta_2\gamma_3$  (filled squares). The solid lines are fits of a Boltzmann equation to the mean data. For rNa<sub>v</sub>1.2a/1891 $\Delta$ 1977: control,  $V_{1/2} = -5.6 \pm 1.10$  mV,  $k = -8.6 \pm 0.47$  mV, n = 9; plus G $\beta_2\gamma_3$ ,  $V_{1/2} = -0.1 \pm 1.55$  mV and  $k = -8.5 \pm 0.48$  mV, n = 7. **F,** Voltage dependence of inactivation from a representative cell transfected with rNa<sub>v</sub>1.2a/1891 $\Delta$ 1977 channels alone (open circles) and cotransfected with G $\beta_2\gamma_3$  (filled squares). Representative cells were chosen to have approximately the mean level of  $I_{\text{Nap}}$ . Mean parameters derived from fits of Boltzmann functions to the data were for rNa<sub>v</sub>1.2a/1891 $\Delta$ 1977: control,  $V_{1/2} = -54.5 \pm 0.15$  mV,  $k = 6.3 \pm 0.13$  mV,  $C = 0.04 \pm 0.002$ , n = 8; plus G $\beta_2\gamma_3$  (fit with 2 Boltzmann components),  $V_{1/2} = -54.5 \pm 0.52$  mV,  $k_1 = 4.0 \pm 0.80$  mV,  $A_2 = 0.43$ ,  $V_{1/2} = -50.8 \pm 2.89$ ,  $k_2 = 15.7 \pm 2.67$  mV,  $C = 0.03 \pm 0.008$ , n = 3.

ability (see Introduction).  $I_{\rm NaP}$  is thought to be conducted by the same sodium channels that generate  $I_{\rm NaT}$  in some neurons (Alzheimer et al., 1993; Taddese and Bean, 2002), but the sodium channel subtypes that generate  $I_{\rm NaP}$  and the mechanisms that regulate  $I_{\rm NaT}$  versus  $I_{\rm NaP}$  in neurons are unknown. Here, we have addressed this gap in knowledge by analyzing the level of  $I_{\rm NaP}$  generated by different sodium channel subtypes, demonstrating subtype-selective effects of  $G\beta\gamma$  subunits on  $I_{\rm NaP}$  and identifying an essential molecular determinant of  $G\beta\gamma$  modulation of  $Na_{\rm v}1.2$  channels.

### Different levels of persistent sodium current conducted by sodium channel subtypes

Our results show that different sodium channel  $\alpha$  subunits intrinsically generate different levels of  $I_{\rm NaP}$ . Na<sub>v</sub>1.1 and Na<sub>v</sub>1.2 both conduct substantial  $I_{\rm NaP}$ , but when expressed transiently in tsA-201 cells, Na<sub>v</sub>1.1 produces significantly more  $I_{\rm NaP}$  than Na<sub>v</sub>1.2. Conversely, Na<sub>v</sub>1.4 and Na<sub>v</sub>1.5 conduct little  $I_{\rm NaP}$ . Although the CT has been implicated in the modulation of  $I_{\rm NaP}$  by G $\beta\gamma$  (Ma et al., 1997; this work) and in setting the different inactivation properties of Na<sub>v</sub>1.5 relative to Na<sub>v</sub>1.2a or Na<sub>v</sub>1.4

channels (Mantegazza et al., 2001; Deschenes et al., 2001; Cormier et al., 2002; Motoike et al., 2004), the CT of  $\mathrm{Na_v}1.4$  did not reduce  $I_{\mathrm{NaP}}$  produced by the  $\mathrm{Na_v}1.2$ a in chimera  $\mathrm{Na_v}1.2/1.4$  CT. Thus, the intrinsic level of  $I_{\mathrm{NaP}}$  is determined by the pre-CT portion of the channel rather than by the CT. However, the CT alters modulation of  $I_{\mathrm{NaP}}$  when attached to a sodium channel that conducts substantial  $I_{\mathrm{NaP}}$ .

### Regulation of persistent sodium currents by G-proteins

Although  $I_{NaP}$  is important physiologically, few experimental conditions have been identified that alter  $I_{NaP}$  relative to  $I_{\text{NaT}}$ . We showed previously that coexpression of G-protein  $\beta \gamma$  subunits can substantially increase  $I_{\text{NaP}}$ , relative to  $I_{\text{NaT}}$ , and we implicated the CT of the Na<sub>v</sub>1.2 channel  $\alpha$  subunit in those effects by demonstrating block of  $I_{NaP}$  by a competing CT peptide (Ma et al., 1997). Our present results extend those findings in three important respects. First, using bicistronic vectors and fluorescence to verify expression of G $\beta$  and Gγ, we substantially reduced cell-to-cell variability in  $G\beta\gamma$  modulation of  $I_{NaP}$ , thereby providing stronger evidence that  $G\beta\gamma$  subunits are important regulators of  $I_{\text{NaP}}$ . Second, with this improved assay, we identified a novel subtype specificity for  $G\beta\gamma$ modulation of  $I_{\text{NaP}}$ . G $\beta\gamma$  subunits can regulate  $I_{\text{NaP}}$  of Na<sub>v</sub>1.1 and Na<sub>v</sub>1.2 channels but not of Na<sub>v</sub>1.4 or Na<sub>v</sub>1.5 channels. However, the CT of Na<sub>v</sub>1.5, but not that of Na<sub>v</sub>1.4, can support modulation by  $G\beta_2\gamma_3$  when attached to Na<sub>v</sub>1.2a. The ability of the Na<sub>v</sub>1.5 CT to support modulation when incorporated in a chimera with Na<sub>v</sub>1.2a but not in Na<sub>v</sub>1.5 highlights the importance of the pre-CT portion of the channel in permitting modulation by  $G\beta\gamma$  acting via the CT. Fi-

nally, our improved methods allowed analysis of deletion mutants to directly identify the site of  $G\beta\gamma$  action in the CT. Surprisingly, these results implicate the final 28 amino acids of  $Na_v1.2$  in  $G\beta\gamma$  binding and regulation. We propose that this short segment forms part of the  $G\beta\gamma$  interaction site and plays an important role in modulation of channel gating.

 $G\beta\gamma$  subunits do not greatly alter the voltage dependence of activation or inactivation of  $I_{\rm NaT}$ . In contrast, the voltage dependence of inactivation of  $I_{\rm NaP}$  is shifted positively with respect to  $I_{\rm NaT}$ . These results are consistent with a mechanism in which  $G\beta\gamma$  generates  $I_{\rm NaP}$  by destabilizing fast inactivation and switching a fraction of sodium channels to a noninactivating gating mode with slowed and positively shifted inactivation (Ma et al., 1997). The molecular basis for this might be  $G\beta\gamma$ -induced destabilization of binding of the inactivation gate to its receptor.

### Molecular determinants of $G\beta\gamma$ modulation in the C terminus

Ma et al. (1997) proposed that  $G\beta\gamma$  bound to the CT of the  $Na_v1.2$  channel to modulate  $I_{NaP}$ , because its effect was blocked

by a peptide containing the QMEER sequence of the CT. Recent biochemical evidence shows that  $G\beta\gamma$  indeed binds to  $Na_v1.2$  sodium channel  $\alpha$  subunits (Marin et al., 2001) and to the CT of the  $Na_v1.3$   $\alpha$  subunit (Lenkowski et al., 2004). These findings are consistent with an essential role for the CT in  $G\beta\gamma$  modulation of  $I_{NaP}$ . Peptides containing a similar QxxER motif reduced  $G\beta\gamma$  modulation of other target proteins, including calcium channels (Chen et al., 1995; Herlitze et al., 1997; Zamponi et al., 1997). Such peptides are expected to bind  $G\beta\gamma$  subunits and inhibit their action. However, we show that the QxxER motif is unnecessary for modulation of  $Na_v1.2$  by coexpressed  $G\beta\gamma$ . Perhaps the QxxER motif tethers and localizes G-protein  $\beta\gamma$  subunits near their site of action in high local concentration, enhancing  $G\beta\gamma$  effects at low levels of G-protein activation.

Our results show that the last 28 amino acids of rNa<sub>v</sub>1.2 are necessary for  $G\beta\gamma$  modulation of Na  $^+$  channels. Modulation was lost when the CT of rNa<sub>v</sub>1.2a was replaced with that of rNa<sub>v</sub>1.4 or when the CT of Na<sub>v</sub>1.2 was truncated at K1890. Addition of only the last 28 amino acids of the rNa<sub>v</sub>1.2a CT to this mutant restored  $G\beta\gamma$  modulation. Thus, these 28 residues are sufficient for modulation of rNa<sub>v</sub>1.2a by  $G\beta\gamma$ , and the intervening residues between K1890 and S1977 are unnecessary.

The distal CTs of sodium channels contain other motifs of potential importance in regulation of channel function, localization, and degradation. An IQ domain starting at position 1912 in Na<sub>v</sub>1.2 has been implicated in interactions of calmodulin with several sodium channel isoforms (Deschenes et al., 2002; Tan et al., 2002; Herzog et al., 2003; Kim et al., 2004). Just N-terminal to the site of G-protein regulation, a sequence (PPSY) is implicated in interaction of Nedd4 ubiquitin ligase and is present in Na<sub>v</sub>1.1, Na<sub>v</sub>1.2, and Na<sub>v</sub>1.5 but not in Na<sub>v</sub>1.4 (van Bemmelen et al., 2004). In addition, the final three amino acids of Na,1.4 and Na<sub>v</sub>1.5 are potential interaction sites for PDZ (postsynaptic density-95/Discs large/zona occludens-1) proteins such as the syntrophin family of dystrophin-associated proteins, which may contribute to channel localization in cardiac and skeletal muscle (Gee et al., 1998). These processes could potentially interact with regulation by G-proteins.

## Comparison of regulation of $I_{\rm NaP}$ in transfected cells and neurons

 $I_{\mathrm{NaP}}$  in neurons is generally smaller than  $I_{\mathrm{NaP}}$  in transfected tsA-201 cells, even without modulation by G $\beta\gamma$ . The ratio of  $I_{\text{NaP}}$  to  $I_{\text{NaT}}$  reported here would probably be incompatible with normal neuronal function in vivo (Kearney et al., 2001). Evidently, other regulation in neurons limits  $I_{\mathrm{NaP}}$ . Nevertheless,  $I_{\mathrm{NaP}}$  in neurons resembles  $I_{\text{NaP}}$  produced by  $G\beta\gamma$  in transfected cells in several respects. Activation of  $I_{NaP}$  of sodium channels expressed in tsA-201 cells is shifted negatively relative to  $I_{\text{NaT}}$  (data not shown), as it is in neurons (Brown et al., 1994; Mantegazza et al., 1998; Taddese and Bean, 2002). In addition,  $I_{\text{NaP}}$  in both neurons and tsA cells has positively shifted voltage dependence of inactivation relative to  $I_{\text{NaT}}$ . Our results with transfection of single sodium channel isoforms demonstrate that  $I_{\text{NaP}}$  can result from modulation of the same sodium channels that produce  $I_{\text{NaT}}$  (Ma et al., 1997). Thus, our working hypothesis is that  $G\beta\gamma$  modulation is an important regulatory influence on  $I_{\text{NaP}}$  in neurons.

The persistent current in a neuron is probably produced by a mixture of sodium channel subtypes with individual propensities for producing  $I_{\rm NaP}$ . The sodium channel  $\alpha$  subunit(s) responsible for  $I_{\rm NaP}$  has not been identified unequivocally in any central neuron, but it has been proposed that Na<sub>v</sub>1.6 is the primary contributor to  $I_{\rm NaP}$  in cerebellar Purkinje neurons and in prefrontal cor-

tex pyramidal neurons (Raman et al., 1997; Maurice et al., 2001). In addition to Na<sub>v</sub>1.6, the other primary brain Na  $^+$  channel  $\alpha$  subunit isoforms, Na<sub>v</sub>1.1, Na<sub>v</sub>1.2, and Na<sub>v</sub>1.3, all can produce  $I_{\rm NaP}$ . Their relative contributions could be modulated according to cell expression pattern and/or degree of neuromodulation of individual channel subtypes.

#### Modulation of persistent sodium current in neurons

Dynamic modulation of  $I_{\text{NaP}}$  would dramatically modify integrative properties of neurons. Activation of muscarinic acetylcholine receptors in hippocampal neurons reduces both  $I_{NaP}$  and  $I_{NaT}$  to comparable extents via protein kinase C signaling (Cantrell et al., 1996). There have been few reports of positive modulation of  $I_{\text{NaP}}$ in neurons (see Introduction). Increase of  $I_{NaP}$  by dopamine has been observed in prefrontal cortex (Gorelova and Yang, 2000) (but see Maurice et al., 2001). Modulation by free  $G\beta\gamma$  in neurons might occur locally in membrane microdomains (Galbiati et al., 2001) strategically positioned to affect action potential generation in the axon hillock, action potential back-propagation at dendritic branches, or other localized electrical events. Such tightly delimited modulation might be critically important for integrative properties of the neuron but would make little contribution to whole-cell sodium current. Additional studies of sodium channel modulation by G-proteins in vitro may provide methods to probe the mechanism and significance of this form of modulation in intact neurons more incisively.

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