

### **REVIEW**

# Pharmacogenetics of new analgesics

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Patient phenotypes in pharmacological pain treatment varies between individuals, which could be partly assigned to their genotypes regarding the targets of classical analgesics (OPRM1, PTGS2) or associated signalling pathways (KCNJ6). Translational and genetic research have identified new targets, for which new analgesics are being developed. This addresses voltage-gated sodium, calcium and potassium channels, for which SCN9A, CACNA1B, KCNQ2 and KCNQ3, respectively, are primary gene candidates because they code for the subunits of the respective channels targeted by analgesics currently in clinical development. Mutations in voltage gated transient receptor potential (TRPV) channels are known from genetic pain research and may modulate the effects of analgesics under development targeting TRPV1 or TRPV3. To this add ligand-gated ion channels including nicotinic acetylcholine receptors, ionotropic glutamate-gated receptors and ATP-gated purinergic P2X receptors with most important subunits coded by CHRNA4, GRIN2B and P2RX7. Among G protein coupled receptors, δ-opioid receptors (coded by OPRD1), cannabinoid receptors (CNR1 and CNR2), metabotropic glutamate receptors (mGluR5 coded by GRM5), bradykinin B<sub>1</sub> (BDKRB1) and 5-HT<sub>1A</sub> (HTR1A) receptors are targeted by new analgesic substances. Finally, nerve growth factor (NGFB), its tyrosine kinase receptor (NTRK1) and the fatty acid amide hydrolase (FAAH) have become targets of interest. For most of these genes, functional variants have been associated with neuro-psychiatric disorders and not yet with analgesia. However, research on the genetic modulation of pain has already identified variants in these genes, relative to pain, which may facilitate the pharmacogenetic assessments of new analgesics. The increased number of candidate pharmacogenetic modulators of analgesic actions may open opportunities for the broader clinical implementation of genotyping information.

#### Abbreviations

AMPA,  $\alpha$ -amino-3-hydroxyl-5-methyl-4-isoxazole-propionate; CB<sub>1</sub>, cannabinoid receptor 1; CB<sub>2</sub>, cannabinoid receptor 2; COX-2, prostaglandin endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase); FAAH, fatty acid amide hydrolase; Il-1, interleukin 1; MAO, monoamine oxidase; mGluR5, metabotropic glutamate receptor 5; nAChR, neuronal nicotinic acetylcholine receptors; Na<sub>v</sub>, voltage-gated sodium channels; NGF, nerve growth factor; NMDA, N-methyl-D-aspartic acid; NR2B, NR2B Subunit of the NMDA receptor; P2X7, purinergic receptor P2X, ligand-gated ion channel, 7; TRPV1, transient receptor potential cation channel, subfamily V, member 1; TRPV3, transient receptor potential cation channel, subfamily V, member 3

### Introduction

The phenotype of patients receiving pain therapy displays a large inter-individual variability that could be partly assigned to the patients' genotype (Lötsch and Geisslinger, 2006; Lötsch et al., 2009a). Pharmacogenetic influences affecting the pharmacodynamic actions of marketed analgesics have been mainly found among the genes coding for their main targets

(*OPRM1*, *PTGS2*) or components of their respective signalling pathways (*KCNJ6*), in a few additional genes (*COMT*, *MC1R*) partly affecting the function of the main analgesic targets, and in genes important for the pharmacokinetics of some classical analgesics (*CYP2D6*, *ABCB1*) (Lötsch *et al.*, 2009a).

With the targets of classical analgesics, that is, opioid receptors and cyclooxygenases, and of substances labelled as co-analgesics, that is, the  $\alpha_2\delta$  subunit of voltage gated calcium

channels, NMDA channels, sodium channels, noradrenaline or 5-HT transporters, there have been remarkable successes in treating pain. However, chronic pain has remained a primary healthcare problem listed by the World Health Organisation. Consistent with the multifactorial nature of pain (Julius and Basbaum, 2001), translational and genetic research have identified several new analgesic targets (Backonja and Woolf, 2010), for which analgesics are being developed (Table 1). From a pharmacogenetic point of view, this will increase the number of candidate genetic modulators of clinical analgesic actions, opening a chance of broader clinical use of genotyping information for pre-selection of analgesics.

The present overview summarizes potential pharmacogenetic modulators of those new analgesic targets for which substances have reached at least the clinical development phase 1. This avoids an inflated set of all possible targets that have not yet left basic research and their pharmacogenetic implementations are not yet acute. A complete set of all targets of analgesics that are presently considered as promising can, therefore, be found elsewhere (Marchand et al., 2009; Rodger, 2009). Due to corporate strategies and partially pending results, this survey does not provide a uniform picture of which compounds will be chosen for further development. Other new analgesics targeting the same structures as classic analgesics are excluded because this pharmacogenetic information has been discussed elsewhere (Lötsch et al., 2009a). Several novel analgesics were identified by a survey of online sources, including the http://www.clinicaltrials.gov database, company websites, presentations and press releases. As most of the new analgesics are nevertheless not yet broadly available, direct information about a pharmacogenetic modulation of their actions is often lacking. Nevertheless, pharmacogenetics can start from knowledge gathered in other context, often neuro-psychiatric disorders, where functional variants in the same genes have been already identified.

# Pharmacogenetics of pain and analgesia in clinical practice

Pharmacogenetics are often expected to provide guidance for clinical drug therapy. This has been successful in several fields such as cancer therapy (Gonzalez-Angulo *et al.*, 2010) or anticoagulation (Caraco *et al.*, 2008), but pain therapy is not yet among them. The utility of genotyping information in clinical analgesia has been viewed from being broadly optimistic (Argoff, 2010) to pessimistic (Mogil, 2009); however, even most promising results on a modulation of common human analgesia are presently unable to provide a comprehensive prediction of individual analgesic response in the clinical setting (Lötsch *et al.*, 2009c; Walter and Lötsch, 2009). Often, phenotypes could be only retrospectively associated with genotypes. This qualifies genotypes as risk factors and provides explanations for extreme phenotypes.

However, a prospective clinical utility has not been proven, as for example for *CYP2C9* genotyping for warfarin anticoagulation (Caraco *et al.*, 2008), neither are genotype-based analgesic therapy plans broadly used in clinical practice. Currently, most genotyping information has been associated with opioid requirements. Since opioids can be adequately efficiently titrated in most patients, there is no

major advantage of genotyping information, beyond explanations for extreme dosing demands.

With the new, in-development, analgesics involving many new targets, the pharmacogenetics of pain and analgesia may be employed as guidance for the choice of the optimum analgesic. This is currently only marginally possible, as for example basing the non-selection of codeine on the CYP2D6 genotype (Eckhardt  $et\ al.$ , 1998), the selection of a  $\kappa$ -opioid agonist on the MC1R genotype and sex (Mogil  $et\ al.$ , 2005) and the non-selection of a coxib on the PTGS2 genotype (Lee  $et\ al.$ , 2006). Most of the new drugs are being developed against neuropathic pain and it is unlikely that a patient would receive all of these. Pharmacogenetic information may, therefore, be of great value in choosing the optimum analgesics, along with non-genetic, for example disease-specific, guidance.

# Targets of new analgesics and their genetic modulation

### Ion channels

Ion channels are integral membrane proteins that contain pathways through which ions can flow (Di Resta and Becchetti, 2010). They are considered likely targets in the treatment of pain (Mathie, 2010).

Voltage-gated sodium channels. Voltage-gated Na+ (NaV) channels are key mediators of neuronal function and essential for neuronal excitability (Mantegazza et al., 2010). They are the main targets of local anaesthetics. From a genetic perspective, the 1.7 subunit seems to play a major role in pain. Specifically, the complete inability to sense pain in otherwise healthy members of three consanguineous families from northern Pakistan was mapped as an autosomal recessive trait caused by a loss-of-function variant in the SCN9A gene (Cox et al., 2006). This gene encodes the α-subunit of the voltage-gated sodium channel, Na<sub>v</sub>1.7. In the three families, three distinct homozygous SCN9A nonsense mutations (S459X, I767X and W897X) were identified. In accompanying whole-cell voltage clamp experiments in HEK293 cells expressing mutant Na<sub>v</sub>1.7, voltage-gated Na<sup>+</sup> currents were no greater than the background level. Additional very rare SCN9A variants have been added to the causes of this extreme phenotype (Nilsen et al., 2009).

The same gene also exhibits increased-function mutations, which cause the rare opposite phenotype erythromelalgia (Norbury et al., 2007; Choi et al., 2010) consisting of episodic symmetrical red congestion, vasodilatation and burning pain in the feet and lower legs. For example, a child with severe pain had a Na<sub>v</sub>1.7I234T mutation that induces a shift of -18 mV in the voltage-dependence of activation, accelerated time-to-peak, slower deactivation and enhanced responses to slow ramp depolarizations, with a -21 mV shift in the voltage-dependence of slow-inactivation (Ahn et al., 2010). Aside from these very rare genotypes, more frequent functional variants may modulate the pain phenotype of average carriers. The variant alleles rs6746030 A (Reimann et al., 2010) (frequency in Caucasians 9.7%) and rs41268673 T (Samuels et al., 2008) (frequency 1.4%) were reported as being associated with higher than average pain sensitivity.



### Table 1

Compounds for which analgesia is the main clinical target, or at least among clinical indications, and which address a molecular target that has not been addressed by classical available analgesics or co-analgesics, or only as a pleiotropic effect, and which have reached at least clinical phase 1 in their development. The molecular targets and their coding genes are given as derived from publicly available information. Most substances are being developed for neuropathic pain

Compound	Company	Target	Gene	Comments
Ralfinamide	Newron	Na <sub>v</sub> 1.7, (and N-type calcium channels, NMDA)	SCN9A (CACNA1B, see below)	Missed primary endpoint (5/2010)
Lacosamide	UCB	Na <sub>v</sub> 1.8, 1.7 and 1.3	SCN10A, SCN9A, SCN3A	
MK-6721 / NMED160	Neuromed	N-type calcium channels	CACNA1B	Suspended in 2007
Ziconotide	Azur Pharma			Approved in 2004
ACV1	Metabolic Pharmaceuticals			
Retigabine	Valeant	KCNQ/Kv7 potassium channels	KCNQ2, KCNQ3	
NGD8243 (MK-2294)	Ligand	TRPV1 channel	TRPV1	
GRC-6211	Glenmark			Partner suspended tri in 2008
AMG986	Amgen			
AMG8562 (back-up)	Amgen			
AZD1386	AstraZeneca			
NGX-4010	NeurogesX			
ABT 102	Abbott			
SB 705498	GlaxoSmithKline			
NGX-1998	NeurogesX			
MK2295 (BGD8243)	Neurogen/Merck			
NGX-4010	NeurogesX			
adlea	Anesiva			
GRC-15300	Glenmark	TRPV3 channel	TRPV3	
Tezampanel / NGX426 = oral prodrug)	TorreyPines/Raptor	AMPA/kainate receptors	GRIA1-4/GRIK1-5	
Indantadol (CHF-3381, V-3381)	Vernalis	NMDA receptor, MAO	GRIN1, GRIN2A-D, GRINA, MAOB	Suspended 5/2010
CNS-5161	Paion/ERGOMED	NMDA receptor	GRIN1, GRIN2A-D, GRINA	Suspended 12/2009
RGH-896	ForestLabs	NR2B receptor subunit	GRIN2B	Phase 2 failed 6/2010
TC6499	Targacept/GSK	nAChR ( $\alpha_4/\beta_2$ ) receptor	CHRNA4	
ABT-594	Abbott			
ABT-894	Abbott/NeuroSearch			Discontinued 2009
EVT 401	Evotec	P2X7 receptor	P2RX7	
CE-224	Pfizer			
CE-535	Pfizer			
GSK1482160	GSK			
ADL5859	Adolor/Pfizer	δ–opioid receptor	OPRD1	Failed in phase 2
ADL5747	Adolor/Pfizer			Failed in phase 2
PF-4856880	Pfizer			
PF-4856881	Pfizer			

**Table 1** *Continued* 

Compound	Company	Target	Gene	Comments
IP751	Endo (Former Indevus)	CB <sub>1</sub> receptor/COX-2/II-1	CNR1, PTGS2, IL1A, IL1B	
KDS2000	Kadmus (aquired by Organon)	CB <sub>1/2</sub> receptor	CNR1, CNR2	
AZD1940	AstraZeneca			Discontinued
Sativex	GW Pharmaceuticals /Otsuka			Approved
SAD 448 /SAD 378	Novartis			
GRC-10693	Glenmark	CB <sub>2</sub> receptor	CNR2	
GW842166	GlaxoSmithKline			
PRS-211,375 (Cannabinor)	Pharmos			
ADX10059	Addex	mGluR5 receptor	GRM5	Terminated 12/2009 due to liver toxicity
AZD2066	Astra Zeneca			
AZD2516	AstraZeneca			
LY545694	Lilly			
SSR 240612	Sanofi-Aventis	Bradykinin B <sub>1</sub> receptor	BDKRB1	
F-13640 / Befiradol	Pierre Fabre	5-HT <sub>1A</sub> receptor	HTR1A	
Tanezumab	Pfizer	NGF	NGFB	Suspended 6/7, 2010
REGN 475	Regeneron/sanofi			
MEDI-578	AstraZeneca/MedImmune			
PG110	PanGenetics/Abbott			
losmapimod	GSK	p38 kinase	MAPK14	
PF-4457845	Pfizer	FAAH	FAAH	
V158866	Vernalis			

While these genetic changes have attracted the interest of pain researchers so far, the translation of the results of genetic research into drug development makes them immediate candidate variants for a pharmacogenetic modulation of  $Na_v1.7$  blocking analgesics. Carriers of increased-function variants might particularly benefit from  $Na_v1.7$  inhibitors because this would be a selective cure for paroxysmal pain (Fertleman *et al.*, 2006). The consequences of carrying decreased-function variants are theoretically possible in both directions but could be easily assessed.

*Voltage-gated calcium channels.* Members of this ion channel family contain  $\alpha_2\delta$ ,  $\beta$  and  $\gamma$  subunits, and play a role in neuronal excitation. The  $\alpha_2\delta$  subunit of L-type calcium channels is the target of the established co-treatments for neuropathic pain, gabapentin and pregabalin (Perret and Luo, 2009). Newer developments such as ziconotide (Schmidtko *et al.*, 2010), the synthetic form of the hydrophilic conopeptide  $\omega$ -MV<sub>II</sub>A found in the venom of the Pacific fish-hunting snail *Conus magus* (Olivera, 2006), target, with high affinity, the  $\alpha_{\rm IB}$  subunit of N-type voltage-sensitive calcium channels. These calcium channels are also key players in chronic pain (Swayne and Bourinet, 2008). They are coded by the *CACNA1B* gene and expressed at the presynaptic terminals of primary afferent neurons that end in the dorsal horn of the spinal cord

(Gohil *et al.*, 1994), an area playing a key role in nociceptive signal transmission. *CACNA1B* gave an above-threshold signal in a genome-wide association study of the risk of schizophrenia (Moskvina *et al.*, 2009), and the gene was deleted in 16 cases of schizophrenia (Glessner *et al.*, 2010).

Voltage-gated potassium channels. The inwardly rectifying potassium channel K<sub>IR</sub>3.2, a two-transmembrane-onepathway potassium channel, is involved in opioid signalling on postsynaptic inhibition (Mitrovic et al., 2003) and mediates a significant component of analgesia (Marker et al., 2004). Delayed rectifying neuronal KCNQ channels (KCNQ2-5) have homologies with cardiac channels involved in long QT syndrome and play a role in benign idiopathic neonatal epilepsy or congenital deafness (Gribkoff, 2008). These slowly inactivating channels are also expressed at the postsynaptic membrane of small diameter nociceptive nerve endings (Brown and Passmore, 2009) and play a key role in the control of the excitability of nociceptors (Passmore et al., 2003). Potassium channels are considered as targets in several CNS diseases that involve neuronal hyperexcitability such as migraine, epilepsy or neuropathic pain (Wua and Dworetzky, 2005). KCNQ<sub>2/3</sub> are not new analgesic targets as the wellknown flupirtine has been recognized primarily to exert its analgesic actions via opening of these potassium channels



(Ilyen *et al.*, 2002). The principle has been recently taken up for the development of new analyseics (Fritch *et al.*, 2010). Flupirtine has not yet been analysed for pharmacogenetic variability. Genetic modulations regarding *KCNQ2* or *KCNQ3* are known as channelopathies causing hereditary epilepsy (Schroeder *et al.*, 1998; Singh *et al.*, 1998).

Voltage-gated transient receptor potential (TRPV) channels. Members of this cation channel superfamily play critical roles in sensory physiology such as in vision, thermosensation, olfaction, hearing and touch (Montell, 2005). These receptors are activated by capsaicin (the pungent ingredient of hot peppers), protons and heat (>43°C), and are expressed at nociceptors and in pain relevant brain areas (Steenland et al., 2006). This stimuli are employed in experimental pain models using either directly heat and capsaicin (Petersen and Rowbotham, 1999) or producing protons via short pulses of gaseous CO<sub>2</sub> applied to the nasal mucosa, where protons are generated by the action of carbonic anhydrase (Kobal, 1985). A further family member, TRPV3, activated at temperatures of 22-40°C, is also expressed at sensory nerve endings (Eid and Cortright, 2009). Aside from these heat receptors, the TRP family includes cold receptors, among which TRPA1 and M8 have been most often associated with pain. TRPA1 is excited by cold stimuli below 15°C (Story et al., 2003), whereas TRPM8 channels are stimulated by cold between 8 and 28°C (McKemy et al., 2002). TRPM8 is also activated by cooling compounds such as menthol (Peier et al., 2002), while TRPA1 channels are additionally activated by pungent chemicals such as isothiocyanates (horseradish, mustard), cinnamaldehyde (cinnamon) and allicin (garlic) (Patapoutian et al., 2009) or cannabinoids (Jordt et al., 2004). New analgesics are either antagonists at the TRPV1 or TRPV3 nociceptors, or agonists (TRPV1) including capsaicin and chemically derived developments, which act via nociceptor desensitization (Novakova-Tousova et al., 2007).

Because of their involvement in pain sensations, TRPV1, A1 and M8 genotypes have been studied for modulation of the pain phenotype. Genetic associations have been reported about a single subject insensitive to capsaicin, who carried seven intronic TRPV1 polymorphisms and had only 50% of the mRNA and protein expression levels of normally sensing subjects (Park et al., 2007). In 17 European-American women carrying the TRPV1 variant rs8065080 G (I585V), cold withdrawal time was 1.6 times longer than in 136 non-carriers (Kim et al., 2004). This was surprising because TRPV channels are stimulated by heat and, therefore, heat pain was the phenotype expected to be modulated, while for a modulation of cold pain, variants in TRPM8 or TRPA1 would have been primary candidates. The authors hinted at properties in the three-dimensional structure of the engaged TRPA1 haploblock for explanation (Kim et al., 2004). In the same gene, a point mutation leading to an N855S amino acid exchange in the S4 transmembrane segment of TRPA1 receptors increased the inward current on activation at normal resting potentials fivefold (Kremeyer et al., 2010). This was associated with an autosomal-dominant familial episodic pain syndrome characterized by episodes of debilitating upper body pain, triggered by fasting and physical stress. For carriers of such TRPA1 mutations, TRPA1 antagonists are an especially promising therapy.

Ligand-gated ion channels. Targets of this kind addressed with new analgesics include ionotropic glutamate-gated receptors, nicotinic cholinoceptors and ATP-gated purinergic P2X receptors.

Glutamatergic ion channels. Ionotropic receptors directly gate ion channels and are divided into three major subclasses: AMPA, Kainate and NMDA (Petrenko et al., 2003). Several NMDA antagonists have been available for a long time, such as amantadine, dextromethorphan, ketamine, memantine, nitrous oxide, phencyclidine, riluzole or tiletamine, some of them being used in pain treatment, others in treatment of neurological diseases or as substances of abuse. New NMDA or AMPA modulators often target ion channel subunits to obtain higher selectivity for pain. One of these targets is the NMDA receptor 2b subunit coded by the GRIN2B gene. The GRIN2B 2664C>T polymorphism plays a role in Huntington pathology where it appears to modulate neuronal response inhibition (Beste et al., 2010) and has been associated with Parkinson's disease (Tsai et al., 2002). Another variant, GRIN2B 366C>G, was more frequent in Parkinson patients displaying impulse control and related behaviours than in non-affected patients (Lee et al., 2009). The GRIN2B rs10845840 variant has been associated with the temporal lobe volume in Alzheimer's disease patients (Beste et al., 2010). A GRIN2B haplotype has been associated with variation in memory performance (de Quervain and Papassotiropoulos, 2006). In addition, the GRIN2B rs1019385 polymorphism was associated with higher glutamate concentrations in the anterior cingulum and was involved in obsessive-compulsive disorder (Lee et al., 2009) and schizophrenia (Hokyo et al., 2010). Finally, rs2284411 showed associations with symptom dimensions of attention deficit hyperactivity disorder (Dorval et al., 2007).

The antagonist at kainate receptors currently developed as a new analgesic, tezampanel, has selectivity toward the GluK1 (GluR5) subtype and coded by the *GRIK1* gene. Variants in this gene are known from associations with alcoholism (Kranzler and Edenberg, 2010) or autism (Haldeman-Englert *et al.*, 2010).

Neural nicotinic receptors. Nicotine exerts antinociceptive effects by interacting with one or more of the subtypes of nicotinic cholinoceptors (nAChRs) present throughout neuronal nociceptive pathways (Marubio et al., 1999), for example forming capsaicin-sensitive and -insensitive nociceptors expressed at dorsal root ganglia (Rau et al., 2005). Therefore, new analgesic compounds target certain subtypes (Gao et al., 2010) of neuronal nAChRs to circumvent the narrow therapeutic window between analgesic efficacy and toxicity of non-selective nicotinic agonists (Vincler, 2005). Specifically, mice lacking the α<sub>4</sub> subunit of the neuronal nAChR displayed reduced antinociceptive effects of nicotine (Marubio et al., 1999). However, these newer analgesics, such as ABT-594, are not without side effects, such as nausea, dizziness, vomiting, abnormal dreams and asthenia, reported in patients with diabetes-induced peripheral neuropathic pain (Rowbotham et al., 2009).

Functional variants in the *CHRNA4* gene, which codes for this receptor subunit, have been associated with epilepsy (Steinlein and Bertrand, 2010). In addition, the *CHRNA4* 

polymorphisms rs4603829 and rs4522666 were reported to modulate financial and psychological risk behaviours (Roe et al., 2009), CHRNA4 rs1044396 was associated with novelty seeking (Etter et al., 2009), whereas rs2236196, rs1044396 and rs2236196 were associated with nicotine dependence (Breitling et al., 2009). More severe consequences have some rare loss-of-function variants associated with the occurrence of amyotrophic lateral sclerosis (Sabatelli et al., 2009). However, as for several other candidate variants, a direct association with pain or analgesia has not yet been shown and possibly not even been studied because they have played, so far, no role in analgesia.

Purinergic receptors. Purinergic receptors have been reported to be involved in pain (Jarvis and Khakh, 2009; Jarvis, 2010). One mechanism by which ATP evokes acute pain is the interaction with P2X receptors that are also involved in the pathophysiology of chronic inflammatory and neuropathic pain (Kennedy, 2005). P2X3 receptors are expressed in capsaicin-sensitive small-sized dorsal root ganglion neurons where they contribute to the generation of rapidly desensitizing inward currents, which are involved in evoking nocifensive behaviours and thermal hyperalgesia. A P2X receptor-mediated excitatory postsynaptic current was also found in pyramidal neurones of the somatosensory cortex (North, 2003; Pankratov et al., 2003). P2X4 receptors induced in spinal microglia mediate tactile allodynia after nerve injury (Tsuda et al., 2003).

Genetic variation in purine receptors has been studied less frequently. *P2RX7* rs1718119 was associated with severity scores in the panic- and agoraphobia scale (Erhardt *et al.*, 2007) and the loss-of-function mutations *P2RX7* 568N (rs1653624), 307Q (rs28360457) and a null allele (splice site mutation, rs35933842) tended to be over-represented among patients who needed a surgical revision after total hip arthroplasty (Mrazek *et al.*, 2010), which had been related to the involvement of P2X7 receptors in inflammation. In addition, a role in the development of depression has been suggested for the *P2RX7* rs2230912 G allele (Nagy *et al.*, 2008).

### *G* protein coupled receptors

G-protein coupled receptors have seven transmembrane segments and sense external molecules triggering activation of internal signalling pathways.

 $\delta$ –opioid receptors.  $\delta$ –opioid receptors are the natural targets of enkephalins and mediate several biological functions including antinociception. Although the action of most current opioid analgesics is simply described as  $\mu$ -opioid receptor agonism, it is well known that they also bind at other opioid receptors (Mignat *et al.*, 1995). Therefore, a  $\delta$ -opioid component is part of the action of most clinically used opioid analgesics (Gharagozlou *et al.*, 2002). More selective  $\delta$ -opioid agonists have not been broadly established clinically, despite demonstrations of better side effect profiles and a proposal of their use to selectively antagonize  $\mu$ -opioid receptor associated respiratory depression (Su *et al.*, 1998). Selective  $\delta$ -opioid agonists are being under development as analgesics.

In *in vitro* transfection experiments, the W284L variant of the  $\delta$ -opioid receptor selectively reduced the affinity of some but not all of the tested  $\delta$ -opioid agonists (Hosohata *et al.*, 2001). *In vivo*, most polymorphisms in the  $\delta$ -opioid receptor gene (*OPRD1*) have been associated with substance dependence (Zhang *et al.*, 2008) and other psychiatric disorders (Brown *et al.*, 2007). For example, *OPRD1* rs569356 may enhance transcription factor binding and increase  $\delta$  -opioid receptor expression and was associated with substance addiction (Zhang *et al.*, 2010). *OPRD1* variants have also already shown to play a role in pain. Thus, men carrying the rs1042114T>G variant (allelic frequency 10.9%) had lower heat pain sensitivity than carriers of the rs2234918T>C variant (allelic frequency 35.6%) (Kim *et al.*, 2004).

Cannabinoid receptors. The involvement of the cannabinoid system in a number of important physiological processes including the regulation of neurotransmitter release, pain and analgesia, energy homeostasis, and control of immune cell function is mediated by CB1 and CB2 receptors (Graham et al., 2009). They are activated by endocannabinoids, which are arachidonic acid derived lipids such as anandamide and 2-arachidonoyl-glycerol, plant cannabinoids such as tetrahydrocannabinol and synthetic cannabinoids including substances under development as analgesics. The two main receptor subtypes, CB<sub>1</sub> and CB<sub>2</sub>, are primarily located in the CNS or in the periphery, respectively, although this separation is not strict, as, for example, the CB1 receptor is expressed also in the lungs, liver and kidneys (Graham et al., 2009). Cerebral endocannabinoid signalling is involved in antinociception (Wilson and Nicoll, 2002). However, the peripheral CB<sub>2</sub> receptor has also been proposed to play a key role in cannabinoid-mediated analgesia (Agarwal et al., 2007). Exogenous cannabinoids have been suggested to decrease the subjective intensity estimates of pain alone or in synergy with opioids (Naef et al., 2003; Roberts et al., 2006) but hyperalgesic cannabis actions on electric experimental pain stimuli in healthy volunteers have also been reported (Kraft et al., 2008). A cannabis formulation has been approved in Canada since 2005 for the treatment of neuropathic pain.

Polymorphisms in the  $CB_1$  gene CNR1 have not yet been associated with pain phenotypes. So far, functional associations were found with obesity (Russo et~al., 2007; Aberle et~al., 2008), schizophrenia (Ujike et~al., 2002; Chavarría-Siles et~al., 2008; Hamdani et~al., 2008), drug (Proudnikov et~al., 2010) and alcohol dependence (Zhang et~al., 2004; Zuo et~al., 2007; Agrawal et~al., 2009). Polymorphisms in the  $CB_2$  gene CNR2 play a role in osteoporosis (Karsak et~al., 2005) and might also modulate the susceptibility to autoimmune disorders (Sipe et~al., 2005).

Metabotropic glutamate receptors. These  $G_q$  or  $G_i$  protein coupled receptors transmit glutamatergic excitatory signals (Swanson *et al.*, 2005), are expressed at nociceptive neurons and involved in sensitization processes to noxious stimulation (Coderre, 1993). Analgesics are being tested that inactivate the mGluR5 receptor, which is coupled with a  $G_q$  protein. Via phospholipase C activation and inositoltriphosphate/diacylglycerol signalling, activation of this receptor leads to liberation of calcium from the endoplasmic reticulum into the intracellular space and to activation of



protein kinase C. *GRM5* variants were associated with schizophrenia (Devon *et al.*, 2001; Choi *et al.*, 2009) or attention-deficit hyperactivity disorder (Elia *et al.*, 2009).

Bradykinin receptors. Bradykinin  $B_1$  receptors (Marceau et al., 1998) mediate hyperalgesia due to kininin up-regulation (Gabra et al., 2006). In a diabetic neuropathic rodent model, blocking of  $B_1$  receptors reversed tactile and cold allodynia (Dias et al., 2007). A variant in BDKRB1 (-699 G>C) was slightly associated with progression of polycystic kidney disease (Tazón-Vega et al., 2007) but also with the risk of inflammatory bowel disease (Bachvarov et al., 1998). BDKRB1 variants were also reported in the context of hypertension (Cui et al., 2005).

5-HT receptors. 5-HT receptors are expressed in the central and peripheral nervous systems where they mediate both excitatory and inhibitory neurotransmission (Hoyer et al., 1994). They exert many physiological and pathophysiological functions and some of their subtypes play a role in nociception. Several 5HT receptor subtypes are involved in nociception (Xu et al., 1994), such as spinal 5-HT<sub>1</sub>, 5-HT<sub>2</sub> and 5HT<sub>3</sub> receptors (Alhaider et al., 1991; Danzebrink and Gebhart, 1991; Giordano, 1997). Human polymorphisms of their genes have been associated with several pathophysiological functions (Hannon and Hoyer, 2008) leading to a complex knowledge of the genetics and pharmacogenetics of the serotonergic system. Currently, only the 5-HT<sub>1A</sub> receptor is being studied as the target of an analgesic, F-13640/befiradol, that has entered the clinical phase of development. Besides several other biological functions in the regulation of blood pressure and penile erection, mood, addiction and memory, the 5-HT<sub>1A</sub> receptor subtype has been described to play a role in nociception (Nadeson and Goodchild, 2002; Pucadyil et al., 2005). An agonist at these receptors possessed anti-allodynic and anti-hyperalgesic properties (Bardin et al., 2003) including efficiency in neuropathic pain models in laboratory animals (Deseure et al., 2007). The HTR1A -1019C>G polymorphism was associated with schizophrenia, substance abuse disorder, panic attack and antidepressant response in mood disorders (Huang et al., 2004), attention deficit hyperactivity disorder (Shim et al., 2010), and has been suggested to be linked to frontal brain electrical asymmetry (Bismark et al., 2010).

### Signalling messengers

Nerve growth factor (NGF). The nerve growth factor (NGF) is a small protein belonging to the class of neurotrophins and identified originally as a survival factor for sensory and sympathetic neurons in the developing nervous system (Fiore et al., 2009). The expression of NGF is high in injured and inflamed tissues, and activation of the NGF receptor tyrosine kinase A (trkA) on nociceptive neurons triggers and enhances pain signalling by multiple mechanisms (Hefti et al., 2006).

trkA is a catalytic receptor being approached as an analgesic's target, (Wang *et al.*, 2009), but the candidate compound has not yet entered phase 1 clinical trial. NGF signalling plays a role in the generation of pain and hyperalgesia (Levi-Montalcini *et al.*, 1996; Fiore *et al.*, 2009) also because the local production of inflammatory cytokines up-regulates NGF (Hefti *et al.*, 2006).

Due to the signal transduction pathway, the actions of NGF targeting dugs may be genetically modulated both at NGFB level, the gene coding for NGF β, and at NTRK1 level, the gene coding for trkA receptors. Loss-of-function variants in the NGFB gene have been identified as the causes of extreme pain phenotypes consisting of complete congenital insensitivity to pain. Since NGF and its receptor trkA are involved in nervous system development and homoeostasis, the genetic variants are associated with other neurological deficits. Thus, the hereditary sensory and autonomic neuropathy type V (HSAN-V) is characterized by a loss of pain perception, impaired temperature sensitivity, ulcers, and sometimes self-mutilation, with variable autonomic involvement (Hilz, 2002). All three affected members of a Swedish family were homozygous for a coding 661C>T SNP (R211W) in the NGFB gene encoding NGF-β, which affects a highly conserved region of the protein (Einarsdottir et al., 2004).

Variants in the NTRK1 gene coding for the trkA receptor have been identified as the causes of the extreme pain phenotype congenital insensitivity to pain with anhidrosis (CIPA), also called hereditary sensory and autonomic neuropathy type IV (HSAN-IV). It is an autosomal-recessive disorder characterized by recurrent episodes of unexplained fever, anhidrosis, absence of reaction to noxious stimuli, selfmutilating behaviour and mental retardation. Since mice lacking the gene encoding the trkA receptor (ntrk1) for NGF display similar phenotypic features as CIPA patients (Smeyne et al., 1994), mutations in the human NTRK1 gene have been studied as candidate causes. Three mutations (1726delC with premature translational stop, IVS15 + 3A > C with altered splicing, 1795 G > C with G571R amino acid substitution) in three unrelated subjects were identified as the molecular basis of HSAN-IV (Indo et al., 1996). Several further mutations have been found in these patients (Indo, 2001), most of them only once but 1726delC was found in more than 50% of Japanese CIPA families (Miura et al., 2000), and 1926-1927insT found in 16 of 19 unrelated CIPA families from Israeli Bedouins (Shatzky et al., 2000).

*Interleukin-1*. Interleukin (IL)-1 is a pro-inflammatory cytokine. Antagonists are developed for the treatment of inflammatory rheumatic and low back pain. Genetic modulations in IL-1-related genes have been found in 131 middle-aged men, among whom carriers of the IL1 receptor antagonist (IL1RN) variant rs2234677 had an increased risk for low back pain. When present with the IL-1α genetic variant IL1A rs1800587 or the IL-1β gene (IL1B) variant rs1143634, a higher risk and more days with low back pain was identified (Solovieva et al., 2004). Higher pain incidence was associated with the IL1A rs1800587 and IL1RN rs2234677 variants and the simultaneous presence of IL1A rs1800587 and IL1RN rs2234677 was associated with increased number of days with pain (Solovieva et al., 2004). The functional variants were associated with IL-1 up-regulation at RNA and cytokine levels (Pociot et al., 1992; Dominici et al., 2002). This makes antagonists primary choices for patients carrying variants that enhance the algesic activity of IL-1.

*P38 MAP kinase.* P38 MAP kinases respond to stress stimuli, such as pro-inflammatory cytokines and cytokines and cellular stresses (Ashwell, 2006). P38 MAP kinases play a role in the

pathogenesis of neuropathic pain. In microglial signal transduction under chronic pain states, downstream effects of p38 produce inflammatory mediators (Ji and Suter, 2007). Selective p38 inhibitors are being clinically evaluated for the treatment of chronic inflammatory disorders including those involving pain (Cottrell *et al.*, 2009). The *MAPK14* gene coding for p38 (named MAP kinase 14) has so far not been positively reported from association studies.

# Enzymes involved in the production of nociceptive or inflammatory mediators

FAAH. The fatty acid amide hydrolase (FAAH) is one of the endocannabinoid metabolizing enzymes. It degrades the fatty acid amide family of endogenous signalling lipids including the endogenous cannabinoid anandamide (Bisogno et al., 2005), which among many other functions has been implicated in the suppression of pain. Lack of FAAH has been associated with a cannabinoid related hypoalgesic phenotype in mice (Lichtman et al., 2004). Moreover, FAAH has been implicated in the antinociceptive effects of paracetamol (Högestätt et al., 2005; Mallet et al., 2008) and other analgesics such as R-flurbiprofen (Ates et al., 2003; Bishay et al., 2010) affecting prostaglandin production and therefore, its polymorphisms may modulate the action of classical and new analgesics.

In pain, a tendency towards increased pain sensitivity associated with frequent *FAAH* alleles was seen in a cohort of 935 subjects. Cold pain intensity was up to 1.4-fold increased in men carrying the variant *FAAH* alleles rs932816 A, rs4141964 C and rs2295633 A, and carriers of the rs4141964 C allele had shorter (0.8-fold) cold withdrawal time than non-carriers (Kim *et al.*, 2006). This would be compatible with increased enzyme activity leading to accelerated endocannabinoid degradation but the molecular consequences of these variants have not yet been assessed.

# Future directions of the pharmacogenetics of analgesia

## Pharmacogenetics of pain and analgesia as a research tool

The genetics of pain and analgesia has proven its value as a superior research tool to discover the role of molecular pathways in human nociception and analgesia. Quantitative sensory trait techniques in rodents (Abiola *et al.*, 2003) have been successfully employed to identify molecular pathways of nociception leading to an increased understanding of pain and in some cases to the identification of new analgesic drug targets. Information about pain pathways from human research employed genotyping of patients with rare and extreme pain phenotypes, thus identifying indispensable components of the human nociceptive system (Oertel and Lötsch, 2008).

Variants in pain-associated genes can be employed to test whether a molecular pathway identified in laboratory animals is relevant in humans. Without modulator molecules that can be applied to humans, genetic variants functionally altering components of the pathway can be taken as a substitute. This requires, however, the demonstration of a molecular consequence of the genetic variant to avoid overinterpretation of an accidental positive association. A genetic association was used as a tool for a proof-of-concept in assessments where genetics was not in the focus. For example, the role of GTP cyclohydrolase (GCH1) activity in pain, first found in laboratory animals, was proven in humans using *GCH1* genetic variants shown to decrease enzyme up-regulation and tetrahydrobiopterin production at the molecular level (Tegeder *et al.*, 2006).

Genetic association studies can also be used as a tool to generate hypotheses but this requires molecular proof and replications of the findings. Genetics has also contributed to identify functionally relevant portions of the gene product, as for example for the  $\mu$ -opioid receptor (Wolf et~al., 1999). Importantly, a demonstrable molecular effect or at least a reproduction of positive associations in an independent cohort has become a scientific standard on which pharmacogenetics results may be based. This has not yet been shown for all so far known polymorphisms affecting pain or other clinical symptoms related to the present drug targets.

## Further pharmacogenetically modulated analysesic targets

The present overview addressed those analgesics targets for which substances are closest to clinical use. It excluded targets for which no drug has so far reached clinical development, such as the GCH1 that may be used to delay the development of pain (Lötsch et al., 2009b). Similarly, T-type voltage gated calcium channels have been shown to play a key role in nociception (Bourinet et al., 2005; Zamponi et al., 2009). Furthermore, hyperpolarization-activated, cyclic nucleotide-modulated (HCN) 'pacemaker' channels play a role in the pathogenesis of neuropathic pain (Chaplan et al., 2003; Papp et al., 2006) rendering them possible further future targets of analgesics. Moreover, acid-sensing ion channels (ASICs) are activated by extracellular protons and can trigger acid-induced pain during inflammation or metabolic stress (Deval et al., 2010). They may be addressed with an existing experimental pain model employing administration of gaseous carbon dioxide to the nasal mucosa where via carbonic anhydrase, protons are generated and, along with TRPV1 activation, stinging pain is evoked (Kobal, 1985).

A further potential target is the inducible microsomal PGE<sub>2</sub> synthase 1 (mPGES-1) that catalyses the formation of prostaglandin E<sub>2</sub> (PGE<sub>2</sub>) from PGH<sub>2</sub>, a cycloxygenase product from arachidonic acid. PGE2 represents an important pain mediator and its pain signalling effects are translated mostly via peripheral prostanoid EP1 receptors and spinal EP2 receptors (Vanegas and Schaible, 2001). mPGES-1-deficient mice showed a reduced pain hypersensitivity and inflammation in some but not all models (Kamei et al., 2004). It therefore qualifies as a target of anti-inflammatory and analgesic drugs, although it is not clear for which diseases such treatment would provide a particular advantage (Rörsch et al., 2010). The PTGES2 gene polymorphism rs13283456 (R298H enzyme) has been found to reduce the risk of type 2 diabetes mellitus (Lindner et al., 2007; Nitz et al., 2007), perhaps through contribution of a lowered body mass index (Fischer et al., 2009).

This overview also excluded new analgesics that are innovative improvements of classic principles but do not add new



targets. For example, tapentadol is an opioid and noradrenaline re-uptake inhibitor, but its pharmacogenetics may be primarily deduced from known pharmacogenetic associations of OPRM1, KCNJ6 and COMT. Some further variants may be added in genes coding for targets of analgesics that have reached phase 2 without a publicly disclosed mechanism of action, such as the 'small molecule' AGN-209323. Candidate genes additional to the present variants affecting the pharmacodynamics of analgesics, may be found in drug metabolizing enzymes or transmembrane transporters potentially affecting the analgesic's pharmacokinetics. However, from the present selection, those variants will be dropped for which the whole target fails clinical development. It is relevant to note that pain drugs under clinical development have failed, for example, ADX10059, RGH-896, ralfinamide and tanezumab. Whether pharmacogenetic reasons played a role in these failures is not known.

### **Conclusions**

For several genes coding for the targets of new analgesics (Table 1), functional modulations by genetic variants are already known. They have so far been found mainly in neuropsychiatric disorders and need to be tested for a possible role in analgesia. However, intensive research on the genetic modulation of pain has provided already substantial knowledge that may serve as a start point. That is, many targets have analysed in terms of pain genetics (Lötsch and Geisslinger, 2007), rather than analgesic genetics (Lötsch and Geisslinger, 2006), and may now be transferred from pain genetic research to pain *pharmaco*genetic research. Variants modulating the pharmacokinetics of new analgesics will possibly increase the number of candidates.

Several new analgesics will soon increase the choice of targets addressed for control of pain. This broader selection of analgesic targets and genetic modulators (Table 1) may increase the clinical utility of genotyping information in pain treatment, which so far with mainly opioid related proposed applications is modest (Lötsch and Geisslinger, 2010). The already considerable specific knowledge of functional variants, summarized here, may allow for specific hypothesis testing and help improving the statistical power of association studies that without a narrow selection of candidate variants would require large samples. Greater benefits of genotyping in pain therapy could be seen in the possibility to choose the individual optimum analgesic before the start of therapy. The chances for a genetics-based individualized pain therapy increase with an increasing number of targets. However, the challenge remains to compile this into clinically feasible guidance to therapy that provides additive value to therapy decisions made without genetics information.

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### **Conflicts of interest**

The authors declare no conflict of interest.

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