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The Utility of Single Nucleotide DNA Variations as Predictors of Postoperative Pain

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Abstract

Objectives: Genetic variation is an important contributor to postsurgical pain and thereby analgesia requirements. A description of the potential predictive power of genetic variants in pain should instruct improvements in pain management postoperatively. We set out to examine whether a set of genetic variants in pain related genes would show any association with actual pain outcomes in a typical surgical population.

Methods: A candidate gene study was carried out in 135 surgical patients with 12 DNA variants (single nucleotide polymorphisms or ‘SNPs’) in known or putative pain pathway genes to detect associations with postoperative pain - measured by a verbal rating score (VRS) and patient-controlled analgesia (PCA) usage rate. Standard PCR based molecular biology approaches were used.

Results: At 20-24h after surgery, patients with the 1032G/1032G variant pair for the A1032G variant of the potassium channel KCNJ6 gene had a slightly higher median VRS than those with 1032A/1032A or 1032A/1032G pairs (p=0.04; dominant genetic model). This small difference was most apparent in the orthopaedic surgery patients where the 1032G/1032G pair associated with VRS (median(interquartile range)) of 5(4-6) vs. 3(0.5-4) in 1032A/1032A or 1032A/1032G groups. For PCA, patients with 3435C/3435C or 3435C/3435T pairs for ATP-dependent efflux pump gene ABCB1 variant C3435T used PCA at a considerably higher rate of 0.89(0.07-1.66) mg.h⁻¹ compared with just 0.11 (0-0.52) mg.h⁻¹ for the 3435T/3435T pair (p=0.03; dominant model). A significantly higher usage rate was also detected for opioid receptor OPRM1 variant IVS2-691 with usage of 0.77(0.01-1.56) mg.h⁻¹ for the IVS2C/IVS2C or IVS2C/IVS2G group vs. 0.24(0-1.26) mg.h⁻¹ in the IVS2G/IVS2G group (p=0.04; recessive model).

Conclusion: While this study has identified some significant statistical associations the potential utility of the studied DNA variants in prediction of postoperative pain and patient-controlled opioid analgesia requirements appears to be quite limited at present.

Keywords: OPRM1; ABCB1; Postoperative; Pain; Morphine; Analgesia

Background

Pain is a complex trait influenced by psychological, social, physical and genetic factors (reviewed [1]). Of the various factors that influence postsurgical pain, genetic variation plays an important role, with many genetic variants contributing to the pain phenotype. Their cumulative small effects occur through alteration of protein expression level or amino acid sequence and thereby protein functions. Accordingly, DNA variants, in particular single nucleotide polymorphisms (SNPs), may produce differences in perception of acute pain [2] or the efficacy of postoperative analgesia [3].

A number of studies have identified genetic associations with acute pain. A survey of the literature for these associations highlights: 1) the ATP-binding cassette (ABC) superfamily, subfamily B p-glycoprotein 170 (ABCB1) gene encoding an ATP-dependent drug efflux pump involved in multiple drug resistance. ABCB1 is a major determinant of morphine bioavailability[4] and the 3435C allele of variant C3435T (rs1045642) in the gene associates with higher expression level and reduced morphine availability in the CNS. 2) The catechol-O-methyl transferase (COMT) gene encoding an enzyme that degrades several analgesic neurotransmitters, including noradrenaline and dopamine [7]. A well-studied variant in the gene, Val158Met (rs4680), encodes a valine-to-methionine variation that associates with reduced metabolic activity of the enzyme, as first reported by Scanlon and colleagues [8]. Reyes-Gibby [9] reports that cancer patients with the 158Val/158Val genotype required 63% more morphine for efficient pain relief compared to patients with the 158Met/158Met genotype. Another group has found that the 158Met variant was actually associated higher pain scores during painful post surgical procedures (with morphine analgesia) [10]. 5) The µ-opioid (OPRM1) gene encodes the µ-opioid receptor and is a very well-studied candidate gene for pain association [18,19]. Gene expression from the 118G allele of OPRM1 variant A118G (rs1799971) – which codes for an asparagine to aspartic acid residue change– produces a receptor with reduced agonist-induced receptor signalling efficacy [20]. Various studies have shown association of this variant with increased pain scores and/or opioid analgesia requirements after surgery [21-24]. 6) The potassium inwardly-rectifying channel subfamily J, member 6 (KCNJ6) gene encoding an ATP-activated channel (GIRK2) that closes with increased intracellular ATP causing membrane depolarization and voltage-sensitive activation. GIRK2 is activated by several G-protein coupled receptors including opioid

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receptors [26]. Nishizawa and co-workers [27] report that two SNPs in the gene - A1032G (rs2070995) and G-1250A (rs6517442) associate with postoperative rescue analgesia requirements. 7) The sodium channel protein type 9 subunit alpha (SCN9a) gene encodes a voltage-gated channel involved in nociception [29]. For SCN9a variant Arg1150Trp (rs6746030), the channel protein expressed from the gene containing the 1150Trp variant shows enhanced levels of depolarizing activation [30].

Other studies have usually looked for associations of single DNA variants with chronic pain conditions, or for pain thresholds in laboratory tests of noxious stimuli on human volunteers. In this study we selected a panel of genetic variants, some with established and some with no previously suggested pain association, and measured whether this broader selection of DNA variants might contribute significantly to the variation in postoperative pain seen in a broad-based representative clinical sample of day-to-day adult postsurgical patients. We aimed to determine whether any of the DNA variants had real clinical usefulness for predicting high postoperative pain.

**Methods**

**Clinical**

We recruited participants who were undergoing elective non-emergent surgery (expected duration <180 min) and were aged 18-65 yr, were competent to consent, were able to comprehend the VRS and were able to activate the PCA device. Subjects with weight >120 kg and/or BMI >35, a preoperative diagnosis of malignancy, epilepsy, pregnancy, a history of chronic opioid use or dependence or severe asthma (i.e. previously necessitating hospital admission), were excluded. Regional anaesthesia, neuraxial blockade or dependency or severe asthma (i.e. previously necessitating hospital admission), were excluded. Regional anaesthesia, neuraxial blockade and total intravenous anaesthesia was not permitted. Patients received standardised general anaesthesia consisting of an intravenous induction and total intravenous anaesthesia was not permitted. Patients received standardised general anaesthesia consisting of an intravenous induction using propofol (1-3 mg.kg⁻¹), muscle relaxant, and maintenance with an equilibrated concentration of 0.7-1.3MAC desflurane. The intraoperative opioid dosing regimen was individualised with a 1.5 mg/hr baseline, 0.5 mg/kg bolus dose of remifentanil and titration as required to achieve satisfactory patient comfort (1.5 mg doses, 5 min lockout interval, and 8 mg/hr maximum dose). Protocols received approval of the New Zealand Northern X regional ethics committee (NTX/09/06/047) with patients giving written informed consent.

Postoperative pain was quantified using a standard verbal rating scale (VRS see Table 1) as well as for morning after surgery (at 20-24hrs) with patients giving written informed consent.

**Selection of DNA variants (SNPs)**

In addition to the variants listed in the introduction (see points 1-7), and after examination of the literature, we chose to also examine: 1) an additional ABCB1 gene variant, T1236C, which has been associated with differential transport of various drug substrates of the ABCB1 efflux pump [6]; 2) an additional variant in OPRM1, IVS2-691, which may encode an altered receptor protein [3,25].

DNA extraction

A 1 ml venous blood sample was collected at the time of surgical closure and stored in 4 ml of a DNA preservation solution (5M GTC, 20 mM sarkosyl, 30 mM sodium citrate, 0.7% mercaptoethanol, pH 7). To extract the DNA, a 1 ml sample of this preparation was collected into a new tube and a 1/10th volume of 3 M sodium citrate and 0.5 ml of phenol-chloroform (pH 7) were added and the tubes centrifuged at 14K RCF for 15 min. The upper (aqueous) phase was collected and DNA precipitated by addition of an equal volume of isopropanol (AR grade), mixing and centrifugation at 14K RCF. The DNA pellet was washed in 70% ethanol and briefly air-dried before resuspension in between 50 and 200 µl of a storage buffer (TE buffer; 10 mM Tris, 1 mM EDTA, pH 8). DNA was quantified using a Nanodrop 2000 instrument (Thermo, NJ).

**Polymerase chain reaction – restriction fragment length polymorphism (PCR-RFLP)**

The first enzyme reaction, to make copies of the DNA of interest (PCR), was performed i-Star Taq polymerase (Intron Ltd, USA) by initial strand separation at 95°C for 2 min followed by 35 repeats of temperature cycling between 95°C 30 s, 60°C 30 s, 72°C 30 s, and a final extension step for 5 min at 72°C. 100 ng of DNA was used in each reaction. Gene annotations, SNP reference numbers, SNP codes used in this report, DNA primer sequences and details of restriction enzyme test are shown in Table 1. Reagents (DNA primers) and specific enzyme-based tests for the variants (namely the restriction fragment length polymorphism method) were designed by us using SNP Cutter (http://bioapp.psyched.uic.edu/SNP_cutter.htm) or WatCut (http://watcut.uwaterloo.ca/watcut/watcut/template.php) or taken from other published studies (as indicated in Table 1). The banding pattern from 10 µL of digested DNA products separated on a gel in an electrical field by electrophoresis at 100 V for 45 min was used to determine which DNA variants were present in each patient sample. Ten percent of the samples were analysed twice as a quality control.

**Study design and SNP data quality controls**

A minimum sample size of 128 individuals was required to achieve a statistical power of 0.9 for individual SNPs; assuming a medium effect size of 0.5, and a type I error rate of <0.05.

A test for suitability of the genetic tests (for Hardy Weinberg equilibrium) was carried out using an online calculator (http://oeg.org/software/hardy-weinberg.html). The measurement of pain intensity is complex. This is particularly evident in a plot of VRS against post-surgical PCA demands that shows many patients tolerating high VRS scores without increasing PCA usage (Figure 1). In this report we used statistical tests to measure potential influences of variants on VRS and PCA.

**Statistical Methods**

**SNP association analysis**

The VRS and PCA data were treated as ordinal. Briefly, for each SNP we analysed each genotype alone (i.e. the additive model, which
### Table 1: SNPs examined in this study: allele frequency, PCR primer sequences and RFLP test details.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Symbol</th>
<th>SNP</th>
<th>Allele1/ position* / Allele2</th>
<th>Type/change</th>
<th>MAF (%)†</th>
<th>PCR primers</th>
<th>Size (bp)</th>
<th>Diagnostic fragments (bp)</th>
<th>Enzyme</th>
<th>Design</th>
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<tbody>
<tr>
<td>ATP-binding cassette, sub-family B, member 1</td>
<td>ABCB1</td>
<td>rs1045642</td>
<td>C3435T</td>
<td>Synon.</td>
<td>C 43</td>
<td>F AGCTGCTTCTGATGGAAAGAT R TGTCAGCACACTTATCCTTCCTT</td>
<td>433</td>
<td>T 357 C 236</td>
<td>MboI</td>
<td>†</td>
</tr>
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<td></td>
<td></td>
<td>rs1128503</td>
<td>T1236C</td>
<td>Synon.</td>
<td>T 44</td>
<td>F TCTTTGTCACCTTACGAC GGCGCAAGACGCGTCGTC</td>
<td>502</td>
<td>C 361 T 416</td>
<td>HaeIII</td>
<td>§</td>
</tr>
<tr>
<td>Catechol-O-methyltransferase</td>
<td>COMT</td>
<td>rs4680</td>
<td>Val158Met</td>
<td>Non-synon.</td>
<td>A 39</td>
<td>F GTGGAGGCGCTGTAGTCCAGGAG R CAGGGATGGACAGGAGCACGCG</td>
<td>199</td>
<td>A 107 G 83</td>
<td>Tsp45I</td>
<td>†</td>
</tr>
<tr>
<td>Cytochrome P450, family 3, subfamily A, polypeptide 4</td>
<td>CYP3A4</td>
<td>rs2242480</td>
<td>C20230T</td>
<td>Intronic</td>
<td>T 33</td>
<td>F ACCCGGTGTCAGCAGAGAAGCT R RTAGAAAAGCGAGAACGAGCC</td>
<td>284</td>
<td>C 216 T 264</td>
<td>Rsal</td>
<td>‡</td>
</tr>
<tr>
<td>Cytochrome P450, family 3, subfamily A, polypeptide 5</td>
<td>CYP3A5</td>
<td>rs776746</td>
<td>A6986G</td>
<td>Splice-3</td>
<td>A 3</td>
<td>F GCATAGGAGATCCACGTATCT R TGGTCACAACGGGAAAGTA</td>
<td>118</td>
<td>G 97 A 118</td>
<td>Rsal</td>
<td>‡</td>
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<tr>
<td>Neurobeachin1</td>
<td>NBEA</td>
<td>rs7990537</td>
<td>A11771G</td>
<td>Intronic</td>
<td>G 28</td>
<td>F CCCCTGATGTGTTTGAACCTG R TTTCTTAGATGCGCTTACTT</td>
<td>433</td>
<td>A 433 G 332</td>
<td>BstII</td>
<td>†</td>
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<tr>
<td>Opioid Receptor, mu 1</td>
<td>OPRM1</td>
<td>rs1799971</td>
<td>A118G</td>
<td>Non-synon.</td>
<td>G 19</td>
<td>F TCACTTTGTCACCTGATAGCGC R TGGACGGAAGTTTCGCAAGAG</td>
<td>190</td>
<td>A 180 G 158</td>
<td>BstUI</td>
<td>†</td>
</tr>
<tr>
<td></td>
<td></td>
<td>rs2075572</td>
<td>IVS2-691</td>
<td>Intronic</td>
<td>G 40</td>
<td>F TACGTCTGTGCAAGGCTAAAGAT R CCCAGTACCGGTGGATGAGA</td>
<td>154</td>
<td>G 154 C 134</td>
<td>MboI</td>
<td>†</td>
</tr>
<tr>
<td>Potassium inwardly-rectifying channel, subfamily J, member 6</td>
<td>KCNJ6</td>
<td>rs2070995</td>
<td>A1032G</td>
<td>Synon.</td>
<td>A 20</td>
<td>F TAGAGGACCCTCCCTGAGACT R CGGAACATCGACGACTGTTT</td>
<td>298</td>
<td>A 197 G 175</td>
<td>Mspl</td>
<td>†</td>
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<td></td>
<td></td>
<td>rs6517442</td>
<td>G-1250A</td>
<td>Upstream</td>
<td>G 24</td>
<td>F TGCCATATCTCGTGTCTGTT R CAGTCATTTTGGAGCAGCA</td>
<td>203</td>
<td>G 203 A 161</td>
<td>HindII</td>
<td>‡</td>
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<tr>
<td>Potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1</td>
<td>KCNS1</td>
<td>rs734784</td>
<td>Ile489Val</td>
<td>Non-synon.</td>
<td>G 40</td>
<td>F AGTTGAGGACCTGCTGAGCGC R ATCATCTGAGGTTGAGGGAGAG</td>
<td>137</td>
<td>A 137 G 115</td>
<td>BstUI</td>
<td>†</td>
</tr>
<tr>
<td>Sodium channel, voltage-gated, type IX, alpha subunit</td>
<td>SCN9A</td>
<td>rs6874030</td>
<td>Arg1150Trp</td>
<td>Non-synon.</td>
<td>A 11</td>
<td>F GTATTCTCTAGTGTTCCACAGATT R TGAAGAAGAGAGCGATCACC</td>
<td>244</td>
<td>A 244 G 172</td>
<td>Rsal</td>
<td>‡</td>
</tr>
</tbody>
</table>

Lower case in primer sequences indicates bases changed to alter restriction sites. Key: Type codes with protein level consequence: Synon.-synonomous, - no amino acid change; Non-synon. - non-synonymous, amino acid change as indicated; Intronic – variant occurs in a non-coding portion of the gene; upstream – in region upstream (5′) of the gene; Splice-3 – causes transcript splice variation in 3′ of the gene; IVS2 – within intron 2 of the gene (full SNP code:IVS2-691 G>C); UTR-3′ - 3′ untranslated region. † Minor allele frequencies (MAF) are from http://www.ncbi.nlm.nih.gov/projects/SNP/. Key chromosome positions are from HumRef sequence and transcript positions are from Genbank NM reference sequences. Primers and test design † (us), ‡[44], §[45], ¶[46], **[48].

**Figure 1:** Scatterplots of VRS against PCA usage for all patients: A) VRSawake vs. PCAmg.h-1; and B) VRSd1A vs. PCAmg.h-1. Line of best fit is shown. Dots represent individual patients.
assumes that heterozygous individuals have a phenotype midway between the two homozygotes and also grouped by the presence of either minor (less frequent) or major (more frequent) alleles (dominant or recessive models). For these models, where ‘d’ is the minor allele and ‘D’ is the major allele, the recessive model compared values from individuals with ‘dd’ against ‘D/D and D/d’ genotypes and the dominant model compared values from individuals with ‘D/D’ against ‘D/d and dd’ genotypes. This approach avoids assumptions regarding mode of inheritance and limits the chance of missing potentially interesting associations and was similar to a method described previously [32,33].

Nonparametric statistical approaches were used including: 1) the 1-way ANOVA (with Kruskal-Wallis Z test) to examine the independent effect of all non-SNP variables on VRS or PCA, and 2) the general linear model (NCSS software) to measure associations between SNPs and VRS or PCA. For all tests a p-value <0.05 was considered statistically significant.

Results

A total of 135 patients from two hospitals in the central North Island of New Zealand (Waikato DHB and Northshore DHB) were recruited into the study. Demographic data, surgery type and duration, and median VRS data are presented in Table 2. No statistically significant associations were found between any pain score or PCA usage and either age, ethnicity or gender. However there was a strong association between VRSawake and surgery type (p < 0.001). To incorporate the influence of surgery type it was included in all SNP association tests for all outcomes using the general linear model (up to 2-way). Hence p values reported here are for the SNP-outcome with consideration of surgery type.

Some samples (<1%) failed to give a conclusive DNA test result and were excluded from further analysis. One NBEA variant (rs9565317) selected for inclusion in the study did not pass genetic testing (Hardy-Weinburg equilibrium) and was removed from the DNA variant panel. All results are expressed as median(interquartile range) unless otherwise stated.

Association Analysis

VRSawake

No statistically significant SNP associations were found for VRSawake.

VRSd1A

An association between KCNJ6 A1032G variant and VRSd1A was found (Table 3). Patients with the 1032G/1032G variant pair had higher median VRS scores when compared to patients with the 1032A/1032A or 1032A/1032G variant pairs (p=0.04; dominant model) (Table 3). The difference in VRS score was only apparent when the actual surgery type was examined (Table 3) and this weak association showed a VRS range of between 2 and 3 for 1032A/1032A or 1032A/1032G pairs and 2.3 to 5 for 1032G/1032G pairs (Table 4). No significant associations were found for any other DNA variants and VRSd1A scores examined.

Patient-controlled analgesia usage rate (PCA_{mg.h^{-1}})

A significant association between PCA usage rate and ABCB1 gene variant C3435T was found (Table 3). For all surgery types individuals with 3435C/3435C or 3435C/3435T genotypes for C3435T consumed at a rate eight times faster in the same period - with median usage of 0.89 (0.07-1.66) compared to just 0.11 (0.0-0.52) mg.h\(^{-1}\) in patients with the 3435T/3435T genotype (p<0.03; dominant model) (Table 5).

Also, for all surgery types combined, patients with the IVS2C/IVS2C or IVS2C/IVS2G genotypes for the OPRM1 variant IVS2-691 had markedly higher median PCA usage rates of 0.77(0.01-1.56) compared to 0.24(0.0-1.26) mg.h\(^{-1}\) in patients with the IVS2G/IVS2G variant pair (Table 5). This association was weakest in the gynaecological patient group where patients with the IVS2C/IVS2C and IVS2C/IVS2G genotype had just a 10% higher PCA\(_{mg.h^{-1}}\) than those with the IVS2G/IVS2G variant pair.

Discussion

The main findings of this study were that, in a broad-based sample of typical postoperative patients, a DNA variant (SNP A1032G in the KCNJ6 gene) was associated with 20-24 h postoperative pain and two DNA variants (SNPs C3435T in ABCB1 and IVS2-691 in OPRM1) were associated with a higher PCA usage rate. As noted above, surgery type had a strong influence on VRS – this was statistically significant for VRSawake - and surgery type was included in our statistical models.

We found that patients with two copies of the 1032G variant (i.e. 1032G/1032G) in KCNJ6 had higher VRSawake when compared to individuals with the variant pairs 1032G/1032A or 1032A/1032A but this was only evident with consideration of the individual surgery types. Nishizawa [27] did not see any association between this variant and pain score but reported an association between the 1032A DNA variant and increased postoperative rescue analgesia requirements. They explain their result by stating that the alternative 1032G variant...
seems to confer an improved efficiency in mediating the transmission of opioid signaling compared with the 1032A variant. Another study found association between eight KCNJ6 variants and postoperative oral analgesia usage but pain scores were not tested (nor were the A1032G or G1250A variants) [34]. The exact function of these genetically synonymous KCNJ6 variants is currently unknown but others suggest that the A1032G variant may regulate gene usage levels via mRNA secondary structure, with lower gene expression in individuals with the IS2G variant pairs had median PCAmg.h-1 pain levels more than two-fold higher than those with the IS2G/IS2G variant pairs across all surgery types. We could not find other studies linking the variant to variation in either postoperative pain or PCA requirements. However, the variant appears to confer an improved efficiency in mediating the transmission of opioid signaling compared with the 1032A variant [27].

The association we describe between the ABCB1 variant 343ST and lower PCA usage rate reflects the findings of another recent study that reports lower PCA requirements in individuals homozygous for the 343ST variant [5]. This effect is very likely due to the higher expression of the efflux pump that is driven from the 343ST variant [35,36]. Individuals carrying this allele therefore have a stronger barrier to opioids at the blood brain barrier so that less of the drug is available at receptors in the CNS [37] and a relatively higher PCA dose is required.

For the OPRM1 variant IVS2-691, patients with IS2C/IS2C or IS2C/IS2G variant pairs had median PCAmg.h-1 pain levels more than two-fold higher than those with the IS2G/IS2G variant pairs across all surgery types. We could not find other studies linking the variant to variation in either postoperative pain or PCA requirements. However, the variant has been studied for effects on oral morphine efficacy in cancer patients although no association was found [38] and another study reported no association between the variant and morphine pharmacodynamics using plasma samples from healthy volunteers [39]. The IVS2-691 variant may exert the observed effects by causing variation in slicing patterns of mRNA transcripts or may be simply ‘tagging’ a nearby variant that actually confers some functional effect and is simply inherited during meiosis with the IVS2-691 variant due to proximity on the same chromosome.

**Possible clinical applicability**

In our patient cohort different DNA variants showed different associations for VRS (i.e. with KCNJ6 gene variant) and PCA (i.e.
with \textit{ABCB1} and \textit{OPRM1} variants). For VRS, the association with the \textit{KCNJ6} variant was weak and is unlikely to have much clinical utility. PCA usage is a composite endpoint that involves a complex relationship including genetic effects acting on the intensity of the pain experienced by the patient and pharmacogenetic effects on the perceived potency of the morphine. Whether preoperative knowledge of genotypes that associated with PCA, for example the 3435T/3435T variant pair for \textit{ABCB1} gene (which had a >8-fold lower PCA usage rate and was found in around 26% of all study subjects), would allow the avoidance of postoperative PCA prescription is as yet untested. Such possible association for the \textit{KCNJ6} variant was weak and is unlikely to have much clinical utility.

### Questions about the neuroscience of postoperative pain

While the \textit{ABCB1} 3435C variant association with higher PCA usage rate for certain types of surgery agree with previous studies, the association for the \textit{KCNJ6} A1032G variant with VRS was unexpected in light of evidence reported by Nishizawa [27]. Although it is possible that some associations we found evidence for may be statistical artefacts, we believe that our results call into question the simplistic pharmacokinetic and pharmacodynamic explanations of the genetic influences on pain and highlights the paucity of our knowledge of the interactions between nociceptive and pharmacological mechanisms.

One notable finding in our study was the lack of any association between the \textit{OPRM1} A118G variant and any of the clinical outcomes. This may be due to a masking of the association due to the low percentage of Asian patients in the study (around 8%). Around 15% of the Asian population are minor allele homozygous for the variant (i.e. have the variant pair A118G/118G) compared to <2% in the Caucasian population. However, other studies have also failed to detect any association with the A118G variant and postoperative pain (VRS). Janicki [42] did not find any association for 118G with either pain score or morphine requirements following surgery and De Gregori [43] did not detect any association with PCA in a similar study (they did not examine pain score data).

### Conclusion

We found evidence for various associations between DNA variants in \textit{ABCB1}, \textit{OPRM1}, and \textit{KCNJ6} and postoperative pain and/or PCA usage. However, these results would appear to be more of scientific than clinical interest because the strength of the correlations do not appear to be strong enough to form the basis for useful clinical prediction. Importantly, we found no pain association for examined variants in \textit{COMT}, \textit{CYP3A4}, \textit{CYP3A5}, \textit{KCN5}, \textit{NBEA} and \textit{SCN9a} genes. This suggests that the particular variants studied in these genes are unlikely to have value in prediction of postoperative pain in a typical population of elective surgery patients. Future studies should focus on defining a more useful panel of DNA variants for reliable prediction of postoperative pain.

<table>
<thead>
<tr>
<th>Gene</th>
<th>SNP</th>
<th>Model</th>
<th>Surgery</th>
<th>Groups</th>
<th>VRS (IRQ)</th>
<th>Count</th>
<th>p value</th>
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<tr>
<td>\textit{ABCB1}</td>
<td>C3435T</td>
<td>Dom.</td>
<td>All</td>
<td>3435C/C or 3435C/T</td>
<td>0.89(0.07-1.66)</td>
<td>100</td>
<td>0.02</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>3435T/3435T</td>
<td>0.11(0-0.52)</td>
<td>36</td>
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<td>General</td>
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<td>Ortho</td>
<td></td>
<td></td>
<td></td>
<td>3435C/C or 3435C/T</td>
<td>1.22(0.19-1.94)</td>
<td>48</td>
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<tr>
<td>OPRM1</td>
<td>IVS2-691</td>
<td>Rec.</td>
<td>All</td>
<td>IVS2C/IVS2G or IVS2C/IVS2G</td>
<td>0.77(0-1.156)</td>
<td>96</td>
<td>0.03</td>
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<td>IVS2G/IVS2G</td>
<td>0.24(0-1.26)</td>
<td>40</td>
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<td>General</td>
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<td>IVS2C/IVS2C or IVS2C/IVS2G</td>
<td>0.69(0.03-1.26)</td>
<td>36</td>
<td>0.04</td>
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<td>Gynae.</td>
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<td>IVS2C/IVS2C or IVS2C/IVS2G</td>
<td>0.24(0-1.05)</td>
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<tr>
<td>Ortho</td>
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<td></td>
<td></td>
<td>IVS2C/IVS2C or IVS2C/IVS2G</td>
<td>0.98(0-1.81)</td>
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<td></td>
<td>IVS2G/IVS2G</td>
<td>0.89(0-1.92)</td>
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<td>IVS2G/IVS2G</td>
<td>0.06(0-1.42)</td>
<td>11</td>
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<td></td>
<td>IVS2G/IVS2G</td>
<td>0(0-1)</td>
<td>5</td>
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</tr>
</tbody>
</table>

Dom. – dominant model; Rec. – recessive model. Underlined p value is for general linear model with 'surgery type' included. Table 4: Details of significant association found between SNPs and VRS.

Table 5: Significant associations found between SNPs and PCAmg.h \textsuperscript{1} with dominant or recessive models.
Acknowledgement

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Authors contributions

GJ selected relevant genes for the study, coordinated sample collection and processing, designed and carried out the RFLP tests and drafted the manuscript. CL assisted in design study, applied for ethics committee approval, recruited Waikato DHB patients, collated drug usage information, interviewed patients for relevant pain score information and helped to draft the manuscript. HJ helped design some RFLP tests, extracted DNA from patient samples and performed genotyping for some variants. MC and MK collected and collated Northshore DHB samples, assisted in study design and commented on the manuscript. RC participated in the design of the study and in data analysis. JS had the initial idea for the study, participated in its design and coordination and helped to draft the manuscript. All authors read and approved the final manuscript.

References


