

Opioids: first lessons from knockout mice

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Opioid receptors of the μ -, δ - and κ -subtypes mediate the potent analgesic and addictive actions of opioid drugs. They also regulate responses to pain, stress and emotions when activated by endogenous opioid peptides. Recently, mice lacking opioid receptors or opioid peptides have been produced by gene targeting, providing molecular tools to study opioid function *in vivo*. Observations on mutant mice have shed new light on the mode of action of opioids, opioid receptor heterogeneity and interactions, and the involvement of each component of the opioid system in mouse physiology. In this article, **Brigitte L. Kieffer** reviews the first reported studies and discusses their therapeutic implications.

Opium has been extracted from poppy seeds (*Papaver somniferum*) for several thousand years to fight cough and diarrhoea, to relieve pain, and also because it evokes euphoria. The active ingredients of opium are alkaloid compounds, the so-called opioids. These molecules display strong analgesic¹ and addictive² properties and have been the subject of intense investigations. Morphine is the most active component of opium and was the first opioid to be isolated in the past century. Today, morphine remains the most potent pain killer used clinically, despite a considerable number of adverse side-effects³. Although the 1980s and 1990s led to the development of many novel potent opioids by the pharmaceutical industry, the ideal analgesic is still awaited eagerly. The illegal abuse of heroin, a diacetylated morphine derivative, represents a major public health problem⁴, and mechanisms underlying opioid addiction are still poorly understood^{5,6}.

Several decades of pharmacology have shown that opioid alkaloids produce their biological action at the level of the CNS and specifically activate membrane receptors, thus interfering with a complex endogenous neurotransmitter system. The opioid system is composed of three receptor types known as μ -, δ - and κ -receptors, which are activated by a family of structurally related endogenous peptides. Genes encoding three families of opioid peptides – pro-enkephalin, prodynorphin and pro-opiomelanocortin – and their receptors – MOR (μ -opioid receptor), DOR (δ -opioid receptor) and KOR (κ -opioid receptor) – have been cloned and characterized^{7–10}. This neuromodulatory system has been implicated in the control of behaviours that are essential

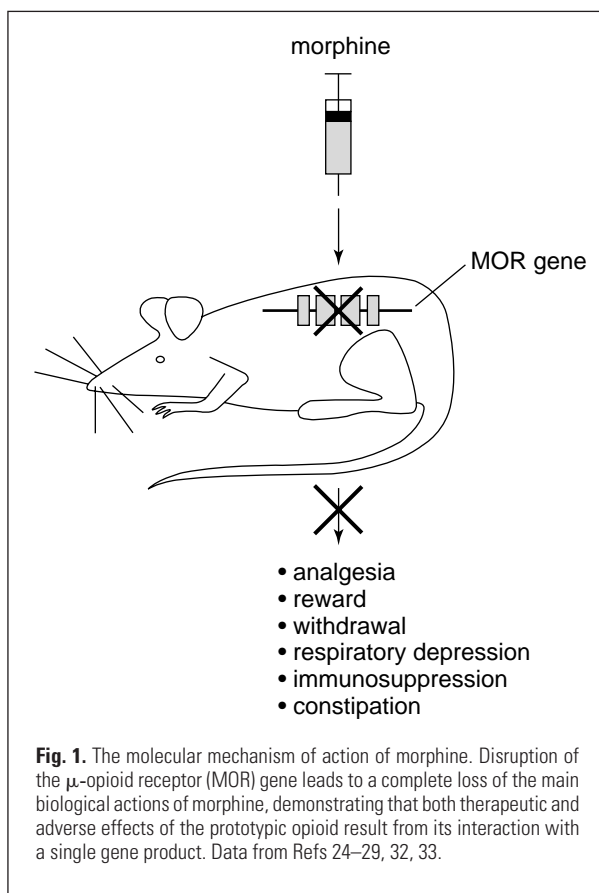
for self and species survival, including responses to noxious information and stress, reward and motivation^{11–14}. Opioid peptides and their receptors also control autonomic functions, including respiration¹⁵, thermoregulation¹⁶, and gastrointestinal motility¹⁷, and they also modulate immune responses¹⁸.

Opioid receptors represent the primary targets for opioid drugs. Because of their high therapeutic potential for the treatment of severe pain, these compounds have spurred decades of pharmacological studies and the development of thousands of novel synthetic derivatives. Most efforts have aimed to increase the selectivity of opioid receptor agonists or antagonists towards μ -, δ - or κ -receptors, with the hope that one could discriminate the biological events mediated by each receptor type and determine whether the desired and adverse effects of opioids could be dissociated. These studies showed that each receptor is distributed differently throughout the CNS (Ref. 19), with some regions expressing all three receptors (striatum and dorsal horn of the spinal cord), although not necessarily in the same neurones, and other regions exhibiting abundant sites for one receptor type only (thalamic nuclei for the μ -receptor or the claustrum for the κ -receptor). They also revealed that each receptor is implicated in opioid function in a distinct manner and to a different extent^{20,21}. Overall, it seems that μ -receptor agonists display the best antinociceptive activity but also the highest abuse liability, that δ -receptor agonists might exhibit less addictive potential, while being poor analgesic compounds and, finally, that the use of κ -receptor agonists for pain treatment should be restricted to the periphery because of the strong dysphoric properties of these compounds.

Until very recently, the issue of the contribution of each receptor type in opioid function was addressed by pharmacological approaches only, because agonists and antagonists were the only available tools. However, interpretation of the data is complicated by poor knowledge of the *in vivo* selectivity of opioid compounds, and their distinct metabolic or pharmacokinetic properties. Although binding affinities and selectivities of the compounds can be determined accurately *in vitro* using brain tissues²² or recombinant receptor preparations²³, one can never exclude the possibility that ligands described as highly μ -, δ - or κ -selective cross-interact with another receptor type *in vivo*. Their mode of action relies on the site of drug administration, the doses involved or the experimental paradigm (acute or chronic treatment). Thus, the exact contribution of each receptor in mediating the biological action of opioid drugs, or in regulating the endogenous opioid physiology, remains to be clarified by other approaches.

Molecular cloning of the receptors and spectacular advances in recombinant DNA methods now make it possible to address the issue by a genetic approach. The activity of known genes can be modified *in vivo* using gene-targeting technology. Recently, mice lacking opioid peptides or receptors have been generated by

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homologous recombination. It is the purpose of this review to summarize what has been learnt from the very early analysis of these mutant mice, and to discuss the future outcome expected from the detailed observation of these exquisite 'tools'. Issues that are being addressed currently in several different laboratories are as follows: (1) How do opioids act at the molecular level, and what are the therapeutic implications? (2) What is the molecular basis for the hypothesized heterogeneity of μ -, δ - and κ -opioid receptor subtypes and the postulated interactions between opioid receptors? (3) How crucial is the opioid system for survival and how are its various components implicated in responses to threatening environmental stimuli?

The mode of action of opioid drugs: which molecular target?

Morphine is the prototypic opioid. In contrast to many synthetic opioids that have been developed in the past 20 years, morphine is an opioid compound with low receptor selectivity. Binding studies performed on rodent brain membranes^{22,24} or recombinant receptor preparations²³ have shown that morphine exhibits a preference for μ -receptors, with K_i values in the nanomolar range, but also binds to δ - and κ -receptors with submicromolar affinities. This two-order-of-magnitude selectivity factor might be sufficient to examine μ -receptor responses using *in vitro* assays, but is rather low to ensure μ -receptor selectivity under *in vivo* testing conditions. Thus, it has

long been believed that morphine activates multiple receptors *in vivo*. The investigation of morphine responses in mice lacking μ -receptors has now elucidated its molecular mode of action unequivocally (Fig. 1; Table 1; Refs 25–34).

Mice that lack μ -receptors (MOR-deficient mice) have been generated by several laboratories, by disrupting exon 1 (Refs 25–27), exon 2 (Ref. 28) or exons 2 and 3 (Ref. 29). Analgesia, the main therapeutic action of morphine, was investigated extensively after acute subcutaneous (s.c.) administration of the drug. Morphine analgesia was abolished at doses that produce potent analgesia in wild-type mice (up to 50 mg kg⁻¹, s.c.) in tail immersion²⁸, tail-flick^{25–27} and hotplate^{25,28} tests. Similar results were obtained following intrathecal or intracerebroventricular (i.c.v.) administration²⁷. The injection of very high doses of morphine in mutant mice indicated a 110-fold increase in the ED₅₀ value when morphine was injected by the s.c. route, and no analgesia following i.c.v. administration (25 μ g, that is, 15 times the ED₅₀ value in wild-type mice)²⁹. Altogether, these data show the absence of morphine antinociception in MOR-deficient mice at doses that classically induce strong analgesia in wild-type mice. This demonstrates that the MOR-encoded receptor is necessary to mediate morphine action on pain pathways and suggests that δ - and κ -receptors do not participate in morphine analgesia under standard experimental conditions. This is corroborated by the finding that morphine analgesia is preserved in mice deficient in the KOR (Ref. 30) or DOR (Ref. 31) genes.

Other major pharmacological actions of morphine have been studied in MOR-deficient mice. One of the most common adverse side-effects of morphine treatment is respiratory depression, a biological action that can be seen after acute administration and which requires tight control in the clinic. Matthes *et al.* showed that an analgesic dose of morphine (6 mg kg⁻¹, s.c.) decreased respiratory frequency and increased respiration time in wild-type mice. However, no change in respiratory parameters could be measured in similarly treated MOR-deficient mice²⁴. Respiratory depression is the primary factor in the lethal toxicity of morphine. Loh *et al.* showed that an extremely high dose of morphine (1600 mg kg⁻¹, s.c.) was required to kill the mutant mice and that death occurred without any of the typical morphine effects²⁹. Another undesirable action of morphine is constipation: Roy *et al.* demonstrated that a single s.c. injection of 15 mg kg⁻¹ morphine greatly inhibits gastrointestinal motility in wild-type mice, whereas no change in gastrointestinal transit was seen in mutant mice at doses up to 35 mg kg⁻¹ (Ref. 32). Acute morphine treatment also induces modification of locomotor activity. Tian *et al.* showed that horizontal locomotor hyperactivity and the inhibition of vertical locomotion, observed in wild-type mice, was absent in MOR-deficient mice²⁶. Morphine also induces euphoria, a response that can be evaluated in animal models using the place-preference paradigm. Matthes *et al.* showed that morphine-

conditioning (repeated low-dose injections, 3 mg kg⁻¹, s.c.) did not induce place preference in mutant mice, under experimental conditions that greatly prolonged the time spent in the morphine-associated compartment in wild-type mice²⁸. Chronic morphine treatment dramatically modifies central as well as peripheral nervous system physiology, including the development of physical dependence, which is generally revealed by morphine withdrawal symptoms. Matthes *et al.* showed the complete absence of somatic signs of withdrawal (jumping, sniffing, teeth chattering, ptosis, wet-dog shakes, paw tremor, tremor and diarrhoea), and vegetative signs (weight loss and hypothermia) in chronically morphine-treated MOR-deficient mice, while all signs were readily observable in wild-type mice²⁸. In addition, the study showed that upregulation of adenylate cyclase activity, a well-described consequence of repeated morphine administration, did not develop in the brain of mutant mice. Therefore, the absence of μ -receptors prevented morphine withdrawal, both at the biochemical and behavioural levels. Finally, another well-documented consequence of chronic morphine treatment is immunosuppression. Gavériaux-Ruff *et al.* demonstrated that repeated morphine administration induced lymphoid organ atrophy, reduced the ratio of immature to mature thymic lymphocytes and greatly impaired natural killer cell activity in wild-type mice. None of these effects, however, could be observed in MOR-deficient mice³³.

In summary, all morphine responses investigated so far are nullified in MOR-deficient mice. The genetic

approach clearly shows that the MOR gene product represents a mandatory molecular target for morphine. In addition, the data show that the main biological actions of morphine, both therapeutic and non-beneficial, are a result of its interaction with the MOR gene product exclusively. Therefore, it appears that activation of the MOR receptor protein triggers a wide spectrum of biological events. A therapeutic implication of these findings is that the development of novel drugs that would specifically target this protein is unlikely to lead to the ideal analgesic drug.

The detailed study of morphine responses in MOR-deficient mice illustrates the usefulness of knockout mice to clarify the molecular mode of action of opioid drugs. The activity of classic opioid compounds that are being used clinically or as pharmacological tools in academic research can now be re-evaluated. Simonin *et al.* showed that the antinociceptive action of the prototypic κ -receptor agonist, U50488H, was abolished in KOR-deficient mice, and that hypolocomotion and aversion produced by the compound were strongly impaired in the mutant mice³⁰. These data establish a direct correlation between the activity of the KOR gene product and the well-documented κ -receptor pharmacology. However, it is noteworthy that residual hypolocomotion is seen at high U50488H doses (20 mg kg⁻¹, s.c.) and some place aversion can occur (with repeated administration of 1 mg kg⁻¹, s.c.) in mutant mice, observations that highlight the limits of *in vivo* selectivity for an agonist which is described as one of the best κ -selective agents. Using MOR-deficient mice, Loh *et al.* demonstrated the absence

Table 1. Mice lacking μ -(MOR^{-/-}), δ -(DOR^{-/-}) and κ -(KOR^{-/-}) opioid receptors: responses to opioids

Opioid (selectivity)	<i>In vivo</i> responses in wild-type mice	MOR ^{-/-}	Refs	DOR ^{-/-} (Ref. 31)	KOR ^{-/-} (Ref. 30)
Morphine (μ)	Spinal analgesia	Abolished	25–29	Maintained	Maintained
	Supraspinal analgesia	Abolished	25, 28, 29	–	–
	Reward	Abolished	28	–	Maintained
	Withdrawal	Abolished	28	–	Decreased
	Respiration depression	Abolished	24	–	–
	Inhibition of GI transit	Abolished	32	–	–
	Immunosuppression	Abolished	33	–	–
	Hyperlocomotion	Abolished	26	–	–
M6G (μ)	Spinal analgesia	Abolished	29	–	–
	Supraspinal analgesia	Abolished	29	–	–
Endomorphin 2 (μ)	Spinal analgesia	Abolished	29	–	–
	Supraspinal analgesia	Abolished	29	–	–
DPDPE (δ)	Spinal analgesia	Decreased	24, 34	Abolished	–
	Supraspinal analgesia	Decreased or maintained	29	–	–
		Decreased or maintained	34	–	–
			24, 29		
Deltorphan II (δ)	Spinal analgesia	Decreased	24	–	–
	Supraspinal analgesia	Maintained	24	–	–
U50488H (κ)	Spinal analgesia	Maintained	24	–	Abolished
	Supraspinal analgesia	Maintained	24	–	Abolished
	Hypolocomotion	–	–	–	Decreased
	Dysphoria	–	–	–	Decreased

DPDPE, *cycli*[D-penicillamine², D-penicillamine³]enkephalin; GI, gastrointestinal; M6G, morphine-6-glucuronide.

of analgesia²⁹ following treatment with morphine-6-glucuronide, a morphine metabolite, and endomorphine 2, a recently reported, highly selective, endogenous μ -receptor-selective peptide³⁵. Zhu *et al.* reported the abolition of spinal analgesia induced by *cyclic*[D-penicillamine²,D-penicillamine⁵]enkephalin (DPDPE, a δ -receptor agonist) in DOR-deficient mice³¹. In the future, mice lacking MOR, DOR or KOR genes will represent unique tools to identify unambiguously the molecular target of novel opioid drugs that are being developed for therapeutic purposes. Also, combinatorial double-mutant mice, expressing one receptor type only, will undoubtedly prove to be useful in this context.

Opioid receptor heterogeneity and cross-talk: what do knockout mice tell us?

A first level of complexity in opioid receptor pharmacology is the postulated existence of functional interactions between opioid receptors^{36,37}. A second consideration is the pharmacological diversity of opioid receptor sites³⁷⁻⁴⁰, which exceeds that of the opioid receptor gene family. Although little has been done so far, the use of receptor-deficient mice has provided some insights into the molecular aspects of these highly debated issues.

The cross-talk between μ - and δ -receptors is best documented from the pharmacology, and is supported by the observation of analgesic responses to combinations of μ - and δ -receptor ligands or by computer analysis of binding data. The analysis of δ -receptor agonist responses in mice lacking μ -receptors now provides a genetic means to determine whether μ - and δ -receptors act in a cooperative manner (Table 1). Three studies describe δ -receptor-mediated analgesia in MOR-deficient mice^{24,29,34}. Spinal analgesia (measured by the tail-withdrawal response) elicited by two highly δ -receptor-selective agonists, DPDPE (Refs 24, 29, 34) and deltorphin II (Ref. 24), was reported to be unchanged²⁹, slightly lower²⁴ or dramatically lower³⁴ in mutant mice compared with wild-type animals. The two latter studies suggest that the presence of μ -receptors is required to obtain full δ -receptor-mediated analgesia in the tail-withdrawal response. Importantly, reversal by a selective δ -receptor antagonist, naltrindole, indicated that the higher δ -receptor-mediated analgesia in wild-type mice was not a result of a nonselective activation of μ -receptors²⁴. The supraspinal antinociceptive response (jumping from the hotplate) measured in a parallel experiment, was found to be diminished³⁴ or preserved^{24,29} in MOR-deficient mice. Although alterations of δ -receptor-mediated analgesia are not concordant in the three studies, presumably as a result of distinct experimental paradigms (Box 1), the data support the existence of synergistic interactions between μ - and δ -receptors, which are revealed under certain experimental conditions. Whether receptor interactions take place between receptors located on distinct neurones, which interact functionally within neural circuits, or from receptor cross-talk in coexpressing cells, is not clear. However the similar potency of

δ -receptor agonists to stimulate G-protein activation or to inhibit adenylate cyclase activity in wild-type and MOR-deficient mice²⁴ provides no evidence for allosteric interactions or receptor crosstalk at the cellular level. Equally important is the observation that δ -receptor agonists retain analgesic properties in MOR-deficient mice^{24,29}, indicating that part of the antinociceptive activity of the δ -receptor is independent from the μ -receptor. This has therapeutic implications and supports the hypothesis that novel highly δ -receptor-selective agonists that are being developed could be clinically useful⁴¹.

There is little evidence for functional interactions between μ - and κ -receptors in nociceptive pathways, both from pharmacological³⁶ or genetic²⁴ approaches (Table 1), but receptor cross-talk might occur in other responses. Of note is the comparison of morphine abstinence in mice lacking μ - (Ref. 28) and κ -receptors³⁰. Morphine withdrawal was abolished in MOR-deficient mice, demonstrating that μ -receptors represent the primary target for the expression of morphine abstinence. This also indicates that morphine dependence does not arise, even partially, from the concomitant nonselective activation of δ - or κ -receptors by the drug. Interestingly, morphine withdrawal, produced under identical experimental conditions, was attenuated in KOR-deficient mice. This indicates that the κ -receptor also participates to the establishment of long-term adaptive changes in response to chronic morphine administration. Altogether, the data suggest that κ -receptors functionally modulate the μ -receptor-mediated response, possibly by acting downstream from μ -receptors along neuronal pathways. Some reports have suggested that κ -receptors might oppose a number of μ -receptor-mediated actions in the brain^{21,42}. However, it seems that both receptors participate in a synergistic manner in the establishment of morphine dependence.

The molecular basis for opioid receptor diversity is unclear. Pharmacological studies have provided arguments for the existence of several subsites for each μ - (μ 1 and μ 2), δ - (δ 1 and δ 2) or κ - (κ 1, κ 2 and κ 3) receptor class. At present, only three homologous genes have been cloned, and the correlation between the biological activity of their encoded proteins and the pharmacological subtypes remains to be established. Pharmacological heterogeneity might arise from the three known MOR, DOR and KOR genes by alternative splicing mechanisms or from variable responsiveness of the three encoded proteins, depending on post-translational modifications, the interacting ligand or intracellular effectors^{40,43}. Another possibility could be the existence of other opioid receptor genes that still need to be isolated. MOR-, DOR- and KOR-deficient mice have made it possible to investigate the latter hypothesis. Binding data performed on the brain of mutant mice suggest that the three known genes account for most reported pharmacological subtypes. Tyr-DAla-Gly-[NMePhe]-NH(CH₂)₂-OH (DAMGO), a prototypic μ -receptor-selective peptide, does not bind to membrane preparations of MOR-deficient mice^{25,27-29}.

Box 1. Methodology

Spontaneous activity of mutant mice (locomotion), their behaviour under threatening situations (acute pain and stress) and their responses to opioid compounds have been evaluated using a large number of classically described behavioural tests.

Locomotion was investigated in all mutant mice. This was done mainly by monitoring horizontal activity in a non-stressful environment using actimetry boxes, or under stressful conditions in an open field. Vertical locomotor activity is reflected by the number of rearings in the open field or actimetry boxes. Motor skills have also been examined using the rotarod test in μ -opioid receptor (MOR)-deficient mice. Animal models that reflect anxiety have been used to examine mice lacking the opioid peptides or κ -receptors. The tests are the open field, the elevated plus-maze or the elevated O-maze, where mice are exposed to an aversive environment. In these tests, exploration or the time spent in central areas (open field) or open sectors (plus- and O-mazes) were monitored, and decreased activity in those parameters was considered to be an indication of increased anxiety. Aggressive behaviour was studied in mice lacking prepro-enkephalin using the resident-intruder test. In this model, mutant males were isolated for several weeks before another male was introduced into their cages. Tolerance to the intruder was then measured and increased aggression was revealed by reduced attack latencies and higher fighting scores.

Pain perception was evaluated by measuring the modification of nociceptive thresholds following a number of acute noxious stimuli. Thermal pain was examined in most mutant mice using the tail-flick or tail-immersion tests. Tail withdrawal from radiant heat (tail flick) or hot water (tail immersion) reflects physiological events that occur mainly at the level of the spinal cord, and increased tail-withdrawal latencies are considered to be a measure of spinal analgesia. Thermal nociception was also investigated in the hot-plate test, where both paw licking and jumping latencies can be measured. Responses in this test involve effects that are integrated at higher brain levels, and decreased thresholds presumably reflect supraspinal analgesia. The two types of tests have been used to measure both basal nociceptive thresholds and opioid-induced analgesia. One model to evaluate inflammatory pain is the formalin test, which was used for prepro-enkephalin- and κ -opioid receptor (KOR)-deficient mice. In this test, injection of formalin into the paw induces local and transient tissue damage, producing inescapable pain, which is quantified by measuring paw-licking, lifting or biting in the early phase of inflammation. Visceral pain was induced in both β -endorphin- and KOR-deficient mice following intraperitoneal acetic acid injections and further measurement of abdominal contractions. In KOR-deficient mice, responses to mechanical pain were also examined in the tail-pressure test, where withdrawal latencies were measured following a locally applied increasing pressure. Stress-induced analgesia was evoked by forced swim in cold water, the water temperature determining the extent of opioid involvement in the analgesic response. Electric foot-shocks were also used to induce stress in the case of prepro-enkephalin-

deficient mice. Post-stress levels of analgesia were evaluated by measuring nociceptive thresholds in tail-flick, hotplate or acetic acid writhing tests.

Commentary

The choice and design of experimental conditions need to be considered carefully when investigating the presence, or absence, of phenotypic changes in the knockout mice and, more specifically, when comparing results from different laboratories. As an example, it is reasonable to think that some apparent discrepancies in behaviours reported for the various MOR^{-/-} mice (locomotion, pain thresholds and responses to δ -receptor agonists) might result from different experimental testing conditions. Another factor of variability stems from distinct genetic backgrounds in the various mutant mouse strains. Classically, homologous recombination is performed in embryonic stem cells from various substrains of the inbred 129 mouse and chimeric animals derived from the recombinant cells are backcrossed further on a more fecund strain, resulting in hybrid mutant mice. Recipient strains are C57BL/6 for two reported MOR-deficient mice^{1,2}, KOR-deficient mice³ and β -endorphin-deficient mice⁴. Another reported MOR-deficient mouse is a Swiss Black hybrid⁵ and mice lacking preproenkephalin are CD1 hybrids⁶. At present, this can obscure some of the conclusions because genetic background is known to influence many behaviours⁷, in particular, responses to opioid analgesics or nociceptive stimuli⁸. The ideal situation would be to standardize backcrossing procedures and produce functionally related mutant mice with an identical genetic background⁹, defined as most appropriate to study the relevant physiology. Although this is an achievable goal, it requires much effort. One must also consider that the several MOR-deficient mice reported to date all derive from different targeting constructs.

Finally, one should note that MOR-deficient mice arise from a targeted manipulation of the mouse genome and, in this respect, differ widely from the previously well-described, inbred, recombinant CXBK mouse strain obtained from the inbreeding of C57 and BALB/c mice. The latter mice exhibit low morphine-induced analgesia as well as other deficient antinociceptive responses, and display low μ -receptor densities in some brain areas; genetic alterations that are responsible for these specific traits remain to be identified¹⁰.

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Table 2. Mice lacking opioid receptors or peptides: behavioural alterations

Behaviour	MOR ^{-/-}	Refs	KOR ^{-/-} (Ref. 30)	Preproenkephalin ^{-/-} (Ref. 46)	β-endorphin ^{-/-} (Ref. 47)
Locomotion	No change in H or reduction in H No change in R No change in V	25 26, 28 25 26	No change in H or OF	Reduction in horizontal and no change in vertical activity in OF	No change in H or OF
Basal nociception:					
Thermal pain	No change in TI and HP Hyperalgesia in TF and HP	28 25	No change in TI and HP	No change in TF Hyperalgesia in HP	–
Mechanical pain (TP)	–		No change	–	–
Inflammation (F)	–		No change	Behavioural alteration	–
Visceral pain (W)	–		Hyperalgesia	–	–
Stress-induced analgesia	–		–	No change after foot-shock (TF) or cold swim (HP)	Reduction after cold swim (W)
Anxiety	–		No change in OF, PM and OM	Increased time close to walls (OF) Less time in open sectors (OM)	No change in OF
Others	Enhanced haematopoiesis Many other immune parameters unchanged Reduced sexual function in males	26 33 26	Larger litter size	Increased aggressive behaviour (RI)	Increased body weight (10–15%)

F, formalin; H, horizontal locomotor activity measured in actimetry boxes; HP, hotplate; OF, open field; OM, elevated O-maze; PM, elevated plus-maze; R, rotarod; RI, resident-intruder; TF, tail flick; TI, tail immersion; TP, tail pressure; V, vertical activity measured in actimetry boxes; W, acetic acid writhing.

Because DAMGO has been reported to recognize both μ 1 and μ 2 receptor sites with high affinity³⁸, the data demonstrate that both μ 1 and μ 2 sites are encoded by the MOR gene. Zhu *et al.* described the absence of DPDPE (δ 1), deltorphin II (δ 2) and naltrindole (δ 1 and δ 2) in mice lacking the DOR gene, showing that δ 1 and δ 2 sites arise from the DOR gene³¹. Finally, Simonin and colleagues report the abolition of CI977 binding and U50488H biological activity *in vivo* in KOR-deficient mutant mice, indicating that κ 1 receptors, the best characterized κ -receptor binding sites, stem from the KOR gene³⁰. The other described κ -receptor subtypes^{38,44} have been difficult to characterize because of the absence of specific ligands³⁹, and the possibility that these sites arise from the three known genes is under investigation by both pharmacological⁴⁵ and genetic means. Ultimately, disruption of the three genes simultaneously in a single animal will indicate if the cloned MOR, DOR and KOR genes encode the entire opioid receptor activity or whether other genes remain to be discovered.

The role of different components of the opioid system in mouse physiology

In addition to MOR-, DOR- and KOR-deficient mice, mutant mice lacking preproenkephalin⁴⁶ and β -endorphin⁴⁷

have been produced. Although the inactivation of all components of the opioid system has not been completed (prodynorphin-deficient mice have not been reported yet), the successful generation of homozygous mutant mice suggests that the absence of a single component of the opioid system is not lethal under home-cage conditions. Furthermore, the adult mice are fertile and display no marked anatomical deficit, indicating that full activity of the endogenous system is not crucial during development. In the future, studies on combinatorial double- or triple-mutant mice might provide evidence about possible redundancy within the opioid system and its implication for survival. Autoradiographic mapping suggests that the lack of opioid receptors induces very few (MOR)⁴⁸ or no (KOR)³⁰ detectable compensatory changes in the expression of the remaining opioid receptor types. The expression of opioid peptide precursor genes also appears to be unchanged in receptor-deficient mice^{28,30}. By contrast, the absence of preproenkephalin induced a marked upregulation of μ -receptors in limbic areas⁴⁹, showing regional-specific control of receptor expression by the peptide. Compensatory modifications in other functionally related neurotransmitter systems have not yet been reported.

Alterations of spontaneous behaviour in the mutant mice have been described in mice lacking μ - or κ -receptors, as well as in opioid peptide-deficient mice (Table 2). Decreased horizontal locomotor activity was reported for mice lacking μ -receptors²⁸ or the prepro-enkephalin gene⁴⁶, which suggests that a basal tone of both ligand and receptor modulate locomotion. It has been proposed that increased anxiety occurs in prepro-enkephalin-deficient mice⁴⁶, on the basis of their modified behaviour in the open-field and elevated O-maze tests. Mice that lack κ -receptors³⁰ do not appear to behave differently from their wild-type littermates in those animal models. Thus, by studying MOR- and DOR-deficient mice, it will be interesting to determine whether the postulated anxiolytic action of enkephalins is mediated by the μ -receptors or δ -receptors.

Responses to noxious stimuli and stressors both involve the opioid system. So far, pain perception has been investigated in acute nociceptive models only (Box 1; Table 2). Increased pain thresholds were observed following thermal stimulation in mice lacking μ -receptors²⁵ and prepro-enkephalin⁴⁶, suggesting a tonic involvement of these two components of the opioid system in the perception of thermal pain. This was not seen in mice lacking κ -receptors³⁰, which otherwise exhibited an enhanced sensitivity to visceral pain. Responses to stress have been investigated in mice lacking opioid peptides and the first evidence indicates an involvement of β -endorphin⁴⁷, but not prepro-enkephalin⁴⁶, in the opioid component of stress-induced analgesia.

Other noticeable changes have been observed in mutant mice (Table 2). To date, however, too few studies have been reported to provide a clear picture of peptide-receptor partnerships in mouse opioid physiology. In addition, phenotypic changes observed in situations that recruit the endogenous opioid system rely on the behavioural paradigm that is used, or on the genetic background of the mutant mice, which influences basal tones and responsivity (Box 1). At present, it is difficult to correlate available data from mice lacking either a peptide or a receptor. Hopefully, in the future, mutant mice will be observed and compared under strictly identical experimental conditions to allow an accurate identification of the specific role of each component of the opioid system in the control of pain and emotions.

Concluding remarks

Mice that lack opioid receptors have proven extremely useful to determine the molecular mode of action of a number of prototypic opioids and represent invaluable tools in drug discovery programmes for the development of novel therapeutic opioids. These mutant mice allow the clarification of some aspects of opioid receptor heterogeneity at the molecular level. Their use for the study of opioid receptor cross-talk is at an early stage, and the issue of functional interactions of the opioid system with other neurotransmitters systems, including dopamine, glutamate or anti-opioid pathways⁵⁰, remains an

entirely open field of investigation. The relevance of opioid receptor occupancy in behavioural and physiological responses might also be investigated by gene dosage effects in mono-allelic or bi-allelic mutant mice. Finally, the use of opioid receptor-deficient mice in sophisticated animal models for the study of chronic pain, stress and reward mechanisms should provide substantial insights into the tonic involvement of μ -, δ - or κ -opioid receptors under challenging environmental situations.

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Chemical names

CI977: (5R)-(5 α ,7 α ,8 β -(–)-N-methyl-N-[7-(1-pyrrolidinyl)-1-oxaspiro(4,5)dec-8-yl]-4-benzofuranacetamide monohydrochloride)

U50488H: (\pm)-*trans*-3,4-dichloro-N-methyl-N-[2-(1-pyrrolidinyl)cyclohexyl]benzenacetamide

Kainate receptors: subunits, synaptic localization and function

Ramesh Chittajallu, Steven P. Braithwaite, Vernon R. J. Clarke and Jeremy M. Henley

Although it is well established that kainate receptors constitute an entirely separate group of proteins from AMPA receptors, their physiological functions remain unclear. The molecular cloning of subunits that form kainate receptors and the ability to study recombinant receptors is leading to an increased understanding of their functional properties. Furthermore, the development of kainate receptor-selective agonists and antagonists over the past few years is now allowing the physiological roles of these receptors and, in some cases, specific subunits to be investigated. As a consequence, the synaptic activation of postsynaptic kainate receptors and the presence of presynaptic kainate receptors that serve to regulate excitatory and inhibitory synaptic transmission have been described, and will be discussed in this article by **Ramesh Chittajallu, Steven Braithwaite, Vernon Clarke and Jeremy Henley.**

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Since the discovery of multiple glutamate receptor subtypes¹, major advances in understanding the structures, distributions and roles that these receptors play in the CNS have been made. However, until recently, research into kainate receptors lagged behind that for AMPA and NMDA receptors owing to the lack of suitable pharmacological tools. The purpose of this review is to discuss how recent advances in molecular biology and pharmacology have led to the identification of the possible physiological roles of kainate receptors in the CNS.

Recombinant kainate receptors**Kainate receptor subunits**

GluR5 was the first mammalian kainate receptor subunit to be cloned, showing ~40% sequence homology to the AMPA receptor subunits GluR1–GluR4 (Ref. 2). To date, another four kainate receptor subunits (GluR6, GluR7, KA1 and KA2) have been identified. These subunits can be divided into two groups on the basis of their structural homology and affinity for [³H]kainate. The low-affinity subunits, GluR5–GluR7, display 75% homology while the high-affinity subunits, KA1 and KA2, are 68% homologous. The homology between GluR5–GluR7 and KA1/KA2 is much lower at ~45%. As with the AMPA receptor subunits, each of the kainate receptor subunits comprises ~900 amino acids with an M_r of ~100 kDa (Refs 2–9) and are believed to have the same membrane topology¹⁰ (Fig. 1). As discussed below, the kainate receptor subunits are subject to both alternative splicing and RNA editing which increase the number of subunit isoforms (Fig. 1).

Alternative splice variants

Alternative splicing of GluR5 yields two variants (GluR5-1 and GluR5-2); the former contains an additional 15 amino acids in the extracellular N-terminal region². Further splice variants of GluR5-2, each possessing one of three alternative C-terminal sequences, have been identified (Fig. 1). The originally identified sequence is designated GluR5-2b, while additional exons located in the C-terminal domain give rise to GluR5-2a and GluR5-2c. This results in the introduction of either a stop codon producing the truncated subunit (GluR5-2a) or an in-frame insertion resulting in the elongated form (GluR5-2c)¹¹. Two C-terminal alternative splice variants of GluR7 (a and b) have also been reported (Fig. 1). The insertion of an additional 40 nucleotide cassette in GluR7b leads to a change in the open reading frame which not only causes an alteration in the amino acid sequence but also an increase in the size of the C-terminal domain. Owing to this splice mechanism, the C-terminal domain of GluR7b possesses no significant sequence homology to other kainate receptor subunits¹². As yet, no alternative splicing has been reported for rat GluR6, KA1 or KA2 subunits. However, additional splice variants have been identified for kainate receptor subunits in other species. For example, human GluR5 and mouse