

REVIEW

Ion channel regulation by β -secretase BACE1 – enzymatic and non-enzymatic effects beyond Alzheimer's disease

Sandra Lehnert^a, Stephanie Hartmann^a, Sabine Hessler^b, Helmuth Adelsberger^c, Tobias Huth^a, and Christian Alzheimer^a

^aInstitute of Physiology and Pathophysiology, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, Germany; ^bSchool of Psychology, University of Sussex, Brighton, UK; ^cInstitute of Neuroscience, Technische Universität München, München, Germany

ABSTRACT

β -site APP-cleaving enzyme 1 (BACE1) has become infamous for its pivotal role in the pathogenesis of Alzheimer's disease (AD). Consequently, BACE1 represents a prime target in drug development. Despite its detrimental involvement in AD, it should be quite obvious that BACE1 is not primarily present in the brain to drive mental decline. In fact, additional functions have been identified. In this review, we focus on the regulation of ion channels, specifically voltage-gated sodium and KCNQ potassium channels, by BACE1. These studies provide evidence for a highly unexpected feature in the functional repertoire of BACE1. Although capable of cleaving accessory channel subunits, BACE1 exerts many of its physiologically significant effects through direct, non-enzymatic interactions with main channel subunits. We discuss how the underlying mechanisms can be conceived and develop scenarios how the regulation of ion conductances by BACE1 might shape electric activity in the intact and diseased brain and heart.

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BACE1 – a major culprit in Alzheimer's disease

Alzheimer's disease (AD)

Alzheimer's disease (AD) is a devastating neurodegenerative illness with increasing socioeconomic relevance.¹ Despite some favorable trends,² prevalence might triple by 2050 in developed countries like the US, which will demand vast effort of the health care systems and caregivers. As first reported in the beginning of the 20th century by Alois Alzheimer, symptoms of AD include cognitive decline, in particular memory deficits, spatial disorientation, aphasia, apraxia, and affective disturbances.³ Histopathological hallmarks in the brains of AD patients are intracellular neurofibrillary tangles, which are composed of hyperphosphorylated tau protein, and extracellular amyloid deposits.^{3,4} The latter mainly consist of aggregated A β peptides, which are generated from the amyloid precursor protein (APP) in a proteolytic cascade.⁵ Once considered the evil moiety, amyloid plaques are now rather seen as inert deposits. Instead, oligomeric assemblies of A β have been identified as the neurotoxic substrate.⁶

Role of BACE1 in AD

In 1999, BACE1 (also: β -secretase 1 or memapsin 2) was identified as a β -site APP-cleaving enzyme,^{7–11} and, 2 years later, confirmed as the major β -secretase *in vivo*.¹² BACE1 initiates the amyloidogenic pathway of APP processing. Sequential cleavage of APP by BACE1 and the γ -secretase complex creates A β moieties, which are prone to aggregation.⁵ Competitively, α -secretase cleaves APP instead of BACE1 and directs proteolysis toward the non-amyloidogenic pathway with shorter metabolites. Interdependence with further APP-cleaving secretases, i.e. δ -secretase and η -secretase, is just beginning to emerge.^{13,14} In healthy brain, non-amyloidogenic and amyloidogenic processing are balanced, with A β peptides being important effectors in synaptic transmission and plasticity.^{15,16} In 2003, Yang *et al.* reported enhanced BACE1-mediated amyloidogenic cleavage in AD.¹⁷ Recent evidence suggests that BACE1 activity can be elevated much earlier and may foster the conversion from mild cognitive impairment to AD.^{18,19} Recent support for the amyloid hypothesis of AD came from a study

which recapitulated the disease in a 3D human neuronal cell culture model, demonstrating that the appearance of prominent neurofibrillary tangles requires A β generation,²⁰ a causality that is still controversial.²¹

While APP triplication in trisomy 21 and mutations in APP and PSEN1 or PSEN2 of the γ -secretase complex are known to engender familial AD, contributions of BACE1 polymorphisms remain to be established.²² Nevertheless, the importance of BACE1 in AD pathogenesis has been demonstrated by mutations in APP, which either promote β -site cleavage causing a familial form of early-onset AD, or, contrarily, hinder APP β -cleavage and thus protect against the disease and even mild cognitive impairment.^{23,24} As a note of caution against a too straightforward interpretation of these findings, it is worth mentioning that the above APP mutations might also affect the aggregation kinetics of A β .^{25,26}

In view of its pathogenic impact, inhibition of BACE1 is considered a highly promising strategy against AD. Almost a decade before BACE1 has been identified as β -secretase, protease inhibition by competing peptides had been proposed.²⁷ Today, enormous effort is devoted to the design of small molecule BACE1 inhibitors, some of which are currently in Phase II/III clinical trials.²⁸ Alternative strategies aim to inhibit BACE1 allosterically by BACE1-binding antibodies or peptides, to target A β by antibodies, or to develop vaccines against A β .^{28,29}

Early alterations of network activity in AD

Long unrecognized in the clinical care of AD patients, in particular at early stages of the disease, epileptiform activity is now receiving increasing attention, as it appears to play an important role in AD pathogenesis and progression.^{30,31} AD is associated with an enhanced risk of seizures, and patients displaying (subclinical) epileptiform activity or overt seizures show earlier onset of cognitive decline and faster transition into severe dementia.³² Pharmacological suppression of aberrant network activity in AD should therefore offer more than symptomatic treatment as it is thought to interfere with a mechanism that contributes to and propels cognitive decline. Support for this hypothesis comes from a study with APP-over-expressing mice, in which the second-generation anti-epileptic drug levetiracetam blocked abnormal EEG activity and reversed synaptic and cognitive

deficits.³³ In contrast, other established anticonvulsant drugs failed to produce similar beneficial effects. Notably, the Na⁺ channel blocker phenytoin even exacerbated the aberrant EEG pattern, which would be consistent with the concept that neuronal hyperexcitability in AD results from decreased levels of Na_v1.1 channels in inhibitory interneurons.³⁴ These findings emphasize the need to identify and specifically target the ionic mechanisms directly involved in the altered network activity in AD.

BACE1-deficient mice

The first BACE1-deficient mouse lines, which were generated, seemed to lack appreciable phenotypic abnormalities.^{35,36} This was a highly welcomed finding as it appeared to indicate that inhibition of BACE1 would not engender unwarranted side effects, thereby lending strong momentum to anti-BACE strategies. Subsequent studies on BACE1-deficient mice, however, revealed significant postnatal lethality, reduced body weight, decreased anxiety-related behavior, and hyperactivity.³⁷ Further investigations found decreased thermal pain threshold, impaired motor coordination, myelination deficits, impaired spatial learning and memory, and altered synaptic function and neurotransmitter metabolism.³⁸⁻⁴⁰ As a putative correlate of their learning and memory deficits, Wang *et al.* found that activity-dependent potentiation at the mossy-fiber - CA3 synapse in the hippocampus of BACE1-deficient mice is substantially impaired.^{41,42} Given that AD patients, in which BACE1 activity should be elevated, often display lowered seizure threshold (see above), it appeared counterintuitive at first that BACE1 knockout mice develop epileptic seizures, too, as reported by 2 groups.^{43,44}

BACE1 - electrophysiological effects beyond Alzheimer's disease

Evidence accumulates that BACE1 does not exclusively affect the brain by cleavage of APP. Rather, a multitude of additional substrates that undergo β -site proteolysis has emerged, in part with remarkably higher affinity for BACE1 compared to APP.⁴⁵ Among them are ion channel proteins, suggesting that BACE1 might directly influence the electrical behavior of excitable cells. Upon closer examination of how BACE1 interferes with ion channels, an entirely unexpected finding was made, going far beyond the starting point of these studies: Whereas the initial work had

been based on the biochemical finding that some accessory β -subunits of Na^+ channels can be cleaved by BACE1, it later became obvious that BACE1 can also act as an accessory subunit itself, directly interacting with the pore-forming α -subunit in a non-enzymatic fashion. In the following sections, we will review the different forms of how BACE1 interacts with ion channels, discuss the underlying mechanisms and elaborate on the functional consequences.

BACE1 and neuronal Na_v channels

Na_v function, structure, and regulation by β -subunits

A decade ago, voltage-gated sodium channels (Na_v) were the first ion channels to be identified as targets of BACE1.^{46,47} Na_v channels are best known for the fast, transient inward current underlying the upstroke of the action potential. In addition, they generate persistent and resurgent Na^+ currents, which have been implicated in the regulation of firing threshold and frequency, membrane oscillations, and synaptic integration (see below). The main, pore-forming α -subunit comes in 9 subtypes ($\text{Na}_v1.1$ – 1.9 , encoded by the genes *SCN1A*–*SCN5A*, *SCN8A*–*SCN11A*). Accessory subunits ($\beta1$ – 4 , *SCN1B*–*SCN4B*) can associate with the α -subunit and influence channel expression, trafficking, and gating.^{48–50} All β -subunits and $\text{Na}_v1.1$, $\text{Na}_v1.2$, $\text{Na}_v1.3$, and $\text{Na}_v1.6$ are expressed in the brain.⁵¹ Mutations in both α - or β -subunits have been associated, among other disorders, with epilepsy.^{52–54}

$\beta2$ cleavage and Na_v expression

In 2005, Wong *et al.* and Kim *et al.* demonstrated that β -subunits are substrates of BACE1 and γ -secretase in model systems and *in vivo*.^{46,55} Five years later, BACE1 cleavage sites were mapped in the $\beta2$ subunit, which plays an important role in hippocampus and cortex.⁵⁶ Our group then showed that proteolysis of $\beta2$ by BACE1 caused a leftward shift in the voltage dependence of reconstituted $\text{Na}_v1.2$ current, demonstrating that the cleavage bears significance for channel gating.⁵⁷ In BACE1-transgenic mice and in temporal cortex of AD patients, increased BACE1 levels were found to be associated with enhanced $\beta2$ cleavage.⁵⁸ Moreover, that study revealed that the generated $\beta2$ intracellular domain acted as transcriptional activator for its $\text{Na}_v1.1$ α -subunit and increased $\text{Na}_v1.1$ protein, which was, however, retained intracellularly. Consistent with the findings in BACE1-over-expressing mice, Corbett *et al.*

reported similar changes in APP-over-expressing mice.⁵⁹ They observed increased BACE1 levels and $\beta2$ cleavage, accompanied by increased $\text{Na}_v1.1$ total, but decreased surface expression in cortical pyramidal cells and interneurons, accompanied by aberrant EEG activity. Verret *et al.* found reduced total $\text{Na}_v1.1$ levels in another strain of APP-over-expressing mice and the parietal cortex of AD patients, which was in line with reduced functional $\text{Na}_v1.1$ in the previous studies.⁶⁰ The authors related abnormal EEG activity to reduced gamma oscillations and impaired interneuron function. Restoring $\text{Na}_v1.1$ levels in these APP-over-expressing mice augmented the function of inhibitory interneurons and rescued cognitive deficits. These findings place the interplay between BACE1, $\beta2$, and $\text{Na}_v1.1$ center stage because the effects on channel expression and trafficking can be causally linked to cognitive deterioration, as had been hypothesized earlier.⁶¹

Compared to their wild type counterparts, neurons from BACE1-deficient mice have lower levels of $\text{Na}_v1.1$ and less channel protein is found in the outer cell membrane, so that, with respect to functional $\text{Na}_v1.1$, BACE1-deficiency and -over-expression appear to produce strikingly similar effects.⁶² As an additional feature, BACE1^{-/-} mice have increased $\text{Na}_v1.2$ surface levels, possibly compensating for reduced $\text{Na}_v1.1$. However, the issue of whether BACE1-deficiency leads to enhanced $\text{Na}_v1.2$ surface levels and, as a consequence, to neuronal hyperexcitability remains controversial, with groups reporting evidence in favor or against effects of BACE1 on $\text{Na}_v1.2$ levels.^{43,44,62}

$\beta4$ cleavage and resurgent Na^+ currents

Resurgent currents (I_{NaR}) have been first reported from cerebellar Purkinje cells, where they are mainly carried by $\text{Na}_v1.6$.⁶³ Mechanistically, they result from transient channel re-openings upon repolarization, when an unorthodox open-channel block, most likely exerted by parts of the $\beta4$ subunit, is relieved.^{64,65} Since BACE1, which is known to cleave $\beta4$, is highly expressed in cerebellum, an obvious question was whether Purkinje cells from BACE1-deficient mice would exhibit altered firing pattern.⁶⁶ When compared to wild type neurons, the spontaneous firing of Purkinje cells from mutant mice was indeed reduced (Fig. 1A1). The reduced discharge activity was ascribed to a faster decay of the resurgent current (Fig. 1A2). Thus, in the absence of BACE1, reduced cleavage of $\beta4$ coincides with impaired open channel

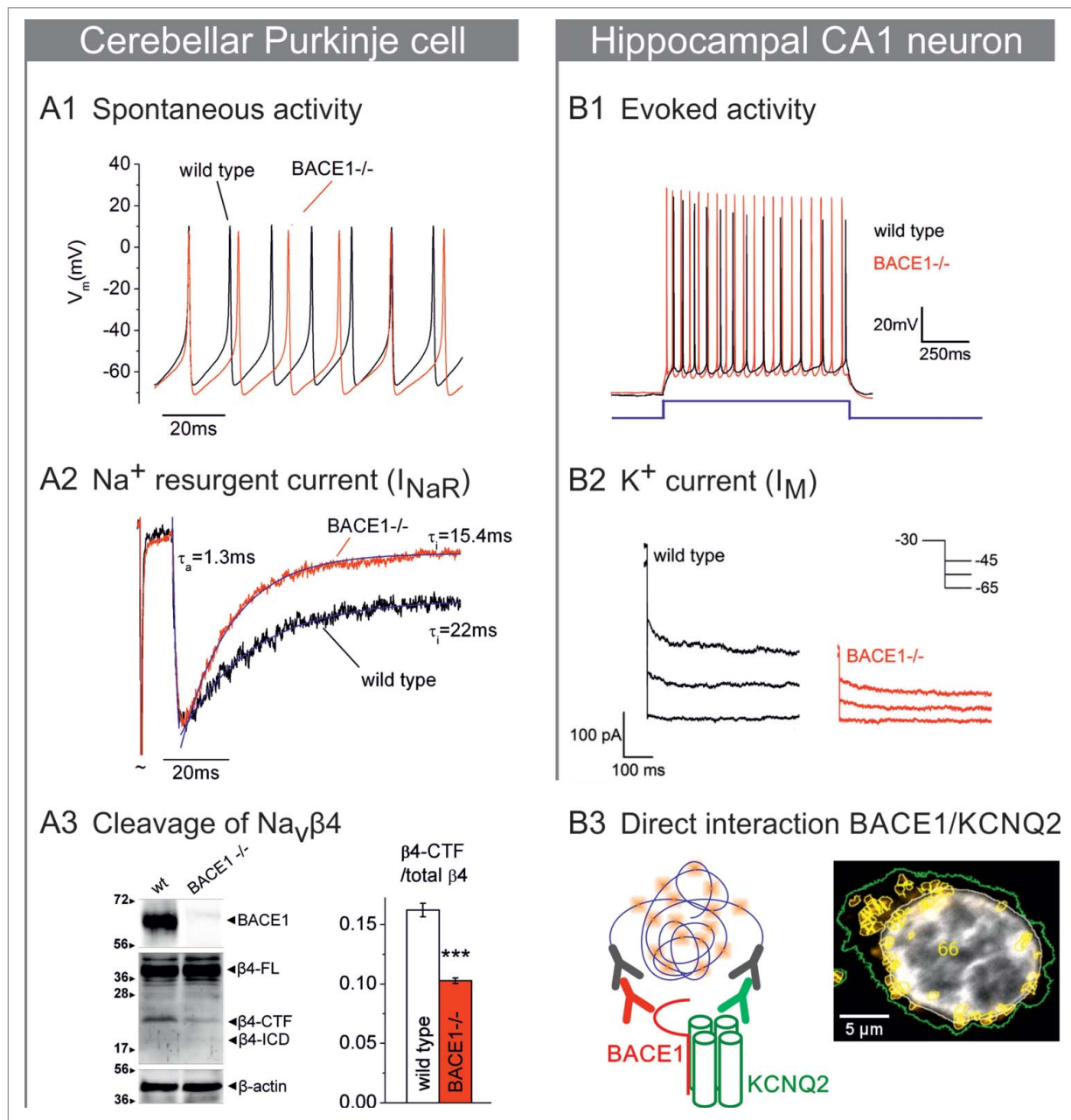


Figure 1. BACE1 modifies gating of Na⁺ and K⁺ channels. (A1) Spontaneous firing of acutely isolated cerebellar Purkinje cells (aligned to first action potential) showed reduced frequency in BACE1^{-/-} cells (red trace) compared to wild type (black trace). (A2) Acutely isolated Purkinje cells were held at -90 mV, then depolarized to +30 mV, which opened Na⁺ channels (peak truncated) that quickly inactivated. Repolarization to -22.5 mV evoked prominent resurgent current (I_{NaR} , normalized to peak I_{NaR}) that decayed faster in BACE1-deficient cells (red) than in cells from wild type mice (black). Solid lines in blue show single-exponential fits to rise and decay of I_{NaR} . (A3) Western blot (left) of cerebellar protein lysates from wild type or BACE1^{-/-} mice at postnatal day 15 shows levels of BACE1, full-length β4 (FL), β4 C-terminal fragment (CTF), β4 intracellular domain (ICD), and β-actin. Densitometric analysis (right) demonstrated reduced β4-CTF in BACE1-deficient mice. (B1) Membrane potential of CA1 pyramidal neurons in hippocampal slices was set to -70 mV, then depolarized by 50 pA current injection (blue inset). Cells from BACE1-deficient mice (red trace) fired more frequently and showed less frequency adaptation, compared to wild type (black trace). (B2) In voltage-clamp mode, acutely isolated CA1 pyramidal cells were hyperpolarized from 30 mV to 45 mV, 55 mV, or 65 mV (inset). Compared to wild type neurons (black current traces), M-current was reduced in BACE1-deficient cells (red traces). (B3) Proximity ligation assay was performed on transiently transfected HEK-T cells expressing BACE1 and KCNQ2-V5 (schematic drawing on the left). Right-hand side: Sites of close proximity are indicated by fluorescent spots (orange, yellow outlines), which were assigned to the respective nucleus (gray, white outline) and cell borders (green outline). A1-3 adapted, with permission, from ref. 66; B1-3 adapted, with permission, from ref. 96.

block and aberrant firing (Fig. 1A3). This finding suggests that proteolysis by BACE1 specifically tailors the $\beta 4$ subunit to become the high-affinity blocking particle, which is required for resurgent current generation.

Does the impaired firing of Purkinje cells engender motor abnormalities in BACE1-deficient mice? When subjected to elevated beam walking, BACE1-deficient mice showed indeed signs of ataxia (Fig. 2B). Furthermore, video analysis of their footprint pattern revealed that, with their hind paws, they significantly stepped outside their body line, which was not observed in wild type mice (Fig. 2C). The motor deficits in BACE1^{-/-} mice strongly resemble those reported from mice with a Purkinje cell-specific ablation of BK potassium channels,⁶⁷ suggesting that the symptoms

after *Bace1* ablation are of cerebellar origin. It is worth noting, however, that, as a consequence of the unprocessed BACE1 substrate neuregulin 1, BACE1-deficient mice also show muscle spindle defects and reduced myelination of peripheral nerves, which also give rise to impaired motor coordination.⁶⁸ Thus, the contributions of cerebellar dysfunction and peripheral deficits to the motor symptoms of BACE1^{-/-} mice remain to be determined in future studies.

Once considered a peculiarity of Purkinje cells, resurgent currents have since been observed in other neurons of the cerebellum as well as in neurons of other parts of the nervous system, most of them expressing $\beta 4$ and showing high frequency firing.⁶⁴ It therefore seems plausible to assume that, by altering

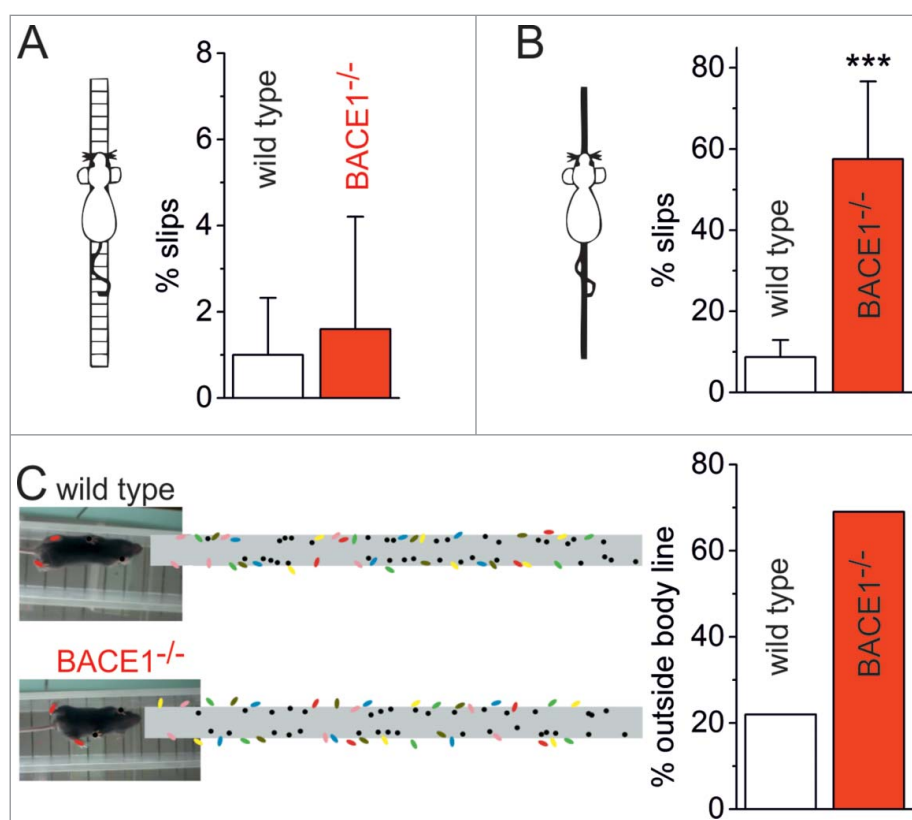


Figure 2. BACE1-deficient mice show ataxia-like motor phenotype. Distinct alterations in motor performance were analyzed in 3 different tasks. (A) In the ladder walking test, the mice had to cross a ladder composed of 38 staves with a diameter of 2 mm placed at intervals of 2 cm. The runs were stored on video tapes and slips of the forepaws and hindpaws were counted off-line in a frame-by-frame analysis. (B) In the elevated beam test, mice had to balance on a circular beam with a diameter of 1 cm and a length of 50 cm. Runs were recorded and analyzed as described above. Whereas both wild type ($n = 9$) and BACE1-deficient mice ($n = 5$) performed the ladder walking test with almost the same precision (A), the more challenging elevated beam task revealed a highly significant difference in performance (B, $p < 0.0001$, One-Way ANOVA). The number of slips was $8.7 \pm 4.2\%$ (SD, $n = 10$) for wild type mice and $57.8 \pm 19.2\%$ (SD, $n = 8$) for BACE1-deficient mice. (C) Foot print analysis was performed by detecting the positions of forepaws (black) and hindpaws (colored) of the mice while running along a transparent bridge. In wild type mice, the foot prints of both forepaws and hindpaws were almost exclusively confined to a path of a width corresponding to the transverse body diameter (8/36 steps of the hindpaws out of $n = 6$ mice outside the body line). By contrast, in BACE1-deficient mice 25/36 steps of the hindpaws (out of $n = 6$ mice) were placed outside the body diameter. The positions of the forepaws were not affected. Tests were approved by the local authorities.

I_{NaR} , BACE1 is capable of influencing the discharge properties of neurons other than Purkinje cells.

Direct interaction and Na_v gating

In addition to Na_v expression and trafficking, BACE1 has also direct impact on channel gating.⁵⁷ As expected, cleavage of $\beta 2$ or $\beta 4$ by BACE1 affected the gating of $Na_v 1.2$ currents. Most surprisingly, however, current modulation was not entirely dependent on BACE1 proteolytic activity. Analyses with proteolytically inactive BACE1 suggested, for the first time, that BACE1 may act as an accessory subunit at $Na_v 1.2$, mimicking $\beta 2$ effects at the $Na_v 1.2/\beta 4$ complex.⁵⁷

Although non-enzymatic actions of a protease that has been evolutionally conserved for β -cleavage may seem enigmatic, BACE1 is by far not the only enzyme endowed with such activity. For example, the G protein-coupled receptor (GPCR) kinase 2 (GRK2) rapidly desensitizes GPCR-coupled potassium currents independent of its phosphorylation capacity.⁶⁹ A whole collection of structural effects has been put together for transglutaminase 2.⁷⁰ Further examples are non-enzymatic functions of matrix metalloproteinase 12 and the γ -secretase component presenilin 1.^{71,72} BACE1 itself has been discussed as a non-enzymatic binding partner for a set of proteins, including BRI3, which is, like BACE1, processed by furin.⁷³ While in Na_v channels, non-enzymatic interactions between BACE1 and channel proteins were clearly discernible but small, such effects became much more prominent when explored in members of the KCNQ family.

BACE1 and neuronal KCNQ currents

KCNQ structure and regulation by β -subunits

The family of KCNQ ($K_V 7$) channels has 5 members, KCNQ1-5 ($K_V 7.1-7.5$, *KCNQ1-5*). The pore-forming α -subunits form homo- or hetero-tetramers.^{74,75} KCNQ1 (also: $K_V LQT$, long QT) is expressed in heart, gastrointestinal tract, and inner ear.⁷⁶ KCNQ2 and KCNQ3 are widely found in the central and peripheral nervous system.^{77,78} KCNQ4 seems to fulfil specific functions in the inner ear and in peripheral sensors, while KCNQ4/Q5 heteromers are important for vessel smooth muscle diameter control and in the vestibular system.⁷⁹⁻⁸¹ KCNQ5 has further been identified as a neuronal KCNQ member.⁸²⁻⁸⁴

A complex molecular network is regulating the expression, localization, and gating of KCNQ channels.

The family of the widely expressed β -subunits KCNE1-5 (*KCNE1-5*) modulates a variety of ion channels and is part of the KCNQ regulation system.⁸⁵ The best studied interaction between a KCNQ α -subunit and an accessory KCNE subunit is that of the KCNQ1/KCNE1 complex, which forms the I_{Ks} and contributes to action potential repolarization in cardiomyocytes.^{86,87} Neuronal KCNQ channels are currently thought to operate without accessory β -subunits.⁷⁴ This view is challenged by our recent work and will be discussed below.

Neuronal KCNQ function

KCNQ2 and KCNQ3 are the main constituents of neuronal M-current, a non-inactivating potassium current with slow activation and deactivation kinetics, which gives rise to a standing outward current below firing threshold.⁷⁷ M-current is suppressed by muscarinic receptor activation (hence its name) owing to depletion of PIP_2 .^{88,77} Depending on its subcellular localization, M-current may regulate various aspects of intrinsic excitability. At the axon initial segment, M-current counteracts the propagation of subthreshold inputs to the axon, while it promotes action potential amplitude at nodes of the distal axon by increasing the availability of Na_v channels.⁸⁹ Somatodendritic M-current mediates spike frequency adaptation during repetitive firing.⁹⁰ M-current further contributes to subthreshold theta frequency oscillations and regulates coherent spiking of neuron populations.^{91,92}

The important role of M-current in keeping the balance between neuronal excitation and inhibition is emphasized by *KCNQ2* and *KCNQ3* mutations, which lead to an infantile epilepsy syndrome (benign familial neonatal convulsions, BFNC).⁹³ Studies with conditional *KCNQ2* or *KCNQ3* knockout mice indicated that *KCNQ2*, rather than *KCNQ3*, is the important player in the regulation of neuronal excitability.⁹⁴ A prominent role of *KCNQ2* has been demonstrated in mice with conditional neuronal *KCNQ2* knockout, which show neuronal hyperactivity and premature death.⁹⁴ Transgenic mice with a dominant-negative variant of *KCNQ2* in the nervous system are epileptic and have impaired spatial memory.⁹⁵ Males are hyperactive and show morphological changes in the CA1 and the mossy fiber region. Intriguingly, these phenotypes closely resemble those of BACE1-deficient mice, raising the possibility that neuronal KCNQ channels might be a target of BACE1, too.

Direct interaction and KCNQ gating

A recent study indeed demonstrated a functionally significant interaction between BACE1 and neuronal KCNQ channels, which may well explain the striking phenotypic similarities between KCNQ2-deficient and BACE1-deficient mice.⁹⁶ In CA1 pyramidal neurons from wild type mice, depolarizing current injection elicited a train of action potentials (APs), which showed frequency adaptation due to M-current activation.^{90,97} By contrast, BACE1-deficient neurons fired APs at higher frequency (Fig. 1B1), similar to neurons in which M-current was suppressed by drugs or genetic manipulations.^{94,98,99} Furthermore, the M-current blocker XE991, which increased input resistance and firing frequency, and reduced latency to first AP in control neurons, failed to do so in mutant neurons. In voltage-clamp recordings, M-currents of acutely isolated CA1 pyramidal neurons from BACE1-deficient mice were reduced by 2/3 and displayed faster decay kinetics when compared to their wild type counterparts (Fig. 1B2). The prominent current decrease in knockout animals markedly exceeds the reduction in human BFNC, where a 25% decrease in M-current seems enough to cause hyperexcitability.^{100,101} Therefore, it is conceivable that the strongly impaired M-current in BACE1-deficient mice is responsible for their epileptic phenotype.

To elucidate the BACE1/KCNQ interplay, we examined KCNQ2 and KCNQ3 in a heterologous expression system.⁹⁶ Co-expression of BACE1 increased KCNQ2/3 current amplitude, shifted activation to slightly more negative potentials, accelerated activation, and decelerated deactivation. Most importantly, the effects of BACE1 were non-proteolytic in nature, since they were reproduced by a proteolytically inactive BACE1 mutant.¹⁰² Thus, the non-enzymatic interaction between BACE1 and the α -subunit of voltage-dependent ion channels first reported for Na_v1.2 (see above) seems to emerge as a more widely applicable mechanism through which BACE1 can influence neuronal excitability. Co-immunoprecipitation and proximity ligation assay served as independent means to confirm direct BACE1/KCNQ interaction (Fig. 1B3). Consistent with findings from KCNQ knockout mice (see above), the effects of BACE1 on reconstituted M-current were mainly due to its interaction with KCNQ2 rather than with KCNQ3. Notably, BACE1 was also capable of increasing currents mediated by heterologously expressed KCNQ4 or KCNQ5.⁹⁶

Since the functionality of KCNQ channels strongly depends on adequate PIP₂ levels, an obvious question is

whether BACE1, as it becomes part of KCNQ channel complexes, enhances their affinity for PIP₂, thereby promoting channel openings. However, BACE1 did not alter the decrease of KCNQ2/3 currents upon PIP₂ depletion, nor did PIP₂ displace BACE1.^{96,103} Thus, BACE1 appears to act differently than KCNE1, which sensitizes KCNQ1 to PIP₂.¹⁰⁴ Furthermore, the current-promoting effect of BACE1 was different from that of the established M-current activator retigabine.⁹⁶ Taken together, these data suggest that the long-held view of M-current arising from neuronal KCNQ channel assemblies lacking auxiliary subunits requires modification. In the absence of KCNEs as binding partners for neuronal KCNQ channels, BACE1 may step in and become an essential constituent of M-current.

BACE1 and KCNQ1/KCNE1 (I_{Ks}) currents

BACE1 is present in murine heart and in human iPSC-derived cardiomyocytes.¹⁰⁵ Underscoring the significance of BACE1 for cardiac electrophysiology, atrial cardiomyocytes from BACE1^{-/-} mice show only about half the I_{Ks} of wild type cells.¹⁰⁵ Since I_{Ks} is thought to be mediated by KCNQ1/KCNE1 channel complexes, these findings strongly point to physiologically relevant BACE1/KCNQ interactions also in the heart. Compared to neurons, however, matters in the heart are complicated by the fact that KCNE1 (and KCNE2) were identified as substrates to sequential cleavage by BACE1 or α -secretase, and γ -secretase.¹⁰⁶ This situation leaves us with a number of possibilities of how BACE1 may influence I_{Ks}. For example, cleavage of KCNE1 by BACE1 may be a prerequisite for proper I_{Ks}. In addition, or alternatively, BACE1 may physically interact with KCNQ1 to augment I_{Ks}, analogous to the boosting of M-current in neurons. If a direct, non-enzymatic interaction holds true, we will have to ask next how BACE1 competes with KCNE1 for binding to KCNQ1 channels. First answers to these questions come from a study, in which KCNQ1, KCNE1, and BACE1 (including its proteolytically inactive variant) were heterologously expressed in various combinations.¹⁰⁵ Major findings from this work are: First, BACE1 modulates currents mediated by KCNQ1 alone and by KCNQ1/KCNE1 complexes independent of its proteolytic function. Second, BACE1 slows activation and inactivation kinetics of KCNQ1/KCNE1 currents, and third, the effects of BACE1 critically depend on cellular ATP levels: BACE1 reduced

reconstituted I_{Ks} in well-supplied cells, but counteracts current decline when ATP levels fall.

With BACE1 emerging as a β -subunit-like binding partner of KCNQ1, the issue of competition between BACE1 and KCNE subunits comes to the fore. Lundquist *et al.* suggested complex channel assemblies when different KCNE subunits are present in a tissue.⁸⁵ BACE1 now further complicates the assembly options and may temper with KCNQ1/KCNE1 stoichiometry, which has been vividly debated in the past years.¹⁰⁷⁻¹¹¹

The interaction between BACE1 and KCNQ1/KCNE1 also raises a number of clinically interesting points. For example, can the increased lethality of BACE1-deficient mice be linked to abnormal cardiac electrophysiology? In the CNS, cellular stress was reported to elevate BACE1 expression and activity. Does this also hold for cardiac stress, and if so, would it protect against arrhythmias, as suggested by the strengthened effect of BACE1 when ATP is depleted?

Outlook

The finding that β -subunits of several voltage-dependent channel families can be split by BACE1 was the starting point to focus on the enzyme in the context of cellular excitability. The more recent finding that BACE1 can act

as a β -subunit itself, thereby regulating channel function in a non-enzymatic fashion, offers an entirely new look at the role of this protein in the healthy and diseased brain and heart (summarized in Fig. 3). It is well conceivable that the list of channels, which can be influenced by BACE1 through proteolytic and, perhaps more so, through non-proteolytic effects, will be growing. Given that BACE1 is a rather ubiquitous protein and channels such as KCNQ1 are also expressed in various non-excitable cells, multiple organ systems and tissues might rely on BACE1/channel interactions. So far, hypotheses related to the physiological and pathogenic implications of the interplay between BACE1 and ion channels have been mainly derived from studies of BACE1-deficient preparations. From a translational point of view, it would be particularly important to gain a deeper understanding of how increases in BACE1 expression and activity, which are associated with Alzheimer's disease, might influence the spectrum of electrophysiological effects related to BACE1. So far, BACE1 is mainly seen as a major culprit in AD owing to its pivotal role in the amyloidogenic pathway. But if BACE1 at the same time augments M-current, wouldn't this non-proteolytic effect help to dampen the heightened propensity of AD patients to develop seizure activity? Another endogenous, putatively anti-epileptic mechanism has already

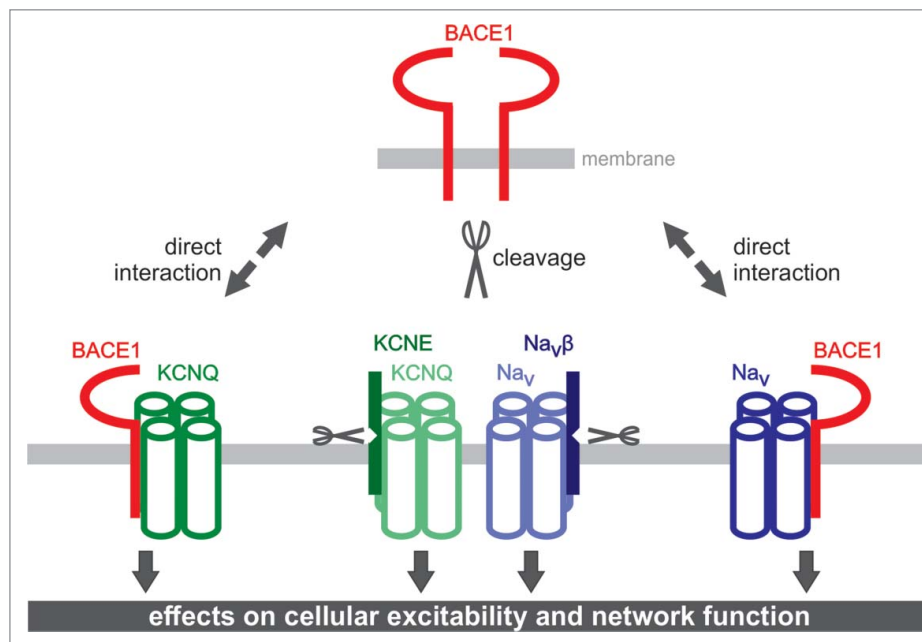


Figure 3. Schematic model of proteolytic and non-proteolytic effects of BACE1 on Na^+ and K^+ channels. Acting like an accessory β -subunit, BACE1 may attach itself to α -subunits of Na_v and KCNQ channels in a non-enzymatic fashion (configurations on left- and right-hand side). In addition, BACE1 may cleave β -subunits ($Na_v\beta$ s and KCNEs) of the respective channels (configurations at center). The different forms of interaction with BACE1 all influence channel function and are thus expected to have an impact on cellular excitability and network activity.

been described for hippocampus and superior cervical ganglia, where KCNQ2 and KCNQ3 mRNA is upregulated as a response to induced seizures.¹¹² If a synergistic and beneficial effect of BACE1 holds true, can we design drugs that suppress the noxious enzymatic actions of BACE1 while at the same time preserving its beneficial actions on certain ion channels? In this context, strategies that aim to render BACE1 harmless by other means, such as blocking peptides that bind to APP and inhibit the fatal BACE1/APP interaction,¹¹³ may gain importance. With issues like these, it becomes evident that studies on the electrophysiological impact of BACE1 hold great promise not only for elucidating the amazingly rich repertoire of targets and actions of this truly protean protein under physiological and pathological conditions, but also to exploit that knowledge to develop specifically tailored therapies.

Abbreviations

A β	amyloid β
AD	Alzheimer's disease
AP	action potential
APP	amyloid precursor protein
ATP	adenosine triphosphate
BACE1	β -site APP-cleaving enzyme 1
BFNC	benign familial neonatal convulsions
BK	large-conductance voltage- and calcium-activated potassium channel
BRI3	brain protein I3
CA1/3	cornu ammonis areas 1/3
CNS	central nervous system
EEG	electroencephalogram
GPCR	G protein-coupled receptor
GRK2	G protein-coupled receptor kinase 2
I _{Ks}	slow delayed rectifier potassium current
I _{NaR}	resurgent sodium current
iPSC	induced pluripotent stem cell
KCNE	voltage-gated potassium channel subfamily E
KCNQ	voltage-gated potassium channel subfamily Q (K _v 7.1-5)
K _v	voltage-gated potassium channel
Na _v	voltage-gated sodium channel
PIP ₂	phosphatidylinositol-4,5-bisphosphate
PSEN1/2	presenilin 1/2

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