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Assessment of the TRPM8 inhibitor AMTB in breast cancer cells and its identification as an inhibitor of voltage gated sodium channels.

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Abstract

Aims: To assess levels of the calcium permeable transient receptor potential cation channel, subfamily melastatin, member 8 (TRPM8) in breast cancer molecular subtypes and to assess the consequences of TRPM8 pharmacological inhibition with AMTB (an inhibitor of TRPM8) on breast cancer cell lines.

Materials and Methods: Cell viability and migration of breast cancer cells was determined using MTS assays and wound healing assays, respectively. RNA-Seq analysis of breast tumours and qPCR in breast cancer cell lines were used to assess mRNA levels of ion channels. Membrane potential assays were employed to assess the effects of AMTB against specific voltage gated sodium channels (Na_v).

Key findings: TRPM8 levels were significantly higher in breast cancers of the basal molecular subtype. AMTB decreased viable cell number in MDA-MB-231 and SK-BR-3 breast cancer cell lines (30 and 100 μM), and also reduced the migration of MDA-MB-231 cells (30 μM). However, these effects were independent of TRPM8, as no TRPM8 mRNA was detected in MDA-MB-231 cells. AMTB was identified as an inhibitor of Na_v isoforms. $\text{Na}_v1.1-1.9$ were expressed in a number of breast cancer cell lines, with $\text{Na}_v1.5$ mRNA highest in MDA-MB-231 cells compared to the other breast cancer cell lines assessed.

Significance: TRPM8 levels may be elevated in basal breast cancers, however, TRPM8 expression appears to be lost in many breast cancer cell lines. Some of the effects of AMTB attributed to TRPM8 may be due to effects on Na_v channels.

Key words: AMTB, breast cancer, TRPM8, sodium channels

Introduction

Changes in cytosolic free calcium ($[Ca^{2+}]_{CYT}$) are often critical for events important in cancer progression (1, 2). Altered expression of specific calcium permeable ion channels has been widely reported in cancers and/or cancer cell lines originating from the lung, prostate and breast (3-7). In some cases, such changes are even specific to the cancer clinical subtype, such as the overexpression of the transient receptor potential cation channel subfamily V member 6 (TRPV6) channel in estrogen receptor negative breast cancers and those of the basal molecular subtype (8). The basal molecular subtype of breast cancer is of particular interest due to its overlap with breast cancers that lack the expression of receptors representing current targets for targeted therapies, such as the estrogen and human epidermal growth factor 2 (HER2) receptors (9, 10).

TRPM8 is a member of the TRP ion channel family and is expressed in primary sensory neurons where it plays an important role in cold sensation (11). The properties of TRPM8 in specific neuronal sensory pathways have seen its identification as a target for a diverse range of conditions including pain, migraine and cough (12-14). However, despite the importance of TRPM8 as a sensor in neurons, it was actually first identified through a study assessing the overexpression of proteins in the prostate, which also demonstrated elevated levels in cancers of the prostate, lung, colon and breast (15). Subsequent to this report, a variety of studies have explored in great depth the contribution of TRPM8 to prostate cancer cell growth and invasion and the potential role of TRPM8 modulators to control prostate cancer disease progression and/or TRPM8 as a biomarker (16-20).

Despite the first report of TRPM8 overexpression in breast cancer occurring in 2001 (15), there have been limited studies of TRPM8 in the context of possible associations with breast cancer subtypes, the role of TRPM8 in breast cancer cells and the suitability of this ion channel as a target for breast cancer therapy (21, 22). An agent which may be useful in defining the possible role of TRPM8 in breast cancer and as a proof of concept tool for targeting TRPM8 in breast cancer therapy is the TRPM8 inhibitor, *N*-(3-aminopropyl)-2-[[3-methylphenyl] methyl]oxy}(20)-*N*-(2-thienylmethyl)benzamide (AMTB) (23). AMTB, a 2-benzyloxy-benzoic acid amide derivative (18), has been used as a TRPM8 pharmacological inhibitor in a variety of studies (23-25) and has been reported to inhibit the migration of LNCaP, PC3 and DU145 prostate cancer cell lines (25). TRPM8 has also been reported to regulate migration, proliferation and also angiogenesis processes (20, 26-32). However, AMTB has not been assessed in breast cancer cell lines.

Hence, in this study, we sought to define the expression of TRPM8 in breast cancer molecular subtypes and assess the consequences of TRPM8 pharmacological inhibition in breast cancer cell lines. These studies yielded the unexpected result that some of the reported effects of AMTB in a variety of disease models may be independent of TRPM8 and could rather be a consequence of the ability of AMTB to inhibit voltage gated sodium channels (Na_v) of the Na_v1 class.

Materials and Methods:

Analysis of TRPM8 expression in breast tumours

RNA-Seq gene expression profiles in human breast tumours ($n = 506$) from The Cancer Genome Atlas (TCGA) study (33) were assessed as previously described (34). Gene expression of TRPM8 in 84 basal-like, 58 HER2 enriched, 233 Luminal A, and 131 Luminal B tumours were evaluated. Statistical significance was measured using Kruskal-Wallis test with Dunn's post-test.

Cell Culture

The human breast cancer cell lines used this study: MDA-MB-231, MCF-7 and HCC1569 were purchased from American Type Culture Collection; SK-BR-3, T-47D and ZR-75-1 cell lines were a kind donation from the late Professor Rob Sutherland (Garvan Institute, Sydney) and MDA-MB-468 cells were a generous gift from Dr Chanel Smart (The University of Queensland Centre for Clinical Research). MDA-MB-231 cells and SK-BR-3 cells were cultured as previously described (35, 36) in antibiotic-free media and routine mycoplasma contamination testing was carried out using the MycoAlert Mycoplasma Detection Kit (LT07-218, Lonza Inc).

Pharmacological agents

AMTB was purchased from Sigma-Aldrich (SML0103). Stock solutions were prepared by dissolving compounds in dimethyl sulfoxide (DMSO) (D8418, Sigma-Aldrich) or sterile distilled water and aliquots were stored at 4°C or -20°C . Lidocaine (N-(2,6-dimethylphenyl)acetamide) stock solution was purchased from Sigma-Aldrich (L7757).

Cell viability assay

CellTiter 96[®] AQueous One Solution Cell Proliferation Assay (G3580, Promega) was used to determine cell viability. Cells were cultured in antibiotic-free media and plated in 96-well plates at a density of 5,000 cells per well for MDA-MB-231 and 6,000 cells per well for SK-BR-3 cells. Pharmacological compounds/toxins were diluted to the appropriate concentrations in cell culture media and added to the cells at 24 h and 72 h post plating. Control wells were treated with 0.1% vehicle (DMSO or absolute ethanol) or antibiotic-free media. MTS assays were performed 96 h post plating using CellTiter 96[®] AQueous One Solution Reagent (Promega). Absorbance at 490 nm was measured using a micro-plate reader ((iMark, BioRAD).

***In vitro* scratch assay**

MDA-MB-231 cells (17 000 cells per well) were seeded in 96-well plates and incubated at 37°C, 5% CO₂ for 48 h. The WoundMaker[™] instrument (Essen Biosciences) was used to produce an equal sized scratch in the cell monolayer of all wells of the plate. Cells were washed twice with fresh media and immediately treated with various concentrations of AMTB for 24 h. Images of the centre of each well were acquired with a JuLI[™] Stage live cell imaging system (NanoEntek) (10X objective), 24 h post-treatment. Analysis of wound closure (confluence) was performed using JuLI[™] Stage automated cell imaging system software (V0.0, NanoEntek). Confluency results were normalised to a control well (media treatment) representing the highest confluence at 24 h.

RNA isolation and real-time RT-PCR

Total RNA was isolated and purified using a RNeasy Plus Mini Kit (74136, Qiagen). Purified RNA was reverse transcribed using Omniscript RT Kit (Qiagen); random primers (C1181, Promega) and RNAase inhibitor (N2111, Promega) were purchased separately. Real-time PCR was performed using TaqMan[®] Universal PCR Master Mix (2X) and TaqMan[®] gene expression assays purchased from Life Technologies. Gene expression assays: SCN1A/Nav1.1 (Hs00374696_m1), SCN2A/Nav1.2 (Hs01109877_m1), SCN3A/Nav1.3 (Hs00366902_m1), SCN4A/Nav1.4 (Hs01109480_m1), SCN5A/Nav1.5 (Hs00165693_m1), SCN8A/Nav1.6 (Hs00274075_m1), SCN9A/Nav1.7 (Hs00161567_m1), SCN10A/Nav1.8 (Hs01045137_m1), SCN11A/Nav1.9 (Hs00204222_m1), TRPM8 (Hs01066597_m1) and endogenous control for 18S rRNA (4319413E) were used in this study. Assays were performed using a StepOne Plus instrument (Applied Biosystems) under universal cycling conditions and data were analysed using StepOne Plus Software, version 2.2.2 (Applied Biosystems). The relative quantification or comparative C_T (cycle

threshold) method (37) was used to determine relative mRNA levels with data normalised to 18S rRNA.

Human TRPM8 cDNA clone (pCMV6-XL5-hTRPM8, un-tagged, homo-sapiens, clone MGC:2849, complete cds, NCBI RefSeq: BC001135.1, 10 µg, Cat#: SC13793, Origene Technologies Ltd) was used as a positive control for TRPM8 real-time RT-PCR assays.

FLIPR membrane potential assay

HEK293 cells heterologously expressing human Na_v1.1–1.8 (SB Drug Discovery, Glasgow, UK) were cultured in MEM containing 10% v/v FBS and selection antibiotics as recommended by the manufacturer. Cells were grown in a humidified 5% CO₂ incubator at 37°C, grown to 70–80% confluence, and passaged every 3-4 days using TrypLE Express (Invitrogen). Cells were seeded in 384-well plates (Corning) at a density of 10,000-15,000 cells per well and cultured for 48 h. Membrane potential dye (Molecular Devices) was diluted in physiological salt solution (PSS; 140 mmol/L NaCl, 11.5 mmol/L glucose, 10 mmol/L HEPES, 5.9 mmol/L KCl, 1.4 mmol/L MgCl₂, 1.2 mmol/L NaH₂PO₄, 5 mmol/L NaHCO₃, 1.8 mmol/L CaCl₂, pH 7.4). Growth media was removed from the cells, 20 µL dye/well added and cells incubated in the dark at 37°C for 30 min. A two-addition FLIPR protocol consisting of addition of AMTB, incubation for 5–10 min and addition of veratridine (20-60 µM) to activate Na_v1.1-1.7 or deltamethrin (150 µM) was used to activate Na_v1.8. The change in fluorescence was measured (excitation 515–545 nm, emission 565–625 nm) every 1-2 s for 5-30 min after addition of agonists using the fluorescence imaging plate reader FLIPR TETRA (Molecular Devices). To quantitate the effect of test compounds on Na_v responses, the area under the curve (AUC) corresponding to 5 min after the addition of veratridine or maximum response corresponding to 30 min after the addition of deltamethrin was computed using ScreenWorks (Molecular Devices, Version 3.2.0.14).

Statistical Analysis

Statistical analysis was performed using GraphPad Prism version 6.04 for Windows, unless otherwise specified.

Results:**TRPM8 levels are elevated in basal-like breast cancers**

TRPM8 levels were significantly higher in basal-like breast tumours, compared to the luminal A, B and HER2-enriched subtypes (Figure 1). Considerable variation in TRPM8 levels was also observed within the basal-like subtype, with the sample showing the highest TRPM8 expression level having 476 times more TRPM8 transcript than the median level among the basal-like samples. Although the most striking elevation was detected in the basal-like breast tumour samples, the HER2-amplified group also had higher TRPM8 levels than both of the luminal subtypes.

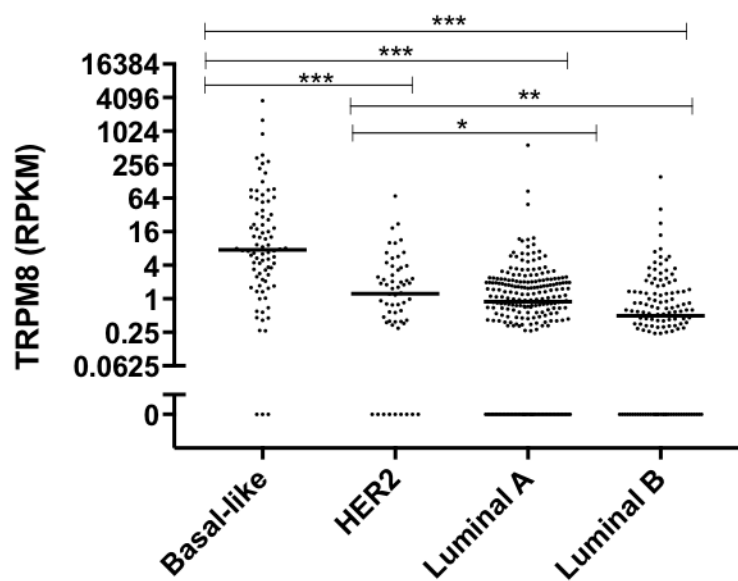


Figure 1: TRPM8 expression in breast cancer clinical samples. Gene expression (Reads Per Kilobase of transcript per Million (RPKM)) of TRPM8 in 506 breast tumours from TCGA breast cancer RNA-Seq data, classified according to breast tumour subtypes. TRPM8 is over-expressed the basal-like subtype compared to HER2 enriched and luminal A/B subtypes. Horizontal lines represent median levels for each subtype, statistical significance was determined using Kruskal-Wallis test with Dunn's post-test; *** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$.

AMTB decreases the proliferation and migration of breast cancer cells via a TRPM8 independent mechanism

Treatment of MDA-MB-231 and SK-BR-3 breast cancer cells with the TRPM8 inhibitor AMTB reduced cell viability by approximately 70% at 30 and 100 μM , with IC_{50} values of 23.7 μM and 17.3 μM in MDA-MB-231 and SK-BR-3 cells, respectively (Figure 2A and B). *In vitro* scratch assays showed that AMTB (30 μM) also significantly decreased the migration of MDA-MB-231 breast cancer cells (Fig 2C). However, this effect was not due to TRPM8, since assessment of TRPM8 mRNA levels in a variety of breast cancer cell lines representing distinct molecular subtypes (38, 39), revealed little or no TRPM8 mRNA (Table 1), including in SK-BR-3 and MDA-MB-231 cells where effects by AMTB were observed. Therefore, the effects of AMTB, a reported selective TRPM8 inhibitor (23), at a concentration (30 μM) used in other model systems (18), occurred independently of TRPM8 inhibition in these breast cancer cell lines. The possibility of off-target effects of AMTB was therefore investigated.

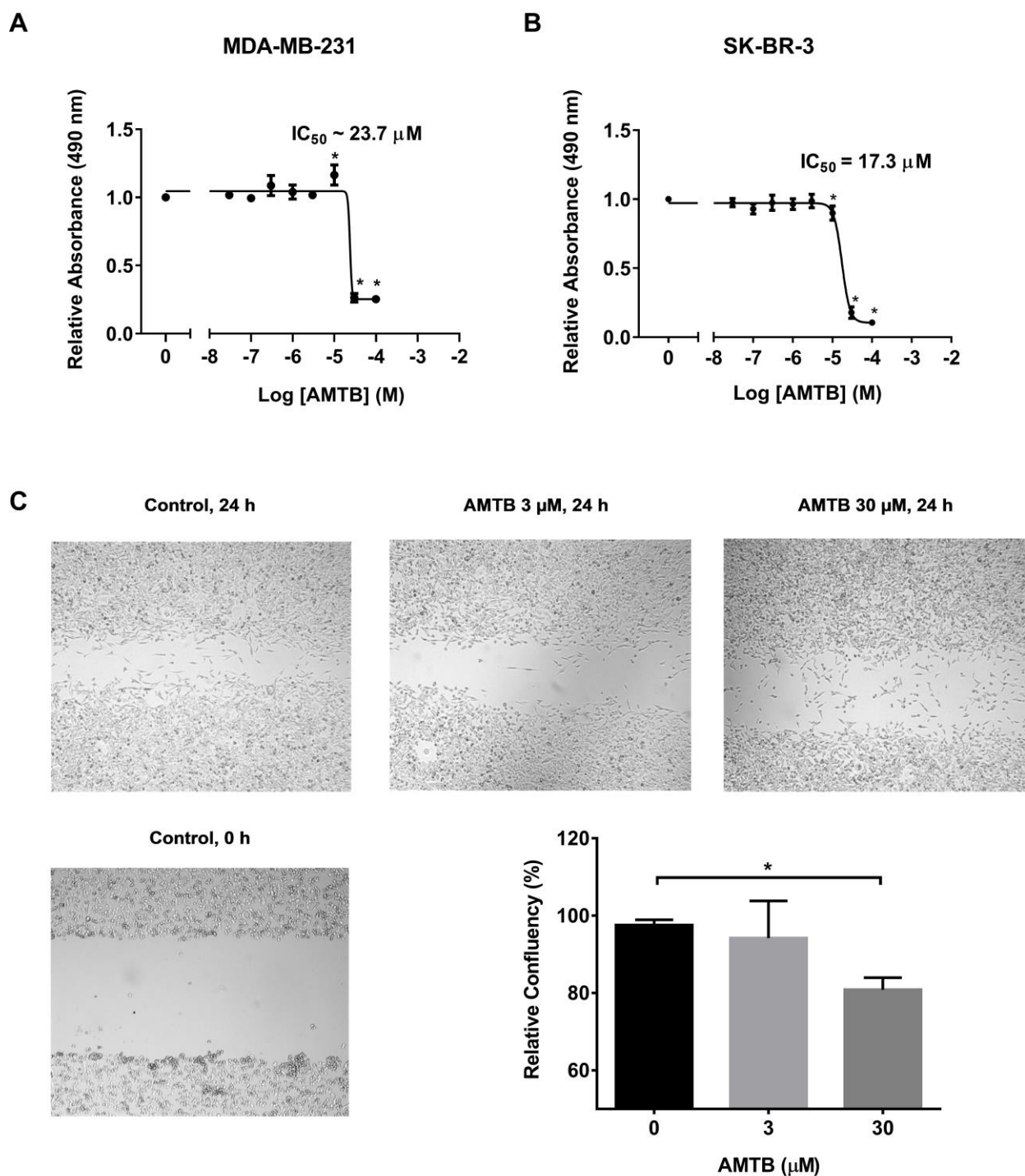


Figure 2: AMTB reduces cell viability and migration of breast cancer cells. Concentration-response curves for AMTB in MDA-MB-231 (A) and SK-BR-3 (B) breast cancer cells. Cells were incubated with AMTB (0 – 100 μM) for 72 h and an MTS assay was used to approximate viable cell number. Absorbance values (490 nm) were normalised to control treated cells and plotted using non-linear regression curve fit: log (inhibitor) vs response – variable slope (four parameters). Data show mean \pm SD, n = 3. Statistical analysis was performed using a one-way ANOVA with

Dunnett's multiple comparisons test; * $P < 0.05$ compared to control. **C:** In vitro scratch assays were performed on MDA-MB-231 cells in the absence (control, 0) and presence of AMTB (3 μM , 30 μM). AMTB (30 μM) decreased the migration of MDA-MB-231 cells by ~20%. Representative images from one experiment after initial scratch (0 h) and 24 h post-treatment. Bar graph represents the relative confluency of each treatment group normalised to control well (24 h with media only); mean \pm SD, $n=3$, * $P < 0.05$.

Table 1: TRPM8 mRNA are very low or undetectable in breast cancer cell lines. Molecular subtypes, receptor status (estrogen receptor, ER; progesterone receptor, PR (38, 39)) and average C_T values for TRPM8 and 18S rRNA (housekeeping control) in different breast cancer cell lines, $C_T > 35$ were assigned not detected (ND); mean \pm SD, $n=3$.

Cell Line	Molecular Subtype and Receptor Status	C_T TRPM8	C_T 18S
HCC1569	Basal, ER-, PR-, HER2+	ND	15.52 \pm 0.62
MCF-7	Luminal, ER+, PR+	ND	15.92 \pm 0.42
MDA-MB-231	Basal, ER-, PR-	ND	14.93 \pm 0.30
MDA-MB-468	Basal, ER-, PR-	34.04 \pm 0.52	15.53 \pm 0.39
SK-BR-3	Luminal, ER-, PR-, HER2+	33.34 \pm 0.57	14.94 \pm 0.11
T-47D	Luminal, ER+, PR+	ND	15.83 \pm 0.16
ZR-75-1	Luminal, ER+, PR-	34.81 \pm 0.62	17.13 \pm 0.18
Positive control: TRPM8 cDNA	-	12.55 \pm 0.05	-

AMTB inhibits veratridine-induced effects on membrane potential

Strikingly, AMTB contains several structural features required for inhibition of voltage-gated sodium channels (Na_V) by local anesthetics, including a substituted benzene ring, an intermediate chain with amide linker, as well as a hydrophilic terminal (Figure 3A and B). In addition to structural similarities of AMTB to such compounds, we also observed profound analgesia of AMTB after intraplantar administration in animal models of chemotherapy-induced allodynia where local anaesthetic provided anti-allodynic effects, but TRPM8 knockout animals lacked a phenotype (data not shown) (40). We thus assessed the effect of AMTB on the function of Na_V 1.1-1.8 using a high-throughput fluorescent imaging plate reader (FLIPR) membrane potential assay (Figure 3C). AMTB blocked veratridine-induced membrane potential changes at each Na_V 1 isoform more potently than the prototypical Na_V blocker lidocaine (Figure 3C and D). The IC_{50} (~2 - 15 μM) for each Na_V placed the actions of AMTB on Na_V s in a similar concentration range as that reported for inhibition of TRPM8 by AMTB (23). Given veratridine has no effect on membrane potential in untransfected HEK293 cells (Suppl. Fig 1), and that AMTB did not affect membrane potential in HEK cells expressing Na_V 1.1-1.8 (data not shown and Suppl. Fig 2), these results are consistent with inhibition of Na_V 1.1-1.8 by AMTB. These results, therefore, suggested that one of the mechanisms by which AMTB could exert effects on MDA-MB-231 cells is via effects on Na_V s. Therefore, the presence of Na_V s in a panel of breast cancer cell lines representing different molecular subtypes was evaluated.

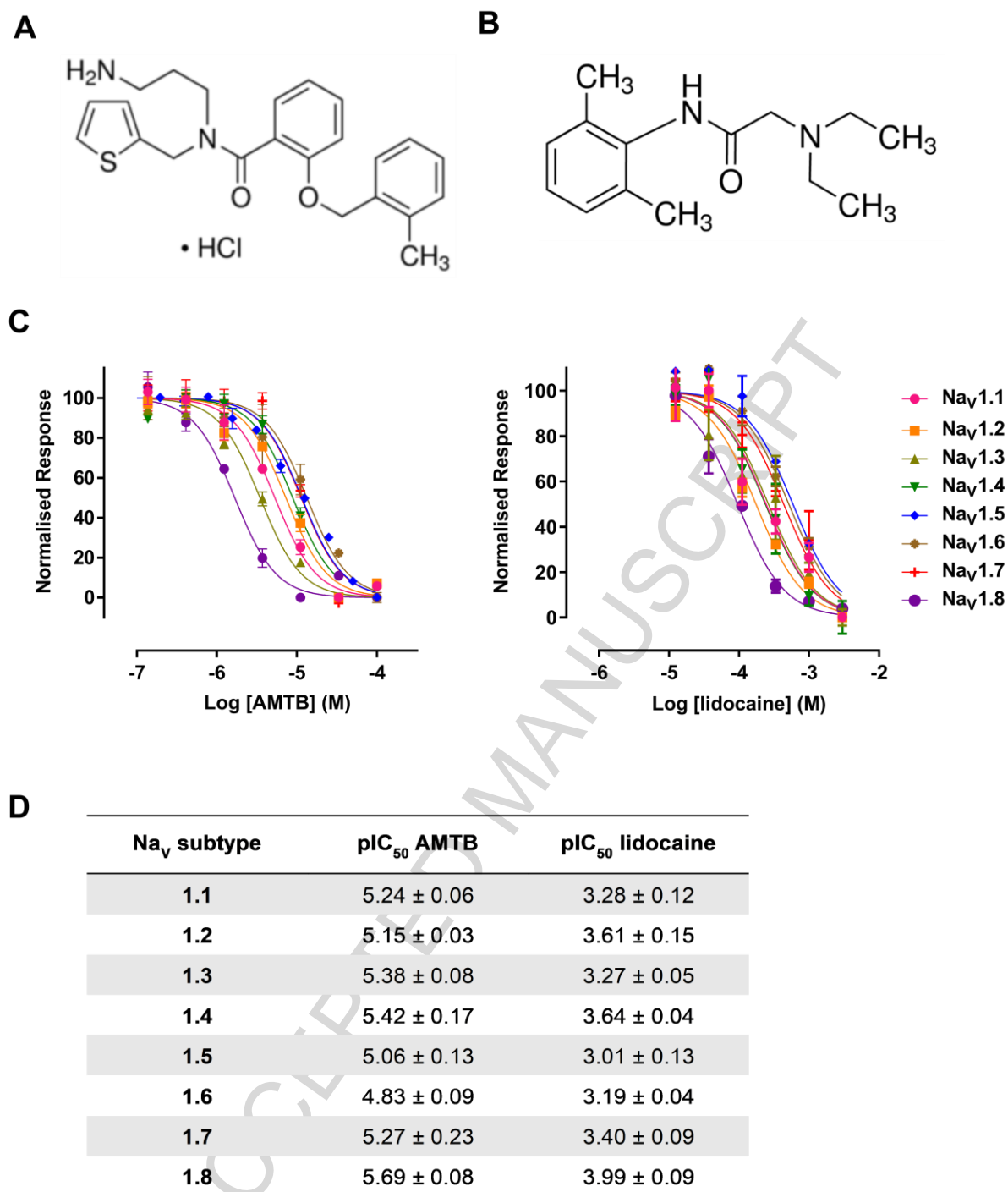


Figure 3: AMTB is a non-selective inhibitor of voltage-gated sodium channels (Na_v). (A)

Chemical structure of AMTB (N-(3-aminopropyl)-2-[(3-methylphenyl)methoxy]-N-(2-thienylmethyl)-benzamide). (B) Chemical structure of lidocaine (N-(2,6-

dimethylphenyl)acetamide). (C) Representative concentration-response curves for AMTB and

lidocaine in HEK293 cells stably expressing hNa_v1.1-1.8. Data are presented as mean ± SEM from

3-6 wells. (D) pIC₅₀ values for AMTB and lidocaine at hNa_v1.1-1.8 obtained from the membrane

potential assays. Data are presented as mean ± SEM from 3 independent experiments.

Differential expression of Navs in human breast cancer cell lines

There have been reports of Navs in human breast cancer cell lines, including the consequences of silencing and/or pharmacological inhibition of specific Nav1 isoforms (41-43). However, there has been no comprehensive study of Nav1 isoforms across human breast cancer cell lines of different molecular subtypes. Our assessment of Nav1.1-1.8 mRNA in luminal, HER2 enriched and basal-like breast cancer cell lines identified that in contrast to TRPM8, all assessed breast cancer cell lines had detectable levels of mRNA for at least one Nav1 isoform.

There were significant differences in the mRNA levels of specific mRNA isoforms between breast cancer cell lines. For example, the HER2 enriched basal-like molecular subtype cell line HCC1569 (38, 39) had the highest levels of Nav1.1 and Nav1.6 mRNA, whereas the basal-like MDA-MB-468 cell line had the highest levels of Nav1.2. The basal, triple negative MDA-MB-231 cell line (38, 39) had the highest levels of Nav1.3, Nav1.5 and Nav1.7. Nav1.8 was undetected or at the limit detection for all breast cancer cell lines examined. Elevated levels of specific Nav1 isoforms is not a characteristic specific to basal-like cell lines since the luminal and estrogen receptor positive breast cancer cell lines MCF-7 and T47D (38, 39) had the highest levels of Nav1.9 and Nav1.4, respectively. Indeed, there was no clear relationship between the expression of a specific Nav isoforms and the molecular subtype of the breast cancer cell line or the expression of any specific biomarker (e.g. HER2 enriched or the estrogen receptor).

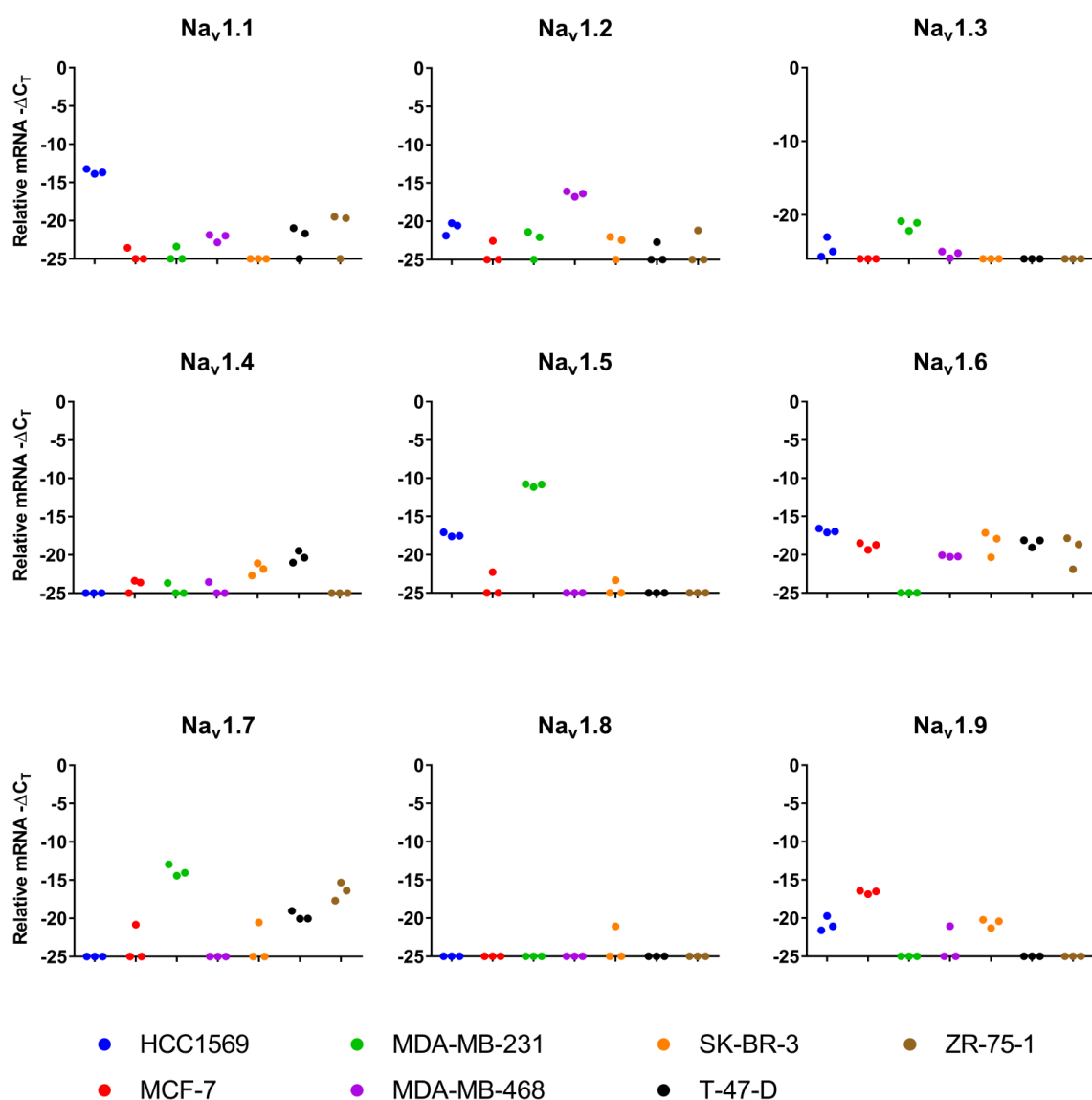


Figure 4: Levels of Nav1.1-1.9 mRNA in seven breast cancer cell lines. $-\Delta C_T$ values ($-C_T$ target- C_T 18S) from qPCR analysis of Nav isoforms in a panel of breast cancer cell lines. A more positive value is reflective of a greater level of target mRNA. Dots on the x-axis signify the target was beyond the designated limit of detection ($C_T > 35$) and was assigned a $-\Delta C_T$ value of -25. Each dot represents an independent biological replicate, ($n = 3$). See Table 1 for molecular subtypes and receptor status of the cell lines used.

Discussion

These studies suggest that basal-like breast tumours express significantly higher levels of TRPM8 compared to luminal A, B and HER2 enriched subtypes suggesting a possible role for TRPM8 as a therapeutic target or biomarker in breast cancer. However, TRPM8 seems to be undetectable in many breast cancer cell lines. Our studies using breast cancer cell lines that do not express TRPM8 suggest that the widely used TRPM8 inhibitor AMTB may exert effects via non-TRPM8 mechanisms in some models, specifically through inhibition Na_v s. Hence, AMTB like the non-selective TRPM8 activator menthol should be used with caution in studies of TRPM8 because of non-TRPM8 mediated effects (44, 45).

An association between TRPM8 and breast cancer was first evident in the initial reports of TRPM8 (previously known as Trp-p8), where TRPM8 levels were reported to be elevated in breast tumours compared to corresponding normal tissues (15). TRPM8 overexpression has also been reported in human breast ductal adenocarcinoma compared to adjacent non-tumoural tissue using RT-PCR and immunohistochemistry (46). Despite these reports and the importance of breast cancer subtypes (47, 48), there has been no published assessment of TRPM8 in the context of breast cancer molecular subtypes. Our studies suggest that elevated TRPM8 mRNA is a feature of basal breast cancers, which represent a subtype with significant overlap with triple negative breast cancer cancers (49), which have been identified as a subtype requiring new therapeutic approaches (9, 10). However, future assessment of TRPM8 in basal breast cancer may be challenging since we found that TRPM8 is undetectable in the basal-like MDA-MB-231 breast cancer cell line and was also undetectable or at the limit of detection in all the other breast cancers (luminal and basal-like) that we examined. This result is in contrast to other studies of TRPM8 in human breast cancer cell lines (21, 22). Clearly, our quantitative RT-PCR assay is distinct from both the endpoint PCR assay and western blots used in the studies of Chodon et al (21). Indeed, it is notable that the short 16 and 17 bp PCR primers used in Chodon et al's study to assess TRPM8 expression lack specificity to this gene as both primers bind to the mRNAs of several genes. Liu et al (22), reported a relatively consistently high level of TRPM8 protein by western blot in a panel of 6 breast cancer cell lines, although the antibody used was not specified. We have tried to resolve this disparity by examining RNA-Seq data from an MDA-MB-231 line cultured in a different laboratory. Analysis of sequencing runs from two independent samples with 13,925,285 and 40,037,205 aligned reads found totals of 0 and 3 sequencing reads, respectively mapping to TRPM8 (data not shown), suggesting that this gene is silent in MDA-MB-231 cells and raising questions about the specificity of the antibody used which

was interpreted as showing very robust expression of TRPM8 protein in this particular cell line (22).

Variations in the origin and batch of foetal bovine serum used in cell culture could also alter TRPM8 gene expression as has been reported for other genes (50). The relatively few studies of TRPM8 in breast cancer cell lines may be reflective of issues related to TRPM8 expression. The loss of TRPM8 in cultured breast cancer cell lines is not totally unexpected. Genes that have roles in proliferation, angiogenesis, migration and invasion can display very different expression profiles in 2D *in vitro* cell cultures compared to *in vivo* conditions (51-53), leading to differences in mRNA and protein levels between clinical samples and cell lines (54). In prostate cancer (where TRPM8 is highly expressed in androgen-dependent tumours (15, 28, 30, 55), TRPM8 mRNA levels in primary cell cultures of prostate tumours are reduced when cells are cultured for extended periods of time (> 20 days) (56). In any case, the absence of detectable levels of TRPM8 mRNA in breast cancer cells indicated that AMTB was not exerting its effects on the proliferation and migration of breast cancer cells via the TRPM8 ion channel in our studies. These findings highlight the need for careful validation of results from experiments using pharmacological modulators due to unknown off-target effects. Examples of off-target effects with other TRP channel inhibitors include the selective TRPV1 channel activator capsaicin, which can modulate Na_v and potassium channel function when used at high concentrations (micro – millimolar) (57, 58).

AMTB possesses several structural features which are recognised as important for the activity of local anesthetics at Na_v channels, such as a substituted benzene ring, an intermediate chain with amide linker, as well as a hydrophilic terminal. In addition, we have previously observed *in vivo* analgesic effects of AMTB that appeared to be mediated via inhibition of Na_v channels rather than TRPM8 (unpublished data). Accordingly, findings from our study indicate that AMTB (pIC₅₀ ~ 4.83 – 5.69 at Na_vs) is a more potent inhibitor of Na_vs (Na_v1.1-1.8) than lidocaine (IC₅₀ = 210 μM / pIC₅₀ ~ 3.67) (59). Further studies would be required to confirm inhibition of Na_v isoforms using electrophysiological approaches, and to assess whether AMTB also binds to the local anesthetic site on Na_v channels.

There was no obvious relationship between the expression profile of Na_v isoforms and common breast cancer subtype markers (e.g. estrogen receptor and HER2 overexpression). However, the basal breast cancer cell lines HCC1569 and MDA-MB-231 showed high mRNA levels for Na_v1.5

compared to the luminal breast cancer cell lines assessed. Studies assessing protein levels of Na_v channels in breast cancer cell lines would enhance our understanding of potential differences between breast cancer cell lines. Na_v s are normally found in excitable tissues (60) but have also been reported in cancer cells (61). Altered expression of Na_v s have been described in prostate (62), breast (43), lung (63), cervical (64), colon (65) and ovarian cancers (66). In many of these cancers, altered mRNA and/or protein expression correlates with metastatic /invasive potential (67). For example, $\text{Na}_v1.8$ is highly expressed in several prostate cancer cell lines (DU-145, PC-3 and PC-3M) and its expression correlates with more advanced pathologic stages of the disease (62) In breast cancer, the upregulation of $\text{Na}_v1.5$ and the neonatal splice variant of $\text{Na}_v1.5$ ($\text{nNa}_v1.5$) is linked to metastatic potential (43, 68). Indeed, the highly metastatic MDA-MB-231 breast cancer cell line (38, 39) has been reported to have greater levels of $\text{Na}_v1.5$ (~1,800 times higher) compared to the weakly metastatic MCF-7 cell line, which was consistent with our data (41, 69, 70). Moreover, $\text{Na}_v1.5$ levels appear lower in non-tumourigenic cells (41, 69, 70) and increased expression of $\text{Na}_v1.5$ mRNA is a feature of some breast tumours (71).

Conclusion

These studies provide evidence that some of the effects of AMTB are not mediated by TRPM8 but instead occur via inhibition of Na_v s. Despite a possible association between TRPM8 levels in basal breast cancers, the absence of TRPM8 in commonly used breast cancer cell lines may represent challenges in defining the applicability of TRPM8 as a therapeutic target in this breast cancer subtype.

Acknowledgments

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Conflicts of Interest

The authors declare that there are no conflicts of interest.

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