Molecular Mechanisms of Opioid Receptor-dependent Signaling and Behavior

Ream Al-Hasani, Ph.D.,* Michael R. Bruchas, Ph.D.†

ABSTRACT

Opioid receptors have been targeted for the treatment of pain and related disorders for thousands of years and remain the most widely used analgesics in the clinic. Mu (µ), kappa (κ), and delta (δ) opioid receptors represent the originally classified receptor subtypes, with opioid receptor like-1 (ORL1) being the least characterized. All four receptors are G-protein coupled and activate inhibitory G proteins. These receptors form homo- and heterodimeric complexes and signal to kinase cascades and scaffold a variety of proteins.

The authors discuss classic mechanisms and developments in understanding opioid tolerance and opioid receptor signaling and highlight advances in opioid molecular pharmacology, behavioral pharmacology, and human genetics. The authors put into context how opioid receptor signaling leads to the modulation of behavior with the potential for therapeutic intervention. Finally, the authors conclude there is a continued need for more translational work on opioid receptors in vivo.

OPIODS are the most widely used and effective analgesics for the treatment of pain and related disorders. Opiates have been used for thousands of years for the treatment of pain, and in the last century we have made huge strides in the development of opioids derived from naturally occurring opiates within the fields of receptor pharmacology and medicinal chemistry. In addition, opioids are used frequently in the treatment of numerous other disorders, including diarrhea, cough, postoperative pain, and cancer (table 1).

Opioid systems are critical in the modulation of pain behavior and antinociception. Opioid peptides and their receptors are expressed throughout the nociceptive neural circuitry and critical regions of the central nervous system included in reward and emotion-related brain structures. To date, four different opioid receptor systems mu (µ), delta (δ), kappa (κ), opioid receptor like-1 (ORL1) and their genes have been characterized at the cellular, molecular, and pharmacologic levels.1

The most commonly used opioids for pain management act on µ opioid receptor (MOR) systems (fig. 1). Although µ opioids continue to be some of the most effective analgesics, they are also mood enhancers and cause activation of central dopamine reward pathways that modulate euphoria. These unwanted side effects have driven researchers at basic and clinical levels to actively pursue other opioid receptors as putative drug targets for pain relief (table 1).

The opioid receptor subtypes were identified pharmacologically and genetically more than 2 decades ago. From that point on, numerous studies have implicated all four opioid receptors in an array of behavioral effects, including analgesia, reward, depression, anxiety, and addiction. In addition, all four receptor subtypes have been characterized at cellular levels with respect to the downstream signal transduction pathways they activate. However, there are fewer studies that have directly linked opioid signal transduction to behavioral events. One of the “holy grails” in opioid pharmacology research has been to identify pathway-specific opiate receptor agonists that could activate antinociceptive signaling without causing µ agonist-mediated euphorogenic responses or κ agonist-mediated dysphoria.2,3 Understanding the diversity of signaling at opioid receptors and how second messenger activation leads to modulation of pain and reward could reveal novel opioid receptor drug candidates.

In this review, we highlight the current status of in vitro molecular pharmacology at opioid receptors and discuss many of the recent advances that connect these molecular stud-
ies with opioid behavioral pharmacology. We discuss the advances in opioid receptor pharmacology and highlight the connections between signaling at opioid receptors, tolerance to opioids, and behavioral responses. The review’s primary aim is to discuss recent efforts in understanding how opioid receptors mediate a diverse array of molecular or cellular responses while also modulating behaviors such as analgesia, reward, depression, and anxiety. We summarize the modern advances in opioid receptor signaling to mitogen-activated protein kinases (MAPK) and receptor protein–protein interaction networks and propose that there is a strong potential for selective ligand intervention at opioid receptors to treat a variety of central and peripheral nervous system disorders by using biased ligands and pathway-selective pharmacology. Moreover, we highlight how a greater connection between these advances at the molecular levels and behavioral pharmacology is imperative to fully understand the field of opioid pharmacology.

**Opioid Tolerance in the Clinic**

Before a detailed understanding of the molecular and cellular actions of opioid receptors is developed, it is important to consider their general effects and those observed in daily clinical settings. Different potencies of opiate drug formulations have been effective in the treatment of a variety of acute, chronic, and cancer-related pain disorders. The clinical utility of opioids continues to be limited by a compromise between efficacy and side effects. The most common side effects of opiates can be divided into peripheral effects (constipation, urinary retention, hives, bronchospasm) and central effects (nausea, sedation, respiratory depression, hypotension, miosis, cough suppression), all of which seriously affect the agents’ clinical utility and patients’ quality of life (table 1). There have been many attempts to develop better opioid drugs, but these have been largely unsuccessful because of our incomplete understanding about the development of tolerance to the analgesic effects.

Opioid tolerance is defined typically in the clinic as the need to increase a dose to maintain the analgesic effects. However, this increase in dose can exacerbate the perpetual problem of the side effects mentioned. This continual cycle of insufficient analgesia and side effects is among the greatest challenges of using opioids in the treatment of pain.

<table>
<thead>
<tr>
<th>Organ Systems</th>
<th>Effects</th>
<th>Additional Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Central nervous system</td>
<td>↑ Analgesia</td>
<td>Leading to risk of addiction and abuse</td>
</tr>
<tr>
<td></td>
<td>↑ Euphoria</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Sedation</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Rate of respiration</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Cough reflex</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Miosis—constriction of the pupils</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Truncal rigidity</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Nausea and vomiting</td>
<td></td>
</tr>
<tr>
<td>Peripheral Gastrointestinal system</td>
<td>↑ Constipation</td>
<td>Codeine used for treatment of pathologic cough</td>
</tr>
<tr>
<td></td>
<td>↓ Gastric motility</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↓ Digestion in the small intestine</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↓ Peristaltic waves in the colon</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Constriction of biliary smooth muscle</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Esophageal reflux</td>
<td></td>
</tr>
<tr>
<td>Other smooth muscle</td>
<td>↑ Depression of renal function</td>
<td>Most apparent when using fentanyl, sufentanil, alfentanil</td>
</tr>
<tr>
<td></td>
<td>↓ Uterine tone</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Urinary retention</td>
<td></td>
</tr>
<tr>
<td>Skin</td>
<td>↑ Itching and sweating</td>
<td></td>
</tr>
<tr>
<td></td>
<td>↑ Flushing of the face, neck, and thorax</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular system</td>
<td>↓ Blood pressure and heart rate if cardiovascular system is stressed</td>
<td></td>
</tr>
<tr>
<td>Immune system</td>
<td>↓ Formation of rosettes by human lymphocytes</td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>Behavioral restlessness</td>
<td></td>
</tr>
</tbody>
</table>

The actions summarized in this table are observed for all clinically available opioid agonists.

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Table 1. Organ System Effects of Morphine and Its Surrogates

Anesthesiology 2011; 115:1363–81 R. Al-Hasani and M. R. Bruchas
pharmacology demonstrated that guanine nucleotides such as guanosine triphosphate (GTP) modulate agonist binding to opioid receptors in membrane preparations from brain tissue. It was later determined that GTPase activity is stimulated by opioid agonists and endogenous opioid peptides. Agonist stimulation of opioid receptors was also shown to inhibit cyclic adenosine monophosphate (cAMP) production in a manner similar to that of other types of G protein-coupled receptors (GPCR). When pertussis toxin was used to selectively adenosine diphosphate (ADP)-ribosylate the G protein, the inhibitory function of opioid receptors on cAMP signaling was found to be Gαi dependent. Today it is widely accepted that all four opioid receptor types couple to pertussis-toxin–sensitive G proteins, including Gαi, to cause inhibition of cAMP formation.

The classic and perhaps most important aspect of opioid receptor signal transduction relates to opioids’ ability to modulate calcium and potassium ion channels (fig. 2). After Gαi dissociation from Gβγ, the Gαi protein subunit moves on to directly interact with the G-protein gated inwardly rectifying potassium channel, Kir3. Channel deactivation happens after GTP to guanosine diphosphate hydrolysis and Gβγ removal from interaction with the channel. This process causes cellular hyperpolarization and inhibits tonic neural activity. In several reports, the inhibitory effects of opioids on neural excitability were shown to be mediated by interactions of opioid receptors with G protein-regulated inwardly rectifying potassium channel (Kir3).

When activated, all four opioid receptors cause a reduction in Ca2+ currents that are sensitive to P/Q-type, N-type, and L-type channel blockers. Opioid receptor-induced inhibition of calcium conductance is mediated by binding of the dissociated Gβγ subunit directly to the channel. This binding event is thought to reduce voltage activation of channel pore opening. Numerous reports have shown that opioid receptors interact with and modulate Ca2+ channels; this has led to the examination of specific Ca2+ channel subunits that may be involved in opioid receptor modulation. For instance, it was reported that MOR stimulation results in G protein-dependent inhibition of α1A and α1B subunits.

It is also clear that the acute administration of opioid agonists reduces Ca2+ content in synaptic vesicles and synaptic cisternae, with compensatory up-regulation of vesicular Ca2+ content during the development of opioid tolerance. In addition, because the activation of μ, δ, and κ opioid receptors inhibits adenylyl cyclase activity, the cAMP-dependent Ca2+ influx is also reduced.

The evidence for opioid receptors positively coupling to potassium channels while negatively modulating calcium channels has been reported in numerous model systems and cell types. For many years this was thought to be the primary action of opioid receptors in the nervous system. This coupling of opioid receptors to potassium and calcium channels has been demonstrated in a wide range of systems, from neurons in the hippocampus, locus coeruleus, and ventral...
The tegmental area to the dorsal root ganglia, supporting the notion that these channels are highly conserved opioid receptor substrates and represent one of the most important targets for opioid receptor modulation. Newer findings, which we highlight later in this review (see Opioid Receptor Regulation), suggest that although opioid receptors have potent effects on ion channel modulation, they also have slower yet robust effects on other signal transduction pathways.

**Molecular Mechanisms of Opioid Tolerance**

To date, the molecular and cellular mechanisms mediating the development of tolerance to morphine remain a matter of controversy. Traditionally, it was thought that the down-regulation of opioid receptors after chronic agonist exposure induces tolerance, as reported in *in vitro* studies. However, recent *in vivo* studies show that down-regulation does not occur consistently with each and every agonist and may not completely explain tolerance. In light of these findings, it has been suggested that MOR proteins are not down-regulated but instead may be desensitized and uncoupled from downstream signaling pathways. It has been observed that after chronic morphine exposure, levels of the second messenger cAMP are increased. However, this elevation in cAMP may not be attributable to opioid receptor uncoupling from inhibitory G proteins but instead could reflect cellular adaptive changes, including the up-regulation of adenyl cyclase, protein kinase A, and cAMP response element-binding protein. It is this ineffective regulation of cAMP by morphine that some believe induces tolerance.

It has also been proposed that the regulation of opioid receptors by endocytosis reduces the development of tolerance and therefore serves a protective role. *In vivo* studies have shown that facilitation of MOR endocytosis in response to morphine prevents the development of morphine tolerance. In addition, it has been shown *in vivo* that the lack of β-arrestin 2 prevents the desensitization of MOR after chronic morphine treatment, and these mice also failed to develop antinociceptive tolerance.

Recent studies have identified how ligand-directed responses, more commonly known as biased agonism, are crucial in understanding the complexity of opioid-induced tolerance. The work of Bohn and colleagues showed how β-arrestin 1 and β-arrestin 2 differentially mediate the regulation of MOR. β-arrestins are required for internalization, but only β-arrestin 2 can rescue morphine-induced MOR internalization, whereas both β-arrestin 1 and β-arrestin 2 can rescue [d-Ala², N-Me-Phe⁴, Gly-ol⁵]enkephalin (DAMGO)-induced MOR internalization. These findings suggest that MOR regulation is dependent on the agonist and may be critical in understanding the mechanism involved in the development of tolerance. Melief *et al.* further showed how acute analgesic tolerance to morphine is blocked by c-jun N-terminal kinase (JNK) inhibition but not G protein-receptor kinase 3 (GRK-3) knockout. In contrast, using a second class of μ agonists (fentanyl, methadone, and oxy-
models. the role and consequences of biased signaling in behavioral Connor34). Here we highlight the key findings in this area as extensively examined (for a detailed review see Bailey and trafficking, desensitization, and phosphorylation have been ical dependence. As a result of this problem, opioid-receptor tolerance. This process is well established in the GPCR liter- nine, and tyrosine residues that are accessible to protein ki-

Opioid Receptor Regulation

Agonist-induced receptor phosphorylation is believed to be one of the many critical molecular components of opioid tolerance. This process is well established in the GPCR liter-

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μ Opioid Receptors (MOR)

One common thread between the opioid receptor subtypes is the interesting observation that receptor trafficking and regulation vary depending upon the agonist. For example, morphine is unable to promote receptor internalization, in contrast to DAMGO, which causes robust internalization.32,35,36 It is thought that morphine tolerance, a major problem in the clinic, is perhaps mediated by these differences in receptor regulatory activity. Several groups are actively working to discern the various mechanisms for the differences in ligand-dependent MOR regulation, but controversy remains, with some groups hypothesizing that MOR internalization does not actually uncouple the receptor from signal transduction pathways but instead induces recycling of uncoupled receptors to the plasma membrane. Alternatively, the morphine-bound receptor, although not internalized, may still signal at the cell membrane, and because signaling is never attenuated, the cellular machinery adapts to produce tolerance. A recent study has shown that morphine acts as a “collateral agonist” to promote receptor G-protein uncoupling (“jamming”) and JNK activation (see MAPK Signaling at Opioid Receptors), whereas fentanyl and DAMGO internalize and desensitize normally.35 It is plausible that many processes work together to produce receptor regulation and opioid tolerance, and additional study is warranted to continue to decipher these discrepancies.

κ Opioid Receptors (KOR)

κ Opioid receptor trafficking shares some common features with MOR regulation because KOR is readily phosphory-

nases, which phosphorylate the receptor. All three intracel-

EDUCATION

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In contrast to MOR and KOR, DOR were thought to exist primarily (more than 90%) at intracellular sites\(^\text{49-51}\) until recently, when mice expressing fluorescently tagged DOR revealed that there was strong membrane localization of DORs \textit{in vivo}.\(^\text{52}\) The reasons for this discrepancy between the numerous studies showing intracellular DOR labeling and membrane labeling remain unclear and continue to be matters of controversy. It is plausible that previous studies using DOR antibodies were flawed because of antibody specificity issues, despite the numerous controls conducted. Although DORs tagged with GFP are a powerful \textit{in vivo} tool, they require careful interpretation given that GFP is a large protein that may interfere with the typical DOR trafficking machinery. Additional investigation is required in both cases, and it is plausible that both concepts are indeed true; the concentrations of DOR expressed on the cell surface may well be higher than originally hypothesized, yet a large intracellular pool of DOR protein remains. Nevertheless, DOR seems to be a dynamic opioid receptor that can readily traffic in response to agonists. Some reports have shown that chronic morphine treatment promotes movement of DORs to the cell surface in the dorsal horn of the rat spinal cord.\(^\text{49}\) This effect was dependent on MOR receptor activity because blocking or deleting MOR genetically (MOR knockout) prevents the effect.

Like MOR and KOR, desensitization of DOR is controlled \textit{via} phosphorylation, after recruitment of arrestins and sequestration of arrestin-bound receptors.\(^\text{53,54}\) Phosphorylation of DOR has been shown with both small-molecule organic ligands and peptide treatments. Once again, c-terminal phosphorylation was shown to be critical for opioid receptor regulation. In DOR, the Ser363 residue is the key phosphorylation site.\(^\text{55,56}\) This phosphorylation event was shown to be mediated by GPCR kinase 2 (GRK-2).\(^\text{56,57}\) Other studies have demonstrated that other amino acid residues are involved in DOR regulation. For example, Thr353 was found to be important for [D-Ala2, D-Leu5]-Enkephalin (DADLE)-mediated down-regulation of DOR, and Leu245 and 246 act as lysosomal targeting motifs that participate in determining agonist-bound DOR localization.\(^\text{58,59}\) Furthermore, ligand-specific variability in agonist-dependent DOR phosphorylation has been observed with potential differences between SCN80- and [D-Pen2,5]Enkephalin (DPDPE)-bound conformations recruiting kinases with various efficacies and potencies.\(^\text{60}\)

Opioid Receptor Like-1 (ORL1)

Opioid receptor like-1 (also called nociceptin or orphanin FQ) receptors are the newest members of the opioid receptor family, and few groups have examined their regulatory properties. Agonist-induced internalization of ORL1 is rapid and concentration-dependent.\(^\text{61}\) Both the endogenous agonist nociceptin and small-molecule selective ORL1 agonist Ro646198 promote rapid internalization of ORL1. Agonist challenge also reduces the ability of ORL1 to couple to inhibition of forskolin-stimulated cAMP production, suggesting that ORL1 undergoes desensitization mechanisms similar to those of the other three opioid receptor subtypes. ORL1 internalization appears to be more rapid than that of the other opioid receptors, with some groups reporting internalization after only 2 min of agonist exposure in Chinese hamster ovary cells.\(^\text{62}\) However, this appears to be dependent on ligand type and cell line expression because ORL1 internalization in human neuroblastoma cells was slower and occurred closer to a 30-min time point.\(^\text{62}\) ORL1 receptors recently were demonstrated to cointernalize with N-type Cav2.2 channels after a 30-min agonist treatment.\(^\text{63}\) The internalization of the entire signaling complex is not unusual in GPCRs; however, the effect in the case of ORL1 is particularly pronounced and is believed to play a major role in how ORL1 selectively removes N-type calcium channels from the plasma membrane to inhibit calcium influx.

Opioid receptor like-1 receptor regulation is increasingly studied, but our understanding remains in the infant stages compared with that of the other three opioid receptor subtypes. To date, few site-directed mutagenesis studies have been conducted, and receptor regulation in primary neurons, dorsal root ganglion, or dorsal horn neurons remains unknown. As we move forward in understanding opioid receptor signaling and identify novel opioid receptor targets, ORL1 receptors become likely candidates for the future of opioid pharmacology.

Opioid Receptors and Arrestin Recruitment

Phosphorylation by GRK-2 or -3 of \(\mu\), \(\delta\), and \(\kappa\) opioid receptors leads to arrestin 2 or 3 recruitment. Arrestin molecules are key proteins that bind phosphorylated GPCRs to regulate their desensitization, sequestration, and sorting and ultimately assist in determining receptor fate. Opioid receptors are regulated by arrestin 2 and arrestin 3 binding (also called \(\beta\)-arrestin 1 and \(\beta\)-arrestin 2, respectively), and this interaction depends on the model system and agonist treatment procedure. Mice lacking arrestin 3 have been shown to have a reduced tolerance to \(\mu\) opioids such as morphine, suggesting that MOR regulation requires arrestin 3.\(^\text{30,64}\)

With the use of surface plasmon resonance methods, glutathione s-transferase pull-down assays, and classic immunoprecipitation methods, the C-terminal tails of DOR, MOR, KOR have been shown to be crucial for arrestin 2 or 3 binding. C-terminal carboxyl mutant opioid receptors have been studied widely, and these serine mutant receptors show decreased agonist-induced receptor internalization and arrestin recruitment. Dominant positive arrestins (such as Arrestin-2-R169E or Arrestin-3-R170E) that bind the nonphosphorylated receptors can rescue internalization of serine mutated MOR/DOR/KOR,\(^\text{58,65}\) further implicating arrestin dependence in opioid-receptor trafficking. Most studies implicating arrestin have been conducted in heterologous expression systems using overexpressed arrestins and opioid receptor subtypes. These conditions are atypical and do not represent...
the likely physiologic state of opioid receptors and arrestins in vivo, so these data should be interpreted with caution, and additional studies using in vivo approaches are needed to increase our understanding of arrestin–opioid interactions.

**MAPK Signaling at Opioid Receptors**

In the discussion above, we highlighted that sustained agonist treatment causes Grk phosphorylation at the carboxyl-terminal domain of opioid receptors activating arrestin-dependent receptor desensitization and internalization (fig. 2). During the last several years, GPCR research has discovered that the phosphorylated arrestin-bound GPCR complex is not simply inactive, but that it recruits alternate signal transduction cascades, including MAPKs. The merging of our previous knowledge regarding opioid receptor phosphorylation, arrestin, and cellular mechanisms of tolerance with an understanding of opioid receptor signaling to MAPKs is becoming more appreciated (table 2).

Mitogen-activated protein kinase pathways are diverse signaling cassettes that govern cellular responses, including cell proliferation, differentiation, apoptosis, transcription, translation factor regulation, channel phosphorylation, and protein scaffolding. The MAPK family is composed of 12–15 gene products with the most well-described forms including extracellular signal-regulated kinases 1 and 2 (ERK 1 and 2), JNK1–3, and p38 (α, β, γ, δ) stress kinase. The MAPKs are distinct in that they have the capacity to respond to a variety of stimuli and transmit a diverse array of intra- and extracellular signals. MAPK signaling is regulated by the kinetics of activation, nearby phosphatase activity, and the cellular domain the MAPKs occupy. Initially, ERK MAPKs were shown to require receptor tyrosine kinase transactivation, through epidermal growth factor receptor activation also initiated phospholipase C signaling to stimulate ERK 1 and 2 phosphorylation, although recent studies have uncovered G-protein-coupled receptor (GPCR) signaling through ERK activation.

**ERK 1 and 2 Signaling at Opioid Receptors.** The most frequently examined opioid-induced MAPK cascade is ERK 1 and 2. Coscia and colleagues have been crucial in developing our understanding of the relationship between opioid receptors and ERK 1 and 2 signaling. In one of the initial studies, MOR and KOR stimulation was demonstrated to initiate ERK 1 and 2 phosphorylation in astrocyte cultures and transfected cell lines. The kinetics of ERK 1 and 2 phosphorylation by MOR and KOR systems vary, yet both receptors can activate ERK 1 and 2 within 5–10 min. MOR-mediated ERK 1 and 2 phosphorylation requires protein kinase C (PKCo) activity, and MOR-dependent ERK 1 and 2 signaling requires Grk-3 and arrestin in primary neurons, glial cells, and heterologous expression systems. The downstream substrates of MOR-mediated ERK 1 and 2 have been defined in some cases and remain unknown in others. In embryonic stem cells, MOR-dependent ERK 1 and 2 signaling positively modulates and directs neural progenitor cell fate decisions. However, in astrocytes chronic morphine can negatively regulate ERK 1 and 2 signaling by tyrosine kinase pathways to ultimately inhibit neurite outgrowth and synapse formation. Most studies use MAPK–ERK (MEK) inhibitors (the proximal upstream kinase) to determine substrates of ERK 1 and 2 signaling in GPCRs; however, few reports have shown direct interaction between μ-opioid–induced ERK and a final substrate. (The in vivo implications of MOR-dependent ERK signaling are explored in Opioid Signaling and Behavior.) Several groups are investigating the potential for ligand-specific ERK agonists at opioid receptors.

δ Opioid receptors have also been shown to activate ERK 1 and 2 through Gβγ and Ras signaling cascades and do not necessarily require receptor internalization or receptor phosphorylation for signaling. DOR-mediated ERK signaling recently was found to require integrin signal transduction through transactivation of epidermal growth factor receptor pathways. DOR-mediated epidermal growth factor receptor activation also initiated phospholipase C signaling to stimulate ERK 1 and 2 phosphorylation. DOR-dependent ERK 1 and 2 signaling requires additional investigation because, coupled with DOR’s critical role in pain and mood regulation, ERK signaling through DOR may reveal a novel mechanism for DOR regulation of neural activity.

KOR-dependent ERK 1 and 2 phosphorylation occurs in a multiphase manner, with an early period of activity between 5–15 min after agonist exposure and a late phase after 2 h of agonist treatment. Similar to other GPCRs, the biphasic ERK 1 and 2 activation for KOR contains an arrestin-dependent late phase and an arrestin-independent early phase. This group identified Gβγ as a crucial mediator in the early-phase ERK 1 and 2 activation by KOR, and showed that arrestin 3 is required for late-phase ERK 1 and 2. KORs activate ERK 1 and 2 through PI3-kinase, PKCo, and intracellular calcium. However, like MOR and DOR, the substrate for KOR-mediated ERK 1 and 2 has not been identified, although a recent study suggests that KOR-induced ERK 1 and 2 also directly affects stem cell fate toward neural progenitor development. ORL1 receptor-dependent ERK 1 and 2 activation has not been extensively examined, although one group has shown that ORL1 receptor activation does initiate ERK 1 and 2 phosphorylation. The signaling pathways for ORL1-mediated ERK 1 and 2 phosphorylation in neuronal cell types and in vivo need additional investigation.

**JNK.** The JNK pathway is activated by environmental triggers, including stress, inflammation, cytokine activation, and neuropathic pain. Classically, JNK activity can result in transactivation of c-jun, a component of the activator protein 1 transcription factor complex, and JNK phosphorylation is caused by cytokines, including tumor necrosis factor and interleukin-1β. JNK activation has also been implicated in numerous other signaling cascades. JNK typically is activated by Ras-related GTP binding proteins in the p
Table 2. A Summary of Current Opioid Receptor-dependent Signaling

<table>
<thead>
<tr>
<th>Receptor</th>
<th>Cascade/Signaling Pathway</th>
<th>Model</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>μ Opioid</td>
<td>↑ ERK 1 and 2 (GRK-3 and arrestin dependent)</td>
<td>In vivo (murine)</td>
<td>Macey et al. 2006&lt;sup&gt;67&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ ERK 1 and 2 (arrestin dependent)</td>
<td>Astrocytes</td>
<td>Miyatake et al. 2009&lt;sup&gt;68&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↓ ERK 1 and 2 (chronic activation)</td>
<td>Astrocytes</td>
<td>Ikeda et al. 2010&lt;sup&gt;69&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ JNK 2 (PKC dependent)</td>
<td>In vivo and HEK293</td>
<td>Melief et al. 2010&lt;sup&gt;35&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ Stat3 phosphorylation</td>
<td>In vivo (murine) and CMT-93</td>
<td>Tan et al. 2009&lt;sup&gt;70&lt;/sup&gt;</td>
</tr>
<tr>
<td>κ Opioid</td>
<td>↑ ERK1 and 2</td>
<td>Astrocytes</td>
<td>Goldsmith et al. 2011&lt;sup&gt;71&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ p38 MAPK (dependent on GRK-3 and arrestin)</td>
<td>Striatal neurons</td>
<td>Belcheva et al. 2005&lt;sup&gt;72&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ JNK 1</td>
<td>Astrocytes</td>
<td>Bruchas et al. 2006&lt;sup&gt;48&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ JAK2/STAT3 and IRF2 signaling cascade</td>
<td>PBMC</td>
<td>McLennan et al. 2008&lt;sup&gt;73&lt;/sup&gt;</td>
</tr>
<tr>
<td>δ Opioid</td>
<td>↑ ERK 1 and 2</td>
<td>HEK293</td>
<td>Bruchas et al. 2008&lt;sup&gt;74&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ ERK 1 and 2 (integrin stimulated, EGFR mediated)</td>
<td>HEK293</td>
<td>Potter et al. 2011&lt;sup&gt;75&lt;/sup&gt;</td>
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<tr>
<td></td>
<td>↑ ERK 1 and 2 (integrin stimulated, Trk1 mediated)</td>
<td>NG108-15</td>
<td>Bruchas et al. 2006&lt;sup&gt;48&lt;/sup&gt;</td>
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<td></td>
<td>↑ PI3K/AKT/↓GSK-3β</td>
<td>DOR-transfected CHO cells</td>
<td>Eisinger et al. 2009&lt;sup&gt;80&lt;/sup&gt;</td>
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<tr>
<td></td>
<td>↑ PI3K/↓GSK-3β (SRC and AMPK dependent)</td>
<td>DOR-transfected CHO cells</td>
<td>Eisinger et al. 2008&lt;sup&gt;83&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>↑ PI3K (SRC and IGF-1 dependent)</td>
<td>DOR-transfected CHO cells</td>
<td>Eisinger et al. 2008&lt;sup&gt;83&lt;/sup&gt;</td>
</tr>
<tr>
<td>ORL1</td>
<td>↑ ERK 1 and 2</td>
<td>Neuro-2a cells</td>
<td>Heis et al. 2009&lt;sup&gt;85&lt;/sup&gt;</td>
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<td></td>
<td>↑ p38 MAPK</td>
<td>Rats NAc</td>
<td>Olianas et al. 2011&lt;sup&gt;84&lt;/sup&gt;</td>
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<tr>
<td></td>
<td>↑ JNK</td>
<td>Rat NAc</td>
<td>Olianas et al. 2011&lt;sup&gt;85&lt;/sup&gt;</td>
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<td></td>
<td>↑ p38 MAPK</td>
<td>NG108-15</td>
<td>Olianas et al. 2011&lt;sup&gt;87&lt;/sup&gt;</td>
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<td></td>
<td>↑ JNK</td>
<td>NG108-15</td>
<td>Shahabi et al. 2006&lt;sup&gt;88&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

↑ = activation; ↓ = deactivation; AKT = serine threonine protein kinase; AMPK = 5′ adenosine monophosphate-activated protein kinase; CHO = Chinese hamster ovary cells; CMT-93 = mouse rectum carcinoma cells; COS7 = monkey kidney fibroblast cell line; DOR = δ opioid receptors; EGFR = epidermal growth factor receptor; ERK1 and 2 = extracellular signal-regulated kinases 1 and 2; GRK-3 = G protein-receptor kinase 3; GSK = glycogen synthase kinase 3; HEK293 = human embryonic kidney cells; IGF-1 = insulin-like growth factor 1; IFN-γ = interferon regulatory factor 2; JAK2 = Janus kinase 2; JNK 1 and 2 = c-jun N-terminal kinase; MAPK = p38 mitogen-activated protein kinase; NG108-15 = neuroblastoma glioma hybrid cell line; ORL1 = opioid receptor like-1; p38 STAT3 = signal transducer and activator transcription 3; PBMC = peripheral blood mononuclear cell; PI3K = phosphoinositide 3-kinase; SRC = proto-oncogene tyrosine-protein kinase.

**Family:**<sup>106</sup> JNK activation by GPCRs and opioid receptors has not been examined thoroughly but has been demonstrated for all the opioid receptor subtypes. Like ERK 1 and 2, arrestin 2 and arrestin 3 have been reported to scaffold JNK signaling complexes, and it is believed that arrestin 3 has JNK 3 specificity, although this remains a matter of controversy.<sup>107</sup> The cellular mechanisms of arrestin-dependent JNK at GPCRs remain unresolved.

**Opioid Signaling:**<sup>88</sup> Opioid-dependent JNK has been demonstrated by only a few groups. DOR causes protein kinase B (Akt)-dependent JNK phosphorylation through a PI3-kinase mechanism, and JNK activity is PI3-kinase independent in others.<sup>108</sup> PI3-kinase is required for μ-opioid–dependent JNK activation. In contrast, U50,488-induced (KOR) JNK activation has been shown to be independent of PI3-kinase.<sup>108</sup> The substrates and in vivo effects of opioid-induced JNK activa-
tion are being studied by several groups. KOR (U50,488, dynorphin) agonists activate JNK in a pertussis toxin-sensitive (Gαi) manner. 35-108,109 U50,488-mediated JNK requires focal adhesion kinases and the GTPase Rac in immune cell types. MOR-induced JNK activation recently was shown to require PKC activity. 35

In two recent studies, KOR- and MOR-induced JNK phosphorylation by norbinaltorphimine and morphine were shown to act as “collateral agonists” to cause JNK phosphorylation and initiate uncoupling of the G protein to block Gαi-mediated transduction. 35,109 The persistent actions of norbinaltorphimine on KOR-agonist-mediated analgesia (21 days) were shown to require JNK because JNK 1 isoform knockout mice show an absence of norbinaltorphimine-dependent 21-day KOR blockade, and selective JNK inhibitors prevented the long-lasting norbinaltorphimine effect. It was also recently identified that the long duration of action of small molecule KOR antagonists in vivo is determined by their efficacy in activating JNK 1. The persistent KOR inactivation by these small-molecule collateral agonists did not require sustained JNK phosphorylation, 32 implicating intermediate protein(s) or alternate JNK substrates in this process. In contrast, acute morphine tolerance was shown to require JNK 2 because JNK 2 knockout mice showed an absence of norbinaltorphimine-dependent 21-day KOR blockade, and selective JNK inhibitors prevented the long-lasting norbinaltorphimine effect.

**Protein–Protein Networks and Opioid Receptors**

In addition to intracellular signaling and receptor modification by phosphorylation, newer biochemical studies strongly suggest that opioid receptors interact with one another, alternate GPCRs, and a whole host of anchoring and membrane protein sets. These interactions are becoming increasingly appreciated as critical to the ultimate functional role of the opioid receptor families. In many ways, the field of protein–protein interactions is at the forefront of opioid receptor molecular pharmacology, as research moves from previous work in heterologous expression systems to in vivo approaches.

**Opioid Dimerization.** Numerous reports have demonstrated that GPCRs exist as dynamic protein complexes with large interactions between proteins and other receptor types. Several studies have shown that GPCRs can form dimers and oligomers. This oligomerization includes two varieties: homodimers (same receptor) and heterodimers (different receptor type) (Fig. 3). The existence of these GPCR homomers and heteromers has been shown in transfected cell line systems, cell lines, and primary cultures and in some cases in vivo (for review see Rios et al. 113 and Prinster et al. 114). Despite that GPCR oligomerization remains a matter of controversy, it continues to generate interest because opioid receptor dimers may reveal novel targets for the development of new opioid drugs.

Devi and colleagues pioneered research into opioid dimerization and originally identified opioid receptor heterodimers. 115 They found that δ receptors can exist as homodimers, and agonist stimulation causes their dissociation. 115,116 In this seminal work, the authors also found that KOR and DOR form heterodimeric complexes, which appear to alter the trafficking properties of these receptors. They showed how agonist-induced internalization of DOR receptors is reduced substantially in cells expressing DOR/KOR receptors. 115 Moreover, it was shown that 6'-guanidinononaltrindole, which selectively targets the KOR or DOR heterodimer, generates a unique signaling entity, giving additional evidence for the existence of opioid heterodimers. 117
It has been shown that MOR can heterodimerize with ORL1, but the existence of MOR or KOR heterodimers remains a matter of controversy. The observation that the antagonism or absence of DOR diminishes the development of morphine tolerance and dependence suggests there may be an interaction between the two receptors, although future biochemical work in vivo is needed to validate these concepts. Studies not only identified the existence of MOR and DOR heterodimers but also revealed that MOR and DOR heterodimers have distinct ligand binding and signal transduction properties, suggesting that heterodimerization may represent an alternative mechanism for the cell to tune and control second messenger activity.

It was hypothesized that the mechanisms and/or proteins that modulate the level of MOR or DOR complexes are critical in the development of tolerance; this theory inspired research into the events that lead to dimerization. Devi and colleagues recently identified additional signaling proteins, such as RTP4, that partake in opioid receptor oligomer trafficking from the Golgi to distribute opioid receptor complexes at the cell membrane. In addition, it was found that MOR activation promotes the formation of complexes between RGS9–2 and Gα subunits. It was shown that pharmacological manipulations were able to disrupt RGS9–2 complexes formed after repeated morphine administration. These data provide a better understanding of pharmacologic approaches that can be used to improve chronic analgesic responses and tolerance.

Some studies have shown that opioid receptors can heterodimerize with other classes of GPCR. For example, MOR can interact and potentially heterodimerize with cannabinoid receptor 1 (CB1) (fig. 3). Interactions between MOR and cannabinoid receptor 1 receptors appear to modulate their effects, as evidenced by the administration of Δ9-tetrahydrocannabinol, a cannabinoid receptor 1 agonist, which can enhance the potency of opioids such as morphine. In addition, the concomitant activation of MOR or cannabinoid receptor 1 heterodimers leads to significant attenuation of ERK activity compared with the response after the activation of each individual receptor.

A number of previous studies have noted interesting functional interactions between the MOR and α2A-adrenergic receptor systems. These studies reported that the presence of α2A receptors is sufficient to potentiate the phosphorylation of MAP kinases in response to morphine, whereas the combination of ligands abolishes this effect. The interactions between MOR and α2A receptors provide an alternate mechanism for the control of receptor function and could have profound effects in the development of opioid-adrenergic analgesics. Neurokinin 1 and MOR have also been shown to heterodimerize. The interaction between these two receptor types does not alter ligand binding or signal transduction but does change internalization and resensitization. In addition, substance P (neurokinin 1 selective ligand) caused cross phosphorylation and cointernalization of MOR. The functional consequences of opioid receptor oligomerization in vivo are largely unknown, unexplored, and matters of controversy. New technological advances in mouse genetics and imaging are crucial in resolving these issues. One major area of continued interest is the in vivo demonstration of opioid receptor homo- and heterodimerization, as well as the development of additional biochemical tools to demonstrate unequivocally that these receptor proteins directly interact with one another.

In addition to receptor–receptor interactions, it is increasingly clear that opioid receptors are highly complex systems and that they interact with a whole host of extracellular, intracellular, and membrane proteins. The notion of opioid receptors existing as dynamic signaling complexes sits at the forefront of the future of opioid-based therapeutics. The reasons for this include the notion that different opioid receptor ligands can induce the formation of a diverse array of receptor complexes. In addition, it is increasingly appreciated that the opioid receptor’s native environment (i.e., cell type, neural circuit) greatly affects the receptor’s ability to signal, traffic, and function. The idea of a binary GPCR as a simple switch mechanism, from off to on, is becoming widely dis-
regarded as new protein–protein interaction networks and ligand-dependent properties are uncovered.\textsuperscript{32,33,35,76,95,131}

**Other Protein–Protein Interactions.** There are multiple lines of evidence pointing to arrestin molecules as crucial proteins that network and engage opioid receptor signal transduction and orchestrate the interaction of proteins within the cellular milieu. The isolation of other opioid-selective protein-interaction networks has been slow, although more studies are examining the important roles in receptor fate. For one, MOR has been shown to interact with numerous cytoskeletal trafficking proteins, most of which participate in membrane protein endocytosis, including GASP-1, spinophilin, glycoprotein M6A, and tama- lin.\textsuperscript{132–134} MOR also has been shown to interact with calmodulin, which is a highly sensitive Ca\textsuperscript{2+} binding protein implicated in cytoplasmic enzyme activity, including adenyl cyclases and CAM kinases.\textsuperscript{135} DORs are similar because they also use GASP-1 and glycoprotein M6A for regulating surface trafficking and endocytosis. KORs have been shown to interact with GEC-1 and EBP50-NHERF proteins, potentially acting to enhance receptor recovery and recycling rates.\textsuperscript{136,137} Given that ORL1 has not been extensively studied, most of our knowledge about its signaling complex centers around the work of the Zamponi group demonstrating ORL1-Cav2.2 complex formation.\textsuperscript{63,138} The increasing specificity and affordability of proteomic technologies, such as tandem affinity purification (TAP tag) approaches,\textsuperscript{139} will help to advance our understanding of opioid receptor complexes. Validating protein–protein interactions \textit{in vivo} continues to be a challenge, but it is expected that with newer mouse genetic tools, proteomic dissection of opioid receptor complexes \textit{in vivo} will become an easier task.

**Opioid Signaling and Behavior**

**μ Opioid Receptors.** The most common behavioral function linked to opioid receptors has been their ability to mediate analgesic effects. Numerous reports have examined how opioid signaling causes opioid-induced analgesia (see Bodnar\textsuperscript{146} \& Walwyn \textit{et al}.\textsuperscript{139}). It is generally accepted that MOR signaling to pertussis toxin-sensitive G\textit{α}i is required for morphine antinociception. In addition, \textit{in vitro} blockade of arrestin 3 expression improves morphine-mediated analgesic responses and acts to prevent morphine tolerance over time.\textsuperscript{141} Spinal cord expression of G\textit{β}y is required for MOR coupling to analgesic responses and is thought to play a key role in how MORs mediate antinociception.\textsuperscript{142} This is likely to be through the modulation of potassium and calcium channels in the dorsal root ganglion and dorsal horn. Morphine-induced analgesia and tolerance have been linked to numerous signaling pathways, including interaction with adenyl cyclases AC1, AC8, and AC5.\textsuperscript{143,144} μ Opioid receptor-dependent behavioral studies linked to MAPKs signaling have begun to become more common in the literature. ERK 1 and 2 phosphorylation has been shown to be up-regulated by chronic morphine treatment and in opioid withdrawal\textsuperscript{145}; consistent with this idea, MOR-induced ERK 1 and 2 activity in the peri-aqueductal gray region acts as a mechanism to counteract morphine tolerance.\textsuperscript{146} Recently, reports have implicated ERK 1 and 2 signal transduction in morphine reward and plasticity, including place preference and psychomotor sensitization.\textsuperscript{147,148} ERK 1 and 2 activity in the amygdala was found to mediate anxiety-like behaviors during morphine withdrawal.\textsuperscript{149} Together, these reports strongly support the concept that ERK 1 and 2 signaling is an essential mediator of μ opioid-induced plasticity in the brain and spinal cord.

**δ Opioid Receptors.** Like MOR, DOR signaling research has been focused primarily on mechanisms of opioid analgesia. In addition, DOR research \textit{in vivo} has been more commonly centered around DOR localization and anatomical characterization, with fewer studies linking DOR signaling with behavioral effects. Ligand-dependent DOR signaling has been an active area of research, with reports suggesting that ligand-mediated trafficking governs agonist-induced analgesic tolerance to δ opioids.\textsuperscript{33,152} These studies demonstrated that the DOR agonists SNC80 and ARM390 differ in their ability to cause receptor internalization and down-regulation of DOR-mediated Ca\textsuperscript{2+} channel modulation. DOR antinociception to thermal stimuli requires phospholipase C, and PKC activation also determines DOR-α\textsubscript{2A} synergistic effects in the spinal cord.\textsuperscript{153} DOR agonists have been studied increasingly for their potential antidepressant and anxiolytic effects in rodent behavioral models.\textsuperscript{154} However, it is not yet known how or where DOR agonists mediate antidepressant-like behavioral responses.

**κ Opioid Receptors.** Contemporary studies linking κ opioid receptor signaling and behavior have been centered around the role of κ opioids in stress (Bruchas and Chavkin\textsuperscript{155} \& Knoll and Carlezon\textsuperscript{156}). Stress-induced opioid peptide release has been reported for all of the major opioid systems, and this release causes stress-induced analgesia \textit{via} action at opioid receptors. In a few crucial reports, it was demonstrated that KOR activation after stress cannot only increase analgesic responses but also can modulate numerous behaviors, including reward and depression.\textsuperscript{73,157,158}
κ Opioid receptor activation of analgesic responses is thought to require Gβγ signal transduction, whereas KOR-induced potentiation of reward and dysphoria are thought to be mediated by more complex events, including but not limited to MAPK activation. Chartoff et al. showed that the KOR agonist salva has a biphasic effect on reward. The acute administration of salva decreased the rewarding impact of intracranial self-stimulation; however, repeated KOR activation caused a net decrease in the reward-potentiating effects of cocaine. Both acute and repeated salva administration increased phosphorylated ERK, but only acute salva increased c-fos, and only repeated salva increased cAMP response element-binding protein. These findings provide more information about the effects of KOR activation on the reward-related effects of cocaine and will assist in the dissection of the relationship between activation of KOR- and ERK-signaling pathways. KOR-mediated p38 MAPK activity has been shown to be required for conditioned place aversion and swim-stress immobility responses, whereas cAMP response element signaling is critical for prodynorphin gene induction and depression-like behavioral responses. It is thought that KOR modulation of dopamine, serotonin, and noradrenergic systems plays a key role in producing the negative behavioral affective responses. Reports include KOR-mediated reductions on dopamine release, along with p38-dependent modulation of serotonergic output. It was shown recently that KOR-induced p38α MAPK signaling in serotonergic circuitry is required for stress-induced social avoidance, depression-like behaviors, and reinstatement of drug-seeking behavior. This report went on to show that KOR-induced p38α MAPK causes a hyposerotonergic state through increased surface serotonin transporter expression. The mechanisms and neural circuits in KOR-mediated dysphoria and analgesia are being studied by several groups; it is hoped those studies will greatly assist in the development of potential antidepressant ligands at KOR and novel analgesics that bypass KOR-mediated dysphoria.

**Opioids and Genetics**

The pathogenesis of addiction involves a series of complex interactions among biological factors, including genetic vulnerability and drug-induced alterations in gene expression and proteins. Despite great efforts, the progress in finding causal variants underlying drug addiction has been somewhat slow. Numerous case-control studies have investigated single nucleotide polymorphisms in opioid receptor genes and their correlation with addiction to opioids. However, these studies often have produced conflicting results. The most extensively researched example is a polymorphism in OPRM1 (A118G, rs1799971), which results in the replacement of asparagine with aspartic acid at codon 40. Three studies found an association with the variant 118G and opioid dependency, two studies observed an association with the common allele 118A and opioid dependency, and nine studies found no overall association with opioid dependency. This polymorphism highlights the conflicting results obtained from genetic studies of opioid receptor genes and drug dependence.

We have summarized the genetic variants that may contribute to vulnerability to develop opioid addiction (table 3). Genetic testing has important clinical applications in the prevention of many diseases, but in the field of addiction, much work remains to be done to understand the associations between these genetic variants and addiction-related phenotypes.

Within the last decade it was learned that the gene encoding the MOR undergoes extensive alternative splicing, resulting in the generation of multiple versions of this receptor protein. However, correlating these splice variants to pharmacologically defined receptors has proven difficult. The relative contribution to the pharmacologic effect of each splice variant could vary from drug to drug and is dependent on each splice variant’s potency and efficacy at a particular site. It has been suggested that the difference in the activation efficacies of various μ opioids for the receptor splice variants may help explain the subtle but clear differences among various μ opioids in the clinic. In addition, understanding the functional significance of some of the truncated receptor splice variants will be beneficial because they have been reported to modulate the activity of opioid receptors in other systems (see Pasternak).

**Conclusions**

In this review, we discuss a wide array of molecular, cellular, and in vivo studies in opioid receptor pharmacology. We highlight the traditional G protein, βγ signaling pathways, and regulatory mechanisms and discuss recent advances in the subfields of biochemistry, MAPK signal transduction, genetics, and behavior. It is important to note that we have not attempted to discuss all of the fine details regarding the properties of each receptor system.

The most common thread in the reports reviewed is that a large body of our understanding of opioid receptor molecular pharmacology continues to stem from in vitro studies. It is also increasingly clear that most molecular and cellular features of opioid receptors remain disjointed and unconnected to any physiological or behavioral effects, which needs to be the focus of future work in this field.

Many of the most important observations and discoveries surrounding opioid receptors have relied on in vitro approaches, and they continue to be the starting point for most laboratories in molecular pharmacology. However, given the diverse functionality of the opioid receptor family and the variety of signaling pathways and interacting proteins, our knowledge of how opioid receptors function in animal models and, more importantly, human populations or disease is limited.

Opioid receptor signaling has been a primary focus of researchers in this field since its discovery. The major reason...
### Table 3. The Association of Polymorphisms in Opioid Receptor Genes with Opioid Addiction and Functional Differences between These Variants

<table>
<thead>
<tr>
<th>Receptor (Gene)</th>
<th>Polymorphism</th>
<th>Synonymous/ Nonsynonymous</th>
<th>Effects and Associations</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>μ Opioid (OPRM1)</td>
<td>A118G (rs1799971)</td>
<td>Nonsynonymous (Asn/Asp, Variant lacks the N glycosylation site in OPRM1 extracellular domain)</td>
<td>118G allele associated with reduced ACTH response to metyrapone</td>
<td>176</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>118G associated with increased endorphin- binding affinity and activity</td>
<td>177</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>118G allele reduces agonist-induced receptor-signaling efficacy</td>
<td>178</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>118G associated with lower OPRM1 expression</td>
<td>179</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>118G altered downstream signaling of ERK 1 and 2 and PKA compared with A118</td>
<td>180</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>118G associated with opioid dependency</td>
<td>162–164</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>118A associated with opioid dependency</td>
<td>165–166</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>118A associated with opioid and alcohol dependency</td>
<td></td>
</tr>
<tr>
<td></td>
<td>C17T (rs1799972)</td>
<td>Nonsynonymous (Ala/Val)</td>
<td>17T allele associated with cocaine dependence</td>
<td>181</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>TT genotype associated with cocaine and heroin use in African American women</td>
<td>182</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>No association with opiate addiction</td>
<td>162; 165;</td>
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<td></td>
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<td>172; 174</td>
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<tr>
<td></td>
<td>A/G (rs510769)</td>
<td>Intron 1</td>
<td>G allele and heroin dependence*</td>
<td>168</td>
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<tr>
<td></td>
<td>C/T (rs3778151)</td>
<td>Intron 1</td>
<td>T allele and heroin dependence*</td>
<td></td>
</tr>
<tr>
<td></td>
<td>C/T (rs6473797)</td>
<td>Intron 2</td>
<td>C allele and heroin dependence*</td>
<td></td>
</tr>
<tr>
<td></td>
<td>A/G (rs569356)</td>
<td>Promoter</td>
<td>G allele significantly higher reporter expression; altered transcription factor binding</td>
<td>183</td>
</tr>
<tr>
<td>δ Opioid (OPRD1)</td>
<td>G/T (rs1042114)</td>
<td>Nonsynonymous (Cys27Phe)</td>
<td>Cys27 compromised ATP-induced intracellular Ca^{2+} signaling</td>
<td>184</td>
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<tr>
<td></td>
<td></td>
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<td>Cys27 ↓ HERP</td>
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<td></td>
<td></td>
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<td>Cys27 reduced maturation efficiency and differential subcellular localization</td>
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<td>C/T rs2236861</td>
<td>Intron 1</td>
<td>T allele and heroin dependence*</td>
<td></td>
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<tr>
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<td>A/G rs3766951</td>
<td>Intron 1</td>
<td>G allele and heroin dependence*</td>
<td>168</td>
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<tr>
<td></td>
<td>A/G rs2236857</td>
<td>Intron 1</td>
<td>G allele and heroin dependence*</td>
<td></td>
</tr>
<tr>
<td>κ Opioid (OPRK1)</td>
<td>OPRK1 Haplotype</td>
<td>—</td>
<td>No association between OPRK1 haplotype and opioid dependency</td>
<td>186</td>
</tr>
<tr>
<td></td>
<td>G36T (rs1051660)</td>
<td>Synonymous</td>
<td>Association of the T allele with heroin dependency</td>
<td>187</td>
</tr>
<tr>
<td>ORL1 (OPRL1)</td>
<td>G501C (rs6512305)</td>
<td>Nonsynonymous (Lys167Asn)</td>
<td>167Asn impairs ERK 1 and 2 activation</td>
<td>189</td>
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<tr>
<td></td>
<td>A/G C206T (rs6090043)</td>
<td>Intron 5’UTR</td>
<td>LDL-induced biosynthesis of LOX-1 receptors is genotype dependent Marginal association with opioid dependence</td>
<td>190</td>
</tr>
</tbody>
</table>

* No association after correcting for multiple testing.

ACTH = adrenocorticotrophic hormone; ATP = adenosine triphosphate; ERK 1 and 2 = extracellular signal-regulated kinases 1 and 2; LDL = low density lipoprotein; LOX-1 = low density lipoprotein-1; ORL1 = opioid receptor like-1; PKA = protein kinase A.
for this interest is that it has been widely accepted that a clear understanding of opioid receptor synthesis, cellular localization, trafficking, and pharmacology will lead to novel therapeutics that either directly act on opioid receptors or modulate opioid receptor signaling pathways. With the advent of conditional genetic approaches, receptor tags, antibodies, fluorescent tools, and optogenetic manipulation of neural circuitry, opioid receptor pharmacology is poised for some major breakthroughs in the next decade. It is hopeful that these new molecular and cellular discoveries will lead to better opioid analgesics in the clinic, with decreased risks of addiction and tolerance. In addition, it is likely that studies at the forefront of molecular and behavioral pharmacology will continue to reveal novel uses for opioids in the treatment of a variety of psychiatric and neurologic diseases.

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