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Ligands for Ionotropic Glutamate Receptors

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Abstract

Marine-derived small molecules and peptides have played a central role in elaborating pharmacological specificities and neuronal functions of mammalian ionotropic glutamate receptors (iGluRs), the primary mediators of excitatory synaptic transmission in the central nervous system (CNS). As well, the pathological sequelae elicited by one class of compounds (the kainoids) constitute a widely-used animal model for human mesial temporal lobe epilepsy (mTLE). New and existing molecules could prove useful as lead compounds for the development of therapeutics for neuropathologies that have aberrant glutamatergic signaling as a central component. In this chapter we discuss natural source origins and pharmacological activities of those marine compounds that target ionotropic glutamate receptors.

1 Introduction

Marine organisms have provided some of the most well-known and widely used ligands for mammalian iGluRs (Fig. 1). Indeed, one family of iGluRs, the kainate receptors, was named for a molecule derived from a common variety of seaweed that was used extensively in Japanese native medicine as an anthelmintic to treat ascariasis. Despite the prominence in neuroscience research of a limited set of marine natural products that target iGluRs, in sheer numbers far more iGluR-active secondary metabolites, particularly amino acid derivatives, have been derived from terrestrial sources (Moloney 1998,1999,2002). Notable examples include quisqualic acid, from the fruit of the Rangoon creeper *Quisqualis indica* (Takemoto et al. 1975;Takemoto 1978), and willardiine, from the pea seedling of *Acacia willardina* (Gmelin 1959;Ashworth et al. 1972), both of which have played important roles in the pharmacological characterization of iGluRs. Wasp toxins also are sources of metabolites with affinity for iGluRs. Philanthotoxins, which are polyamine-containing toxins from the digger wasp *Philanthus triangulum*, and Joro spider toxins (JSTX) from the Joro spider *Nephila clavata* are open-channel blockers for a subset of glutamate receptors (Clark et al. 1982;Bruce et al. 1990;Blagbrough et al. 1994;Usherwood 2000;Estrada et al. 2007). Numerous other examples of molecules derived from terrestrial organisms exist whose activity on iGluRs have been characterized to varying degrees (e.g., Takemoto et al. 1964;Evans and Usherwood 1985;Konno et al. 1988;Shin-ya et al. 1997a,b;McCormick et al. 1999;Watanabe and Kitahara 2007). This rich abundance of iGluR ligands from terrestrial sources perhaps explains why comparatively few new molecules have been isolated from marine organisms, which are often more difficult to collect and exhibit more limited diversity at the species level. Nevertheless, molecules isolated from marine sources are structurally novel in many cases and for that reason could serve both as important tools in neurobiological research and as templates for development of clinically relevant drugs.

In this chapter we will discuss several broad families of marine-derived iGluR ligands, including peptides isolated from *Conus* snails that target *N*-methyl-D-aspartate (NMDA) receptors and rigid analogs of the excitatory amino acid L-glutamate that predominantly activate non-NMDA receptors, which consist of (S)- α -amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid (AMPA) and kainate receptor families. Molecules that target non-NMDA receptors include kainic acid (KA) and domoic acid (DOM), which are algal products collectively referred to as kainoids because they share a 2,3,4-trisubstituted pyrrolidine core structure (Laycock et al. 1989). The terrestrial excitotoxin acromelic acid, from the Japanese mushroom *Clitocybe acromelalga*, also falls into this structural class. More recent studies discovered two new natural iGluR ligands, dysis herbaine and neodysis herbaine A (Sakai et al. 1997, 2001a), underscoring the potential utility of screening marine benthic organisms for neuroactive molecules. These molecules are structurally distinct from the kainoids and thus constitute a third family of marine-derived ligands for ionotropic glutamate receptors. As a necessary introduction to the molecules themselves, we first briefly review the genetics, pharmacology, and neurophysiology of the three primary members of the iGluR family of subunits, the AMPA, kainate and NMDA receptors.

2 Ionotropic Glutamate Receptors

Ionotropic glutamate receptors are essential to the appropriate function of the mammalian CNS. They mediate chemical synaptic transmission at the vast majority of excitatory synapses, underlie well-characterized cellular models of learning and memory, modulate excitability of neuronal networks, and are required for maturation of synaptic connections during early development (reviewed in Mayer et al. 1992; Hollmann and Heinemann 1994; Aamodt and Constantine-Paton 1999; Dingledine et al. 1999; Huettner 2003; Lerma 2006; Paoletti and Neyton 2007). Modulation of the strength of excitatory synaptic transmission by enhancing or inhibiting glutamate receptor function is under active investigation for therapeutic benefits in a number of neuropathologies, including mild to moderate cognitive impairment and chronic pain (Bleakman et al. 2006; Lynch and Gall 2006; Planells-Cases et al. 2006).

Ionotropic glutamate receptors have been highly conserved during evolution of marine and terrestrial organisms. They subserve similar functional roles in neurotransmission in higher and lower vertebrates, including fish (Nawy and Copenhagen 1987; Kung et al. 1996), and structurally related homologues have been identified from invertebrates such as *Drosophila melanogaster* (Schuster et al. 1991) and *Caenorhabditis elegans* (Hart et al. 1995; Maricq et al. 1995). Their central role in excitatory neurotransmission in a wide variety of organisms in part accounts for the occurrence of natural iGluR ligands used aggressively for prey immobilization (e.g., conantokins). In the following section we confine our brief discussion to the structure, physiology and pharmacology of mammalian iGluRs, because the vast majority of such research has been focused on these molecules. The general principles of receptor function, however, are likely applicable to the true targets of marine excitotoxins in fish and other predatory marine organisms. Reviews with significantly greater detail on the structure, function and significance of each type of mammalian iGluR are available in the recently published book *The Glutamate Receptors* (Gereau and Swanson 2008).

2.1 iGluR Gene Families and Structure

Ionotropic glutamate receptors are ligand-gated cation channels formed from subunit proteins of the AMPA, kainate, NMDA or delta receptor gene families. In mammals, these gene families are known by the acronyms *GRIA*, *GRIK*, *GRIN*, and *GRID*, for Glutamate Receptor, Ionotropic, AMPA (Kainate, NMDA, or Delta) (Fig. 2a). While these subunits have shared structural features and similar primary amino acid sequences, assembly of functional tetrameric receptors is strictly controlled so that each subunit only oligomerizes with partners within its gene family. This restriction ensures, for example, that functional AMPA receptors in the

mammalian CNS only contain AMPA receptor subunits; similar stoichiometric restrictions exist for other iGluRs.

A functional iGluR is composed of four subunit proteins, which can be identical (homomeric receptors) or heterogeneous (heteromeric receptors). The secondary structure of a single iGluR subunit has a generally modular design, with different domains in the proteins playing distinct roles in receptor biogenesis, trafficking, or function (Madden 2002; Greger and Esteban 2007) (Fig. 2b). All iGluR subunits have three transmembrane domains (M1, M3 and M4) and one re-entrant P-loop (M2) similar to that found in voltage-gated channels. The M2 domains form the pore of the channel, whereas other membrane domains are intimately involved in channel gating processes. The large extracellular amino-terminal domain (NTD) is critical for appropriately restricted oligomerization during early steps in receptor assembly and contains allosteric modulatory sites in NMDA receptor subunits (Paoletti and Neyton 2007). The extracellular ligand-binding domain (LBD) is formed from two discontinuous segments of the protein, with the first (S1) located immediately before M1 and the second (S2) between M3 and M4 (Stern-Bach et al. 1994). Each subunit protein contains one binding site for its primary ligand, which in most cases is the excitatory neurotransmitter L-glutamate. While several subunits bind ligands other than glutamate, the tertiary structures of the ligand binding domains of each iGluR subunits are remarkably conserved (e.g., Armstrong et al. 1998; Furukawa et al. 2005; Mayer 2005; Naur et al. 2007), suggesting the fundamental mechanisms for ligand binding and channel gating are common to the different receptor families. Finally, the intracellular carboxy-terminal domains of receptor subunits interact with signaling systems and other protein complexes to modulate function and control trafficking and targeting to synaptic and non-synaptic sites in neurons (Perez-Otaño and Ehlers 2004; Jaskolski et al. 2005; Greger and Esteban 2007).

2.2 AMPA Receptors

AMPA receptors are the “workhorses” of mammalian excitatory synapses. Glutamate release from presynaptic vesicles binds to closely apposed receptors, resulting in channel gating and a brief, localized depolarization of the postsynaptic neuron. Typically, AMPA receptor-mediated excitatory postsynaptic potentials (EPSPs) have a half-time of less than 10 ms, ensuring that receptors are available for re-activation during periods of relatively high frequency input. Summation and propagation of these depolarizing signals to the cell soma can result in initiation of action potentials. Generalized inhibition of AMPA receptors results in cessation of excitatory neurotransmission and, essentially, brain activity.

AMPA receptors are formed from a combination of four individual gene products known as GluR1–4 (with the corresponding genes named *GRIA1–4*) (Hollmann and Heinemann 1994). All AMPA receptor subunits contain a binding site for glutamate and form channels that are permeable primarily to monovalent cations. Notably, receptors lacking the GluR2 subunit are also weakly permeable to calcium (Hollmann et al. 1991). Incorporation of a GluR2 subunit restricts divalent cation permeability as a result of a single amino acid difference from GluR1, GluR3, and GluR4 subunits in the critical pore-forming M2 domain (Dingledine et al. 1992). This amino acid difference (an arginine instead of a glutamine) arises not from a difference in the gene sequence, but rather from a post-transcriptional enzymatic alteration (RNA editing) of an adenosine within the glutamine codon in the mRNA, resulting in its translation as an arginine (Sommer et al. 1991). Functional diversity between receptor subunits is further introduced by an additional RNA editing event, as well as alternative splicing in both extracellular and intracellular domains (Sommer et al. 1990; Lomeli et al. 1994).

Neurons in the mammalian brain appear to use AMPA receptors with distinct stoichiometric combinations of subunits. For example, AMPA receptor excitatory postsynaptic currents (EPSCs) at hippocampal Schaffer collateral–CA1 pyramidal neuron synapses are thought to

arise primarily from GluR2/GluR3 receptors. This is altered during periods of strong synaptic stimulation, which induce insertion of GluR1/GluR2 or GluR2/GluR4 AMPA receptors (Hayashi et al. 2000; Zhu et al. 2000; Shi et al. 2001). In contrast to pyramidal neurons, hippocampal interneurons tend to express AMPA receptors that lack the GluR2 subunit and thus have calcium-permeable populations of receptors (Geiger et al. 1995), which make them sensitive to open-channel blockage by natural polyamine toxins such as philanthotoxin and Joro spider toxin (Iino et al. 1996; Washburn and Dingledine 1996). In principle, this diversity suggests that specific populations of receptors could be targeted pharmacologically, but in actuality there are few identified ligands that exhibit high degrees of selectivity between AMPA receptor subunits.

As will be discussed in subsequent sections, a number of marine-derived agonists that activate kainate receptors with high affinity also act upon AMPA receptors with lower affinity. Kainic acid itself is the best-known example of an agonist with overlapping but divergent affinities for AMPA and kainate receptors. It is clear now, however, that the potent excitant activity elicited by kainoids and dysiherbaines arise largely (though perhaps not exclusively) from their affinity for and activation of kainate rather than AMPA receptors (Mulle et al. 1998; Sakai et al. 2001b).

2.3 Kainate Receptors

Kainate receptors play a variety of roles in the mammalian CNS (Lerma 2006). They modulate excitatory and inhibitory synaptic transmission (Rodriguez-Moreno et al. 1997; Contractor et al. 2000; Kamiya and Ozawa 2000; Schmitz et al. 2000; Frerking et al. 2001; Jiang et al. 2001), modulate some forms of synaptic plasticity (Bortolotto et al. 1999; Contractor et al. 2001; Lauri et al. 2001; Schmitz et al. 2003), control neuronal excitability through inhibitory actions on intrinsic conductances (Melyan et al. 2002, 2004; Fisahn et al. 2005), and can contribute to temporal summation of postsynaptic depolarization in response to bursts of action potentials (Castillo et al. 1997; Vignes and Collingridge 1997; Frerking and Ohliger-Frerking 2002; Jin et al. 2006). Despite these widespread actions in neuronal function, inhibition of kainate receptors (or genetic ablation of one or more subunits) does not have the profound impact on brain activity observed upon inhibition of AMPA receptors (Mulle et al. 1998, 2000; Simmons et al. 1998; Smolders et al. 2002; Contractor et al. 2003; Alt et al. 2007; Pinheiro et al. 2007). This has led to the hypothesis that the roles subserved by kainate receptors are largely modulatory, fine-tuning the balance between excitation and inhibition in the CNS, rather than being obligatory constituents of central synaptic transmission.

Kainate receptors are formed from a combination of five individual gene products, which are further subdivided into two groups based on primary sequence identity and pharmacological specificity. GluR5, GluR6, and GluR7 comprise the first sub-family to be isolated (with the corresponding genes *GRIK1–3*) (Hollmann and Heinemann 1994). These three subunits are collectively referred to as “low-affinity” kainate receptor subunits, because they have a lower affinity for the eponymous ligand, kainic acid, than do the two members of the second sub-family, KA1 and KA2 (*GRIK4 and GRIK5*), which consequently have been referred to as the “high-affinity” kainate receptor subunits. There are important differences in the physiological function of these receptor subunits as well: low-affinity subunits can assemble into functional homo-oligomeric receptors, whereas high-affinity subunits KA1 and KA2 must combine with GluR5, GluR6 or GluR7 to form functional hetero-oligomeric receptors (Egebjerg et al. 1991; Herb et al. 1992; Sommer et al. 1992; Schiffer et al. 1997; Ren et al. 2003). For this reason, KA1 and KA2 are also denoted “auxiliary” subunits to the “principal” GluR5, GluR6 and GluR7 subunits. This concept is somewhat misleading, however, because the majority of neuronal kainate receptors are likely composed of one or more members of both sub-families of subunits as heteromeric receptors (Wisden and Seeburg 1993; Bahn et al. 1994), and thus

both “principal” and “auxiliary” subunits are obligatory to the appropriate functioning of these receptors in the brain.

While inhibition of kainate receptors appears to be well-tolerated by mammalian nervous systems, activation of neuronal kainate receptors with potent and high-affinity agonists, such as kainic or domoic acid, elicits characteristic stereotyped behaviors, tonic-clonic seizures, or even death at high concentrations (Nadler 1979; Ben-Ari 1985). Long-term pathological consequences of sub-lethal exposure to kainate receptor agonists include deterioration of hippocampal pyramidal neurons and lesions similar to that observed in human patients with mTLE (Nadler 1981; Ben-Ari 1985). A similar neuropathology can arise from ingestion of marine organisms (fish or shellfish) containing highly concentrated domoic acid, as is discussed in more detail in the subsequent section.

2.4 NMDA Receptors

NMDA receptors are essential mediators of many forms of learning and memory, and NMDA receptor activation is a requisite early step in most models of long-term synaptic plasticity of excitatory neurotransmission in the mammalian CNS (Dingledine et al. 1999). These receptors have a number of unusual functional features central to their important roles at excitatory synapses. For example, they are the only type of glutamate receptor that requires binding of two distinct agonists, glutamate and glycine, for channel gating (Johnson and Ascher 1987).

As well, NMDA receptors are occluded at physiological membrane potentials by the presence of a Mg^{2+} ion bound to a high-affinity site within the channel pore (Nowak et al. 1984). Voltage-dependent channel block by Mg^{2+} is relieved upon strong depolarization of the postsynaptic membrane, which can occur as a result of robust AMPA or kainate receptor activation or from back-propagating action potentials in the dendritic arbor (Bliss and Collingridge 1993; Spruston et al. 1995; Magee and Johnston 1997). Thus, NMDA receptors function as “coincidence detectors”: in order to gate current, they must receive both a presynaptic signal (glutamate released from the synaptic vesicle) and a postsynaptic signal (depolarization). If these conditions are met, NMDA receptors will open and allow permeation of both monovalent and divalent cations. Relative to AMPA and kainate receptors, NMDA receptors are highly Ca^{2+} permeable (MacDermott et al. 1986; Mayer and Westbrook 1987; Burnashev et al. 1995), and this Ca^{2+} entry through the channel plays a unique role in mediating downstream signals that lead to alterations in synaptic strength. Calcium- and calmodulin-dependent kinase II (CaMKII) and the Ca^{2+} dependent phosphatase calcineurin are perhaps the best-characterized signaling proteins that play central roles in synaptic plasticity downstream of Ca^{2+} entry through NMDA receptors. In addition, Ca^{2+} entry stimulates gene expression to effect protein synthesis-dependent stabilization of alterations in synaptic strength (Nicoll and Malenka 1999; Xia and Storm 2005).

NMDA receptors are formed from heteromeric combinations of three subfamilies of gene products: the NR1, NR2, and NR3 subunits. A single NR1 gene exists in mammals (named *GRIN1*). NR2 subunits are encoded by four distinct genes (*GRIN2A–GRIN2D*). NR3 subunits, the most recent sub-family to be cloned and characterized, are produced by two distinct genes (*GRIN3A and –3B*). Further diversity is introduced into the NR1 family of subunits by alternate splicing events in both the amino- and carboxy-terminal domains, such that a total of eight unique transcripts are utilized in mammalian brains. Functional NMDA receptors are composed of NR1 in combination with either NR2 or NR3 subunits (or, potentially, both types of subunits) (Dingledine et al. 1999; Chatterton et al. 2002; Awobuluyi et al. 2007; Smothers and Woodward 2007). As with all ionotropic glutamate receptor subunits, each NMDA receptor subunit contains a single binding site for a neurotransmitter, but the identity of the endogenous agonist molecule differs between NMDA receptor subunits. Glycine is the native ligand for NR1 and NR3 subunits (Kuryatov et al. 1994; Chatterton et al. 2002), whereas

glutamate binds selectively to NR2 subunits (Laube et al. 1997). Thus, NR1/NR2 NMDA receptors (likely the predominant form found in the brain) have glutamate and glycine as obligate coagonists and are the primary contributors to plasticity in the CNS. NR1/NR3 “NMDA” receptors, in contrast, can be gated by glycine alone (Chatterton et al. 2002); the importance of these unusual receptors in excitatory neurotransmission is not well-characterized.

2.5 Delta Receptors

Delta receptors are a fourth family of receptors that are classified as iGluRs based on structural, rather than functional, similarity (Araki et al. 1993; Lomeli et al. 1993). Glutamate does not bind to or activate either delta-1 (δ_1) or -2 (δ_2) receptors to produce a current. Indeed, the endogenous ligand remains unknown for these receptors, which were classified for many years after their cloning as “orphans.” Recent data suggests that glycine or D-serine could represent physiological ligands (Naur et al. 2007), based on binding studies and resolved crystal structures, but neither elicit a detectable current from the receptors when applied in voltage-clamp experiments. Thus, their mechanism of action remains a mystery. No marine-derived molecules have been identified that target delta receptors, and for that reason we limit our discussion here of these interesting molecules. Several in-depth reviews discuss their potential function and role in development and neuropathology (Yuzaki 2004; Hirano 2006).

3 AMPA/Kainate Receptor Ligands: Kainoids

3.1 Natural Sources and Synthetic Analogs of Kainoids

Kainic acid (KA), the original member of the kainoid family of molecules, was first found from marine red alga *Digenea simplex* (Ceramiales, Rhodomelaceae) (Fig. 3a, b). Aqueous extracts of *D. simplex* were used as anthelmintics in traditional Chinese and Japanese medicine for many centuries (Nitta et al. 1958; Pei-Gen and Shan-Lin 1986), but the isolation and structural determination of KA as the vermifugal principle was first achieved by Takemoto in 1953 (Murakami et al. 1953; Takemoto and Daigo 1958). KA has also been isolated from other species of Ceramiales red algae such as *Alsidium helmithochorton* (Calaf et al. 1989), *Caloglossa leprieurii* (Pei-Gen and Shan-Lin 1986), *Centroceras clavulatum* (Impellizzeri et al. 1975), and certain variety of non-Ceramiales red algae *Palmaria palmata* (Laycock et al. 1989). Tank cultures of a naturally occurring “dwarf” mutant of *P. palmata* provided a source for isolation of KA and other excitatory amino acids such as D-homocysteic acid and glutamate (Laycock et al. 1989). A survey of 46 marine red and green algae found KA or the structural analog domoic acid (DOM) in four and five Rhodomelaceae species, respectively. Interestingly, *D. simplex* itself contained a small amount of DOM (100-fold less than KA), which had not been noted previously (Sato et al. 1996).

In addition to use as a veterinary anthelmintic, KA is well-established as a standard probe in neurological research to elicit currents from neuronal or recombinant kainate receptors and to induce seizure-related behaviors and pathology in animal models of epilepsy. Production of KA for these purposes has relied on both total synthesis and isolation of natural product from algae. The latter process provided a stable and economical resource until the last decade, when isolation from *D. simplex* for commercial purposes ceased, leading to a widespread shortage of KA (Tremblay 2000). Recently, cultivation of *P. palmata* by Ocean Produce International Inc. and synthetic production by other commercial agents re-established a stable production of KA.

Two natural congeners of KA have been isolated from marine organisms. Allokainic acid is the C-4 epimer of KA and was isolated from *D. simplex*. 1'-hydroxykainic acid was found from a KA-producing mutant of *P. palmata* (Ramsey et al. 1994). In addition, a “kainic-peptide”

was isolated from a red alga *A. helminthocorton*; this molecule appears to be a naturally occurring peptide that contains kainic acid as two of its 37 amino acid residues (Calaf et al. 1989), but no further structural information, beyond amino acid analysis, or biological activities have been described.

Recently Sakai and co-workers determined the cellular and subcellular localization of KA in *D. simplex* using immunohistochemical and immunocytochemical techniques (Sakai et al. 2005). A KA-specific antibody localized immunoreactivity within the outmost layer cells in the algal thallus. In subcellular observations using transmission electron microscopy, KA immunoreactivity was found in electron dense cytosolic granule bodies, nuclei, and pit plugs of the cells. No immunoreactivity was observed in epibionts, including bacteria attached to the outer surface of the thallus. Localization of KA in nuclei is of particular interest because the accumulation of secondary metabolites in this structure had not previously been reported. The function of KA in the nucleus, however, remains unknown. The pit plugs are cell-to-cell connective apparatus unique in Rhodophyceae; their physiological role(s) have been elusive but could involve transport of nutritive materials based on morphological observations. Localization of KA immunoreactivity in the pit plug constitutes the first evidence for translocation of cellular material through this structure.

The distribution and occurrence of another marine-derived kainoid, domoic acid (DOM), bears significant importance in the realms of public health and food hygiene. This kainoid is produced by algae that enter the food chain of marine mammals and seabirds, and potentially humans, through accumulation in marine primary producers and higher filter feeders, such as anchovies and certain shellfish (Olney 1994; Watters 1995; Clark et al. 1999; Lefebvre et al. 1999; Mos 2001). DOM was first isolated from red alga *Chondria armata* (Takemoto 1978), and several related compounds – isodomoic acids A to D, isodomoic acid G and H, and domoic lactones A and B – were later identified from the same source (Takemoto 1978; Maeda et al. 1986, 1987; Zaman et al. 1997). To date, ten stereo- and regio-isomers or congeners of DOM have been detected (Clayden et al. 2005).

The ecological and toxicological threat posed by DOM has become evident over the last two decades. DOM-containing algae were also used as vermifugal agents in Japanese folk medicine, similar to *D. simplex*, because DOM is a potent neuronal excitant in both vertebrates and invertebrates arising from its high affinity for kainate receptors (indeed, significantly greater affinity than that of KA itself) (Debonnel et al. 1989; Lomeli et al. 1992). The use of DOM-containing algae for medicinal purposes in humans did not result in any reported incidences of severe toxicity. However, an outbreak of food poisoning resulting from ingestion of DOM-containing blue mussels on Prince Edward Island Canada in 1987 demonstrated its potential for toxicity in humans and was the proximal cause of three deaths (Bates et al. 1989; Wright et al. 1989; Perl et al. 1990b). The clinical manifestation of DOM toxicity included moderate to severe gastrointestinal disorders and neurological symptoms that included disorientation, seizure and memory deficits in a subset of individuals (Perl et al. 1990b; Teitelbaum et al. 1990). One elderly individual who survived the initial intoxication later developed complex partial seizures and exhibited hippocampal neuronal loss and sclerosis similar to that observed in animals following KA-induced toxicity (Cendes et al. 1995). As a result of the striking degree of acute and, in some cases, long-term anterograde amnesia, the term “Amnesiac Shellfish Poisoning” (ASP) was used to describe the clinical consequences of DOM intoxication resulting from consumption of contaminated shellfish (Perl et al. 1990a; Jeffery et al. 2004).

Pennate diatoms belonging to *Pseudo-nitzschia multiseries* species were identified initially as the source organisms that led to ASP after consumption of blue mussels in Canada (Bates et al. 1989). The toxic events localized to the western coast of North America are attributed to

Pseudo-nitzschia australis (Fritz et al. 1992; Lefebvre et al. 1999; Scholin et al. 2000). Additionally, DOM has been detected in diatoms in Japan (*P. multiseriata*) (Fig. 3c, d) (Kotaki et al. 1999), the United Kingdom (*P. australis* Frenguelli, *P. seriata* f. *seriata*) (Cusack et al. 2002; Fehling et al. 2004), and Vietnam (*Nitzschia navis-varingica*) (Kotaki et al. 2000; Lundholm and Moestrup 2000; Kotaki et al. 2004), demonstrating that DOM-producing diatoms can occur throughout many marine ecologies (Bates 2000). Accumulation and depuration of DOM following ingestion of *Pseudo-nitzschia* algae occur at variable rates and in distinct tissues in marine organisms, with the highest concentrations found in anchovies, razor clams and blue mussels following algal blooms on the Pacific coast of North America (Wekell et al. 1994; Lefebvre et al. 2002a, b, 2007).

Mass mortalities of sea mammals and coastal birds of California and Baja California, including the sea lions *Zalophus californianus* (Lefebvre et al. 1999; Scholin et al. 2000), brown pelicans *Pelecanus occidentalis* (Fritz et al. 1992; Work et al. 1993; Sierra Beltran et al. 1997), and Brant's cormorants *Phalacrocorax penicillatus* (Fritz et al. 1992; Work et al. 1993), were attributed to consumption of DOM-containing anchovies *Engraulis mordax*. A decade long monitoring study suggested that increasing numbers of California sea lions with neurological dysfunction and neuroanatomical damage (hippocampal atrophy and sclerosis) was attributable to chronic sub-lethal exposure to DOM (Goldstein et al. 2008). As well, krill (*Euphasia pacifica*) have been identified as a potential source of DOM toxicity that pose a risk to planktivorous organisms (Bargu et al. 2002; Lefebvre et al. 2002a). Governmental and fisheries organizations now routinely screen marine food sources for DOM levels. The US Food and Drug Safety sets a critical limit of 20 ppm DOM in the "edible portion of raw shellfish" (Guide for the Control of Molluscan Shellfish, 2005, available at <http://www.cfsan.fda.gov>), which is well below the levels toxic to humans (Iverson and Truelove 1994). Detection of supra-threshold DOM accumulation in marine organisms has resulted in several instances of temporary bans on fishing of particular species or within affected geographical areas (Trainer et al. 1998; Lefebvre et al. 2002a; Bill et al. 2006).

The physiological function of unusual secondary metabolites such as the kainoids within their marine ecosystem remains a matter of speculation. The most obvious possibility is that their potent and excitotoxic activity on vertebrate and invertebrate iGluRs serves in a defensive capacity to discourage attack.

Intraperitoneal or intracoelomic injection reproduces neurotoxicity observed in vertebrates, but oral gavage or ingestion of DOM is not neurotoxic in fish; (Hardy et al. 1995; Lefebvre et al. 2001, 2007). Furthermore, DOM accumulates without apparent lethality in a variety of benthic organisms (Lefebvre et al. 2002a, b, 2007), although more subtle neurological effects have been observed following exposure during development (Tiedeken et al. 2005). DOM also does not appear to subserve an allelopathic role to discourage competition between algal species (Lundholm et al. 2005). More recently, it was suggested that the excitotoxin might serve as a physiological defense mechanism against krill, which consume the diatoms (Bargu et al. 2006). In this intriguing study, the authors found that DOM effectively reduced krill grazing behaviors and thereby could serve to perpetuate algal blooms.

3.2 Biological Activities of Kainoids

All kainoids elicit currents from both kainate and AMPA receptors. In general, they exhibit higher affinity and potency for kainate receptors, depending on structure and stereochemistry of the side chain functional groups. KA itself exhibits >10-fold higher binding affinity for kainate receptors as compared to AMPA receptors (reviewed in Hollmann and Heinemann 1994). It is a full (or nearly so) agonist that elicits desensitizing currents from most combinations of kainate receptors (see examples in Fig. 4), but only weakly activates AMPA receptors to produce steady-state currents with a very small desensitizing component. Within

the kainate receptor subunit family, KA1 and KA2 kainate receptor subunits have a higher binding affinity for kainate (K_D values of 5–15 nM) than do GluR5, GluR6, and GluR7 (K_D values of 13–95 nM) (Bettler et al. 1990, 1992; Werner et al. 1991; Herb et al. 1992; Lomeli et al. 1992; Swanson et al. 1997). As mentioned previously, KA1 and KA2 have been referred to as “high-affinity” kainate receptor subunits and GluR5–7 as “low-affinity” subunits; it is important to keep in mind that this nomenclature, while useful for categorizing the two sub-families of subunits, is not relevant to their sensitivities to the endogenous neurotransmitter, glutamate.

Application of KA to almost all types of neurons in the mammalian brain causes marked depolarization through the activation of kainate and AMPA receptors, in a concentration- and receptor composition-dependent manner. Thus, KA is only a moderately selective agonist and, in general, currents evoked by high concentrations of kainate (>100 μ M) will arise largely from AMPA receptors, because these receptors tend to be present at much higher density in neuronal membranes compared to kainate receptors. The respective contributions of AMPA and kainate receptors to KA-evoked currents can be differentiated more effectively using a selective AMPA receptor antagonist, such as GYKI 53655, to isolate kainate receptor currents (Paternain et al. 1995, 1996; Wilding and Huettner 1997). Currents evoked by low concentrations of KA (<5 μ M) are largely carried by kainate receptors because of their significantly higher affinity for the marine toxin. This approach has been used, for example, to characterize the modulatory action of presynaptic kainate receptors on AMPA receptor-mediated synaptic currents in the hippocampus (e.g., Kamiya and Ozawa 1998; Contractor et al. 2000). KA played an important role in the early pharmacological and structural differentiation of iGluRs. It was central to definitively establishing its cognate receptor family as a distinct pharmacological entity from AMPA receptors (or Quisqualate receptors, as they initially were denoted) in seminal studies from dorsal root ganglion sensory neurons (Agrawal and Evans 1986; Huettner 1990), which constitute a relatively unique population of neurons that predominantly express kainate receptors as their sole type of iGluR. KA was a critical tool in the iGluR pharmacologist’s armamentarium for nearly a decade because of its unparalleled selectivity, commercial availability and low cost.

A variety of synthetic analogs of KA have been generated, but in large part these molecules have not been characterized as extensively on defined combinations of recombinant kainate or AMPA receptors or on neuronal iGluRs. Structure-activity relationship studies with the KA template indicated that the configurations at C2 and C4 and the composition of the C4 side-chain are particularly critical determinants of receptor selectivity. For example, dihydrokainate, which has a fully saturated C4 isopropenyl group, is a potent competitive substrate for electrogenic glutamate transporters rather than a high-affinity kainate receptor agonist (Johnston et al. 1979; Shinozaki 1988), whereas *trans*-2-carboxy-3-pyrrolidineacetic acid, which lacks the C4 group entirely, exhibits agonist activity on NMDA receptors (Tsai et al. 1988). Also, high affinity binding to and agonist activity on human recombinant GluR6 receptors was maintained in a variety of analogs with aryl substitutions of the C4 side-chain, but stereochemical reversal of the C4 position greatly reduced affinity for the receptor subunit (Cantrell et al. 1996). The natural terrestrial toxin acromelic acid is a C4 aryl-substituted KA analog (Konno et al. 1988) and thus may show a similar high affinity for a subset of kainate receptor subunits, although this has not been demonstrated formally.

The pharmacological actions of DOM are similar to that of KA; it is a high-affinity kainate receptor agonist and somewhat lower affinity AMPA receptor agonist. It binds, activates and desensitizes all homomeric and heteromeric kainate receptors, albeit to differing degrees and with distinct potencies. GluR5–2a receptors, which exhibit a particularly high affinity for domoate, gate a slowly desensitizing current upon activation by the marine toxin, whereas GluR6a receptors rapidly desensitize to a stable equilibrium current (Fig. 4) (Herb et al.

1992;Swanson et al. 1997). DOM is more potent and has a higher binding affinity for kainate receptors than KA (K_i values of ~2–60 nM) (reviewed in Hollmann and Heinemann 1994). Like KA, it is a partial agonist for AMPA receptors that elicits steady-state currents with a minimal desensitizing component. The actions of KA and DOM on non-NMDA receptors have been compared in a detailed review (Hampson and Manalo 1998).

Those natural analogs of DOM (the isodomoic acids) that have been examined generally display a lower potency and affinity for kainate and AMPA receptors. The radioligand binding affinities of isodomoic acid A and C for the GluR6 subunit are ~40- and ~240-fold lower than that that of DOM, respectively (Holland et al. 2005; Sawant et al. 2007); consistent with this observation, isodomoic acids A and C were less effective than DOM in reducing hippocampal population spike amplitudes (an effect known to be mediated predominantly by neuronal kainate receptors) (Sawant et al. 2007). Isodomoic acids D, E, and F have 5–280-fold lower affinities for high-affinity KA binding sites in the rat brain, which (at low radioligand concentrations) primarily arise from kainate receptors (Hampson et al. 1992).

In addition to its central importance to iGluR pharmacology research, KA has been widely used as an excitotoxic agent in behavioral and neuropathological studies (Nadler 1979, 1981; Ben-Ari 1985; Ben-Ari and Cossart 2000). Acute administration of kainoids induces characteristic acute behavioral changes in rodents, including stereotyped movement such as scratching behavior, head bobbing, and frequent grooming after ~10 min (Sperk 1994). The symptoms progress into more frequent and violent behaviors and, dependent upon the concentration of the toxins, animals display clonic whole body convulsions. At high doses, animals die after severe seizure episodes similar to those observed in humans. Repeated administration of KA will induce a permanent hyperexcitable state in animals marked by recurring convulsions, thought to mimic status epilepticus in humans (Ben-Ari and Cossart 2000). The seizurogenic action of DOM is more potent than that of KA, and it can induce long-lasting status epilepticus persisting for hours in mice (Chiamulera et al. 1992; Sakai et al. 2001b).

The neuroanatomical alterations and damage to the limbic regions produced by kainoid injection into rodents or ingestion of environmental DOM by some marine organisms partially reproduces that observed in patients with mTLE (Ben-Ari 1985). The rodent kainate-induced neuropathology model continues to be used as one diagnostic assay in screening potential anti-epileptic drugs (Loscher 2002). A discussion of the extensive literature on this model is beyond the scope of this chapter, but it has been the subject of a number of excellent reviews and book chapters (Sperk 1994; Dudek et al. 2006; Ratte and Lacaille 2006).

4 AMPA/Kainate Receptor Ligands: Dysiherbaines

4.1 Natural Sources and Synthetic Analogs of Dysiherbaines

Dysiherbaine (DH) is the first member of a new structural class of marine-derived iGluR agonists with a high degree of specificity for kainate receptors. In the course of screening for new excitatory amino acids from marine benthic organisms, Sakai and co-workers found that an aqueous extract of a sponge initially identified as *Dysidea herbacea*, which later analysis revealed was instead *Lendenfeldia chodrodes* (Fig. 3e), exhibited potent convulsant activity when injected into mice. The active principal isolated from the sponge extract was unprecedented and was comprised of a functionalized perhydro furanopyrane skeleton furnished with a 2-ami-nopropanoic acid side-chain (Sakai et al. 1997,2006). Similar to kainoids, the structure of L-glutamate was embedded in DH and thus the toxin can be considered a C di-substituted analogue of L-glutamate. Subsequent searches for related compounds from the same sponge species resulted in an isolation of neodysiherbaine A (NDH A), an analog of DH with similar convulsant activity in mice (Sakai et al. 2001a). In addition

to DH and NDH A, several structurally novel betaines, denoted dysibetaine PP, CPa and CPb, were isolated from the same sponge (Sakai et al. 2004). Weak affinity for NMDA and kainate receptors was observed in ligand-binding assays, but the pharmacological activity of the dysibetaines is not well-characterized beyond these preliminary results. The production of this array of structurally unusual molecules in the marine sponge underscores its diverse biosynthetic machinery and suggests that additional bioactive molecules await discovery (Sakai et al. 2006).

Recently Sakai and co-workers examined the localization of DH within the sponge tissue using immunohisto- and immunocytochemical techniques. Molecular analysis of the ribosomal DNA sequence revealed that the taxonomy of the sponge was in fact *Lendenfeldia chodrodes* rather than *D. herbacea*. Moreover, localization of DH using a selective antibody found the toxin exclusively in the cells of endosymbiotic cyanobacteria, of *Synechosystis* sp. (Fig. 3f), suggesting that DH is in fact a metabolite of the cyanobacteria rather than the sponge itself (Sakai et al. 2008).

Because of its intriguing structural and biological features, intense efforts were undertaken towards the synthesis of DH. The first total synthesis by Hatakeyama and co-workers confirmed the proposed structure and absolute stereochemistry of DH (Masaki et al. 2000). To date, four total and one formal syntheses of DH, four total syntheses of NDH A, and structure-activity relationship (SAR) studies of NDH A have been reported (Masaki et al. 2000; Sasaki et al. 2000, 2007; Snider and Hawryluk 2000; Phillips and Chamberlin 2002; Lygo et al. 2005; Takahashi et al. 2006). A variety of DH analogues have been described, although only DH and NDH A are natural products derived from the sponge (Sasaki et al. 1999, 2006; Cohen et al. 2006; Shoji et al. 2006). Extensive molecular pharmacological and electro-physiological characterizations, as well as in vivo pharmacology, demonstrate that DH and its structural analogues are a new generation of excitatory amino acids with distinct receptor selectivity and agonist actions as described in the next section.

4.2 Biological Activities of Dysiherbaines

DH and neoDH are extraordinarily potent convulsants with high-affinity agonist activity on mammalian kainate receptors, a lesser potency for AMPA receptors, and (in the case of DH) an extremely weak activity on mGlu5 metabotropic glutamate receptors (Sakai et al. 2001b). Their pharmacological specificity for different KAR subunits diverges significantly from kainoids, which likely underlies their marked convulsant activity. Whereas KA exhibits highest affinity for the KA1 and KA2 subunits, DH and neoDH instead bind with very high affinity to GluR5, GluR6 and GluR7 KAR subunits (K_i values of ~0.5–1.5 nM) (Sakai et al. 2001b) but only have very weak interaction with KA2 subunits (K_i value of 4.3 μ M, comparable to their affinity for AMPA receptor subunits) (Swanson et al. 2002). The action of DH on homomeric GluR5 and GluR6 receptors is unusually long-lived because the marine toxin effectively promotes a stable, desensitized conformation of the receptor, which can prevent unbinding of the agonist and subsequent re-activation by agonists (Swanson et al. 2002). While the nanomolar binding affinities exhibited by these molecules for the “primary” KAR subunits are indeed quite high, they are not so high as to suggest that the ligand-receptor interaction would be effectively irreversible (as is the case of DH and homomeric GluR5 receptors, for example). Receptors composed of both high- and low-affinity subunits, and in particular GluR5/KA2 receptors, exhibit a further twist in their biophysical response to DH. Application of DH to GluR5/KA2 receptors elicits a slowly desensitizing current, as is typical for many agonists, but upon removal of the agonist from the bathing solution a slowly developing, steady-state current emerges that arises from the stable association of DH with GluR5 subunits, resulting in a tonic partial activation of the heteromeric GluR5/KA2 receptors (Swanson et al. 2002). Thus, the pharmacological activity of the DH molecules on KARs is critically determined by

the subunit composition of the receptors, which can be complex and which is not well understood at the molecular level. A more detailed review of this topic can be found in Sakai et al. (2006). Kainate receptors have diverse compositions in the mammalian brain, and therefore DH will impact neuronal function dependent upon a variety of factors, including toxin concentration and neuronal site of action (Sakai et al. 2001b).

DH has been shown to be the most potent seizurogenic excitatory amino acid isolated from natural sources (Fig. 5a) (Sakai et al. 2001b). The convulsant activity of DH was found to be approximately six-fold more potent than that of DOM (Table 1). Seizure behaviors induced by injection of DH in mice were chiefly distinguished from those elicited by kainoids in the duration of the status epilepticus. Mice receiving DH (40 pmol/mouse, i.c.v. or 1.6 mg/kg, i.p) experienced severe whole body convulsions for more than 3 h, which then stabilized into periodic recurrent seizures. This state, which was not replicated by KA or DOM, lasted for more than 24 h. It is possible that this unique behavior arises from stable binding of the toxin with a subset of kainate receptors similar to that observed with recombinant receptor subunits. Indeed, a recent study showed that the seizurogenic potency of a diverse panel of DH-related molecules was strongly correlated with their affinity for the GluR5 KAR subunit (Fig. 5b), suggesting that activation of receptors comprised of this subunit primarily underlies toxin convulsant activity (Lash et al. 2007). It remains unknown whether the longer-term neuropathological consequences of seizure induction with DH closely resemble the well-characterized pattern of limbic structural reorganization, neuronal loss, and sclerosis produced in the kainate model of mTLE.

The structural determinants that underlie DH and neoDH affinity for kainate receptors have been explored in studies with synthetic analogs (Shoji et al. 2006). The C8 and C9 functional groups, in particular, confer specificity for the GluR5 and GluR6 KAR subunits. Elimination or epimerization of the C9 hydroxyl essentially eliminates binding to GluR6 subunits, as does similar alterations to the C8 group; in contrast, binding to GluR5 subunits is more tolerant to modification at C9 and is unaffected by elimination of the C8 moiety (Lash et al. 2007). This likely arises from the spatially larger binding pocket and the presence of favorable hydrophobic and polar interactions in the GluR5 binding domain as compared to GluR6 (Mayer 2005; Naur et al. 2005; Sanders et al. 2006). Interestingly, removal of both functional groups to produce dideoxy-neoDH (also known as MSVIII-19) fundamentally altered pharmacological activity; this molecule was an antagonist for homomeric GluR5 receptors, rather than an agonist (Sanders et al. 2005). Molecules with similar pharmacological profiles are under active examination for efficacy in a variety of animal models of neuropathologies, including epilepsy and chronic pain. MSVIII-19 is weak convulsant that additionally promotes an reversible unconscious state when injected intracerebroventricularly (i.c.v) in mice (Sasaki et al. 1999) but has relatively modest effects on motor function when introduced via intrathecal or intraperitoneal injection. Finally, epimerization of neoDH at the C4 position, which disrupts the glutamate congener in the molecule, reduced but did not eliminate affinity for GluR5 and GluR6 subunits (Lash et al. 2007). Given these precedents, further modifications to the DH template structure may yet produce molecules with distinct pharmacological profiles or activities on kainate receptor subunits.

5 NMDA Receptor Ligands: Amino Acids

5.1 Natural Sources of Amino Acid Ligands Acting on NMDA Receptors

Several compounds with selectivity for NMDA receptors have been identified from marine organisms. NMDA itself was detected from foot muscle of blood shell, *Scapharca broughtonii* (Sato et al. 1987). More recently, endogenous NMDA was discovered in the tunicate *Ciona intestinalis* (D'Aniello et al. 2003), where it is biosynthesized from precursor D-aspartate; in the tunicate gonads, NMDA induced synthesis of gonadotropin-

releasing hormone (GnRH), which in turn led to production of sex steroid hormones. A survey in marine algae for *N*-methyl aspartic acid (with an unspecified stereochemical configuration) found that eight out of 42 algae collected contained the compound (Sato et al. 1996); the physiological function of these amino acids in the algae is unknown.

Two 4,5-substituted analogs of pipercolic acid with activity on NMDA receptors have been isolated: cribronic acid [(2*S*,4*R*,5*R*)-5-hydroxy-4-sulfooxy-piperidine-2-carboxylic acid], from the Palauan sponge *Cribrochalina olemda*, and (2*S*,4*S*) 4-sulfooxy-piperidine-2-carboxylic acid (*trans*-4-hydroxypipercolic acid sulfate, *t*-HPIS) from the Micronesian sponges *Axynella carteri* and *Stylotella aurantium* (Sakai et al. 2003). Cribronic acid was a new compound while *t*-HPIS had been isolated previously from the legume *Peltophorum africanum* and characterized as NMDA agonist (Evans et al. 1985; Moroni et al. 1995).

Lophocladines are alkaloids with 2,7-naphthyridine skeletons isolated from red algae *Lophocladia* sp. collected in the Fijian Islands. One of the isolates, Lophocladine A, was shown to have affinity for the MK-801 binding site in the channel pore of NMDA receptors, suggesting that this compound might represent a novel class of naturally occurring small-molecule NMDA receptor antagonists. Validation of this possibility awaits physiological studies. A closely related analog, Lophocladine B, did not show equivalent affinity for NMDA receptors; rather, it inhibited microtubule formation and was cytotoxic (Gross et al. 2006).

5.2 Biological Activities of Natural NMDA Receptor Agonists

Both cribronic acid and *t*-HPIS were potent convulsants when injected i.c.v. in mice, producing dose-dependent behaviors, from running, jumping, and tonic extension to lethal convulsions, with ED₅₀ values of ~20–30 pmol/mouse (Sakai et al. 2003). *t*-HPIS and cribronic acid displaced CGP 39653, a ligand for the glutamate binding site on NMDA receptors, from rat cerebrocortical membrane preparations with IC₅₀ values of 214 nM and 83 nM, respectively. Neither compound displaced radiola-beled ligands from AMPA and kainate receptors. The agonist activity of *t*-HPIS on NMDA receptors was confirmed earlier in mouse cortical wedge preparations, in which the molecule caused dose-dependent depolarizations that were reduced by AP-5, an NMDA-receptor antagonist (Moroni et al. 1995). The relative depolarization potency of *t*-HPIS was about 5 times that of NMDA in the cortical preparation. Nothing is known regarding the NMDA receptor selectivity of these compounds. Interestingly, structurally related three- and four-substituted pipercolic acid analogs act as potent NMDA receptor antagonists and have been modified and studied extensively in pursuit of neurotherapeutic drugs (e.g., *cis*-4-phosphonomethyl-2-piperidine carboxylic acid, CGS 19755, Selfotel) (Lehmann et al. 1988). Thus far, however, this pharmacological approach has not proven beneficial in clinical trials for stroke mediation, and instead have tended to exacerbate neurotoxicity associated with ischemia (Davis et al. 2000).

6 NMDA Receptor Ligands: Conantokins

6.1 Natural Sources of Conantokins

Venoms from fish hunting snails, a genus of *Conus*, are a rich source of diverse neuroactive peptides targeting various voltage-gated ion channels, neurotransmitter receptors and transporters (Terlau and Olivera 2004). *Conus* peptides are categorized into a variety of families based on pharmacological targets and structural characteristics. Until very recently, the conantokin family of cone snail peptides contained four members, conantokin-G, -L, -R and -T (con-G, con-L, con-R, and con-T), which were shown to act as NMDA receptor antagonists (reviewed in Prorok and Castellino 2007). Conantokins are relatively unusual because they lack the disulfide bridges critical for structural integrity in most conopeptides and because the conantokins contain four to five γ -carboxyglutamates, a modified amino acid, in their structure.

These first four conantokins range in size from 17 (Con-G) to 27 amino acids (Con-R). Con-G, from *Conus geographus* (Fig. 3g), was the first member of the family discovered and was isolated on the basis of its unusual bioactivity in mice: it produced a sleep-like state (McIntosh et al. 1984). This “sleeper peptide” was proposed initially to target NMDA receptors based on indirect biochemical assays (Mena et al. 1990) and later confirmed using physiological recordings from NMDA receptor channels (Hammerland et al. 1992). Con-T was isolated from *Conus tulipa* based on similar behavioral effects (“sleep” induction) in mice and found to have structural similarities to con-G (Haack et al. 1990); namely the initial glycine-glutamate- γ -carboxyglutamate- γ -carboxyglutamate residues were conserved in the two peptides. This sequence is also present in con-R, from *Conus radiatus* (White et al. 2000), and con-L, from *Conus lynceus* (Jimenez et al. 2002). A new, closely related series of conopeptides targeting NMDA receptors, conantokin-Pr1 to -Pr3 (con-Pr1 to -Pr3), was recently discovered from *Conus parius* (Teichert et al. 2007). Notably, this species of cone snail is the first whose venom contains multiple conantokin peptides. They diverge structurally from the four original conantokins, primarily in that the con-Pr toxins have only three γ -carboxyglutamate residues and two of the members (con-Pr2 and con-Pr3) contain another modified amino acid, 4-*trans*-hydroxyproline. Con-Pr peptides also induce a sleep-like state in mice (Teichert et al. 2007).

6.2 Biological Activities of Conantokins

Conantokins are peptide antagonists selective for NMDA receptors (Haack et al. 1990; Mena et al. 1990; Hammerland et al. 1992; Jimenez et al. 2002; Prorok and Castellino 2007). Con-G, the most extensively characterized conantokin, has appeared to have both competitive and noncompetitive antagonist activity in different assays for NMDA receptor function (Prorok and Castellino 2007). Competitive antagonism occurs at the glutamate binding site on the NR2 subunit (Hammerland et al. 1992; Donevan and McCabe 2000; Wittekindt et al. 2001), with an IC_{50} of ~ 0.5 – $1 \mu M$ for inhibition of NMDA-evoked currents in cultured mouse cortical neurons or for inhibition of synaptic NMDA-EPSCs in CA1 pyramidal neurons in rat hippocampal slice preparations (Donevan and McCabe 2000; Barton et al. 2004). The molecular binding site of con-G could be heterotropic, because the inhibitory activity is enhanced by polyamines such as spermine (Donevan and McCabe 2000), which binds to an extracellular allosteric modulatory site. Con-G also exhibits a high degree of subunit selectivity; inhibition of NR1/NR2B NMDA receptors is potent, whereas NR1/NR2A receptors (or those containing NR2C or NR2D) are relatively unaffected by the peptide (Donevan and McCabe 2000; Klein et al. 2001). This degree of selectivity does not extend to all conantokins, however, as con-R and con-T inhibit both NR2A- and NR2B-containing receptors (White et al. 2000; Klein et al. 2001). Conantokins, and in particular con-G, have attracted significant attention for their potential as therapeutics in a variety of neuropathologies (Layer et al. 2004). Con-G and con-T are effective antinociceptive agents in models of chronic pain (Malmberg et al. 2003), although their peptide structures restrict potential routes of administration. Con-G and con-R, but not con-L, also show anticonvulsant efficacy in a number of mouse seizures models (White et al. 2000; Jimenez et al. 2002; Barton et al. 2003). Con-G, which in its pre-clinical form is known as CGX-1007, also has neuroprotective effects in stroke models (Williams et al. 2000, 2003). While CGX-1007 was found to be safe in Phase I clinical trials, further clinical trials have not been disclosed (Olivera 2006).

Con-Pr peptides also induced the characteristic sleep-like state after injection observed decades earlier with con-G (McIntosh et al. 1984) and inhibited recombinant NR1/NR2 NMDA receptors expressed in *Xenopus* oocytes, with varying degrees of selectivity for NR2B-containing receptors (Teichert et al. 2007). Their pharmacological profiles were distinct from those of the earlier conantokins and consequently will provide additional tools and clues for understanding how the structure of these unusual peptides determines their functional activity and subunit specificity.

7 Unpurified Bioactive Extracts

Several studies found crude extracts with bioactivity that appeared to target iono-tropic glutamate receptors. For example, extracts of cultured bacteria associated with the marine sponge *Halichondria panacea* activate rat cortical NMDA receptors; the active principle(s) were not further isolated, however (Perovic et al. 1998). Garateix and colleagues carried out an ecologically-inspired search for iGluR ligands from marine organisms that prey on crustaceans, leading to the discovery of bioactive peptide-containing fractions from a sea anemone, *Phyllactis flosculifera* (Garateix et al. 1996). Peptide fractions of extracts from the animal diminished both the excitatory and the inhibitory responses to glutamate agonists in neurons of the land snail *Zachrysis guanensis*. Similarly, a crude extract from the sea anemone *Bunodosoma caissarum* induced convulsions following intracerebro-ventricular (i.c.v.) injection in mice. The convulsion was suppressed by chlorokynurenic acid, an antagonist of the glycine site on the NMDA receptor (Gondran et al. 2002). Isolation and structures for these sea anemone products have not been reported to date.

8 Conclusion

Marine-derived compounds have played key roles in iGluR research. The recent discovery of the dysiherbaines and the con-Pr peptides, and the variety of bioactive extracts with unknown active principles, suggest that additional and novel molecules await the attention of neuroscience researchers. One of the central challenges for finding new molecules lies in the very early steps of characterizing bioactivity. While stereotypic seizure behavior and convulsions or sleep-inducing activity are obvious behavioral responses that lend insight into potential biological activity, extracts containing bioactive molecules that elicit less dramatic responses, but which have novel pharmacological profiles, could potentially be overlooked. It is clear, however, that synthetic modification of natural analogs can dramatically alter their pharmacological action (see, for example the DH analog MSVIII-19), and thus it is worthwhile to pursue even those active principles lacking obvious clinical application (such as convulsants). A revived appreciation of the potential utility of drugs from the sea and other natural sources is evident in the form of new initiatives, from funding bodies such as the US National Institutes of Health, which hope to spur development of higher-throughput identification and isolation of natural source compounds that could impact human health. It is likely that these efforts will produce molecules with new structures and specificities for iGluRs to supplement those described in this chapter.

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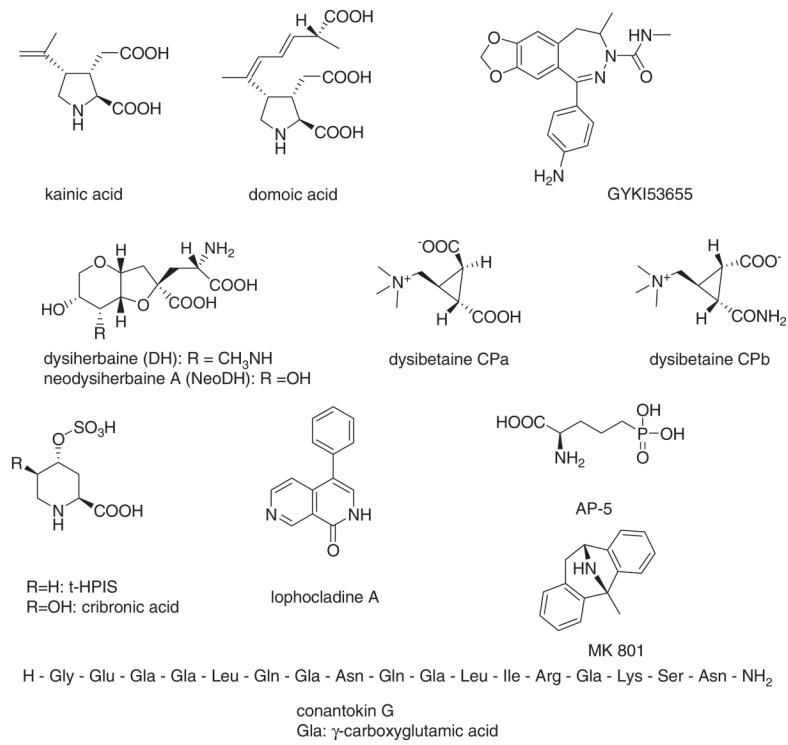


Fig. 1. Chemical structures of representative iGluR ligands discussed in this chapter

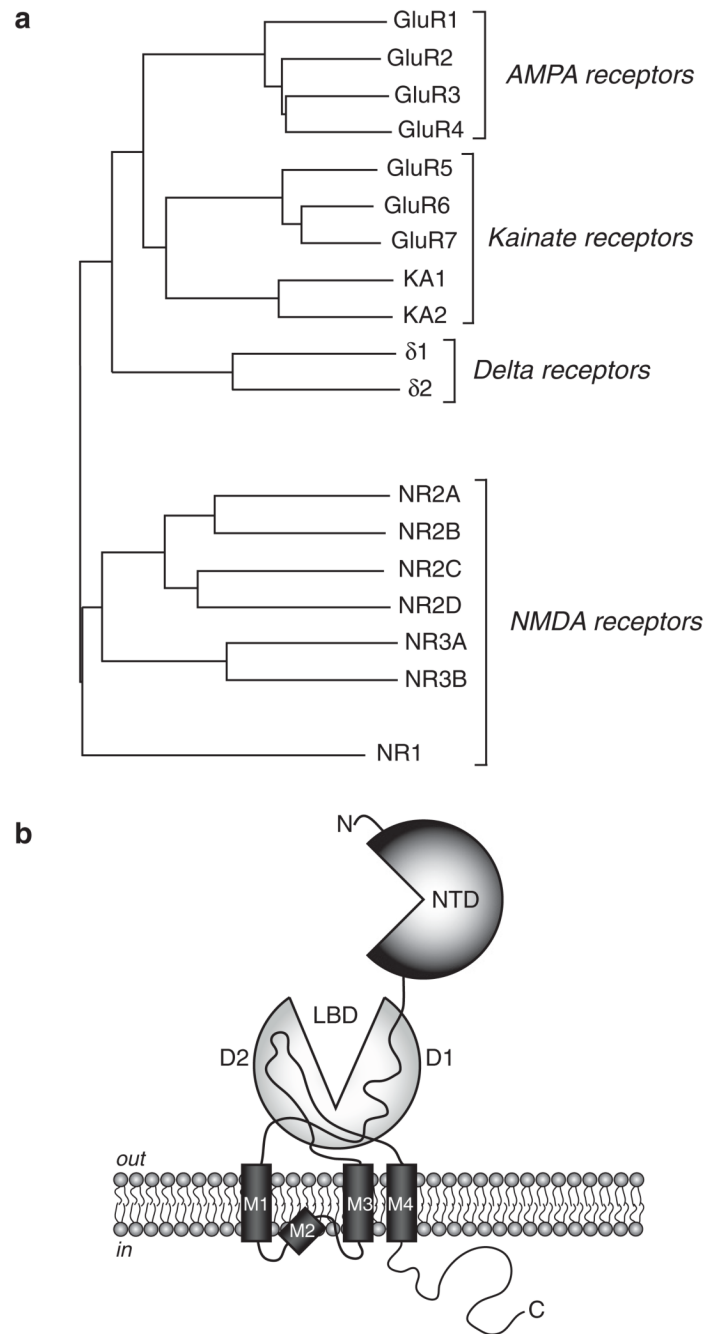


Fig. 2.
a The mammalian ionotropic glutamate receptor gene families represented in a dendrogram, with the distance of the connecting lines proportional to primary sequence identity. **b** The structure of a representative iGluR subunit. The N-terminal domain (NTD) is involved in assembly of tetrameric receptors. The ligand-binding domain (LBD) is extracellular and a bi-lobate structure composed of two distinct domains (D1 and D2). Four membrane domains are noted (M1–M4), with the M2 domain constituting a P-loop. The c-terminal domain contains trafficking, targeting and modulatory determinants.

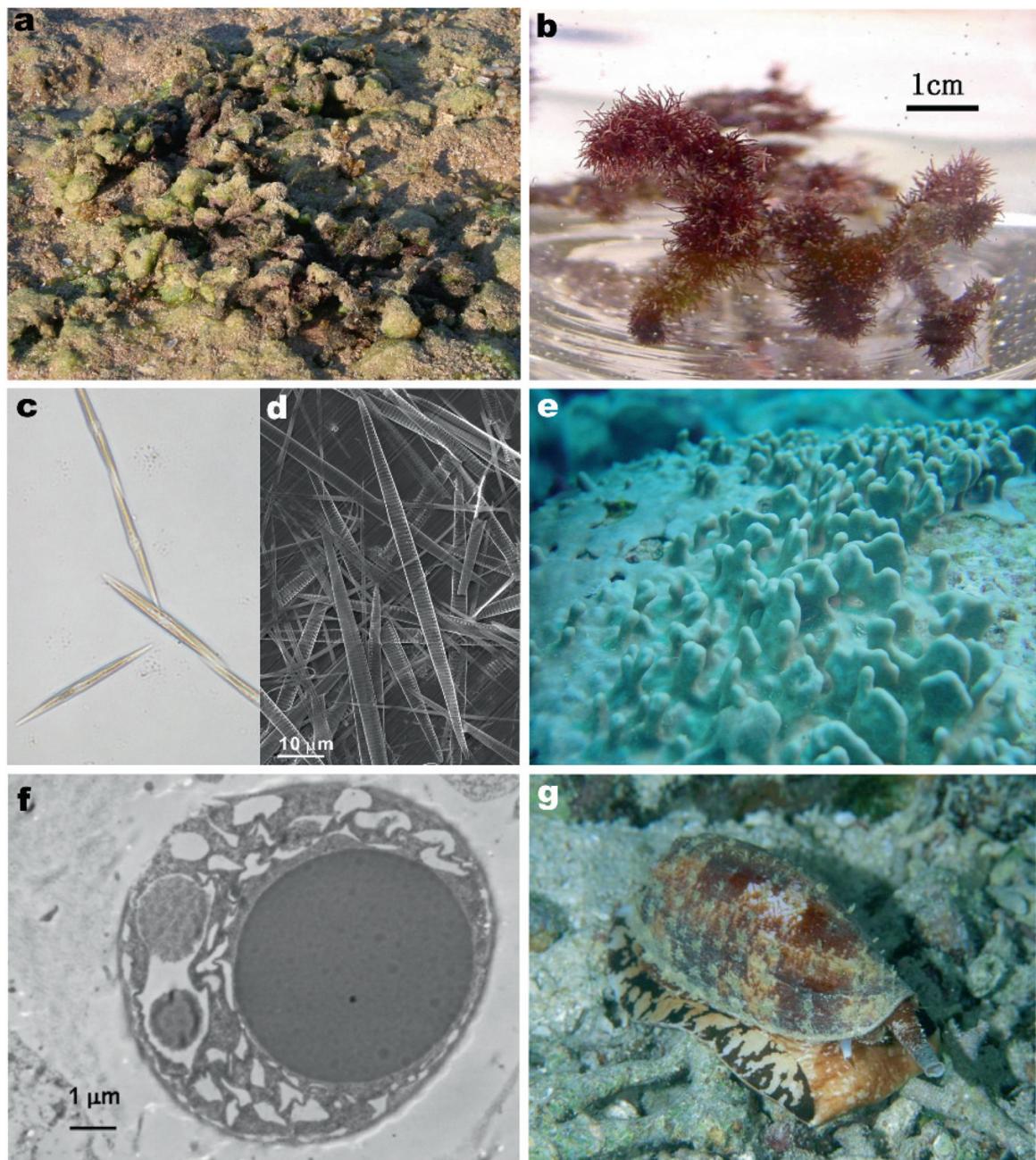


Fig. 3. Marine organisms that contain iGluR compounds. **a** *Digenea simplex* (Iriomote, Okinawa). The algae are often covered by sand. **b** *Digenea simplex* in culture. **c** Light micrograph of *Pseudonitzschia multiseriis*. **d** Scanning electron micrograph of *P. multiseriis*. **e** *Lendenfeldia chondrodes* (Yap, Micronesia). **f** Transparent electron micrograph of a symbiotic *Synecocystis* sp. in mesohyl of *L. chondrodes*. **g** *Conus geographus* in Palau. Images acquired by G. T. Swanson (A), R. Sakai (B, E, F) Y. Kotaki (C), K. Koike (D), and K. Nomura (G)

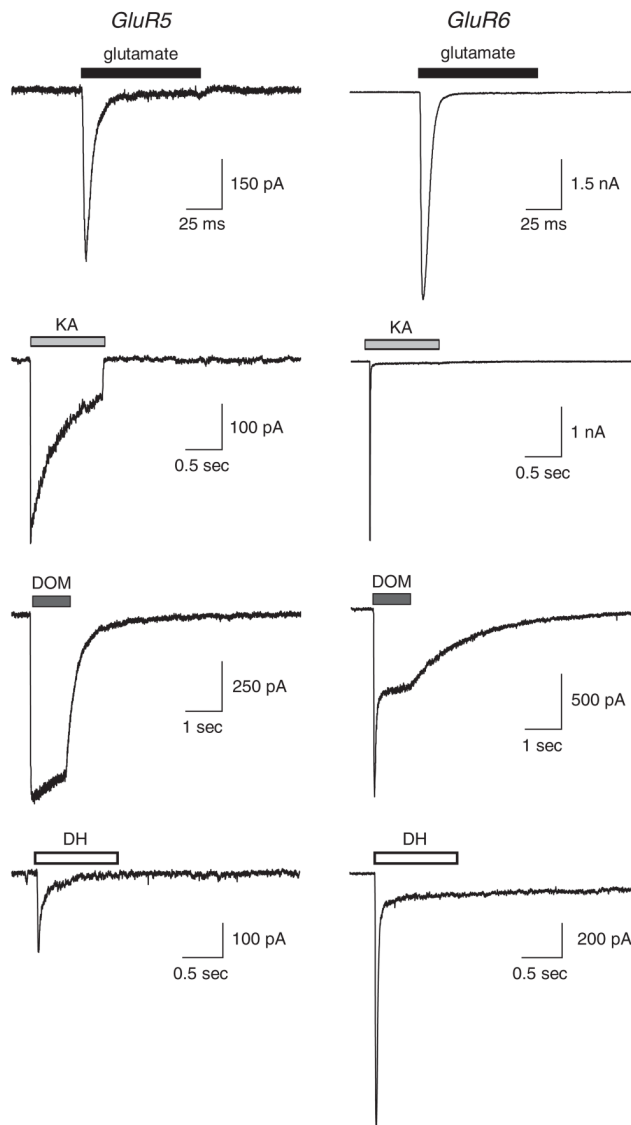


Fig. 4. Representative currents evoked by natural products from kainate receptors. Homomeric GluR5–2a (left column) or GluR6a (right column) receptors were expressed in HEK 293 cells. L-glutamate (10 mM), kainate (KA, 1 mM), domoate (DOM, 30 μ M), or dysiherbaine (DH, 100 μ M) were rapidly applied to cells in whole-cell voltage clamp recordings

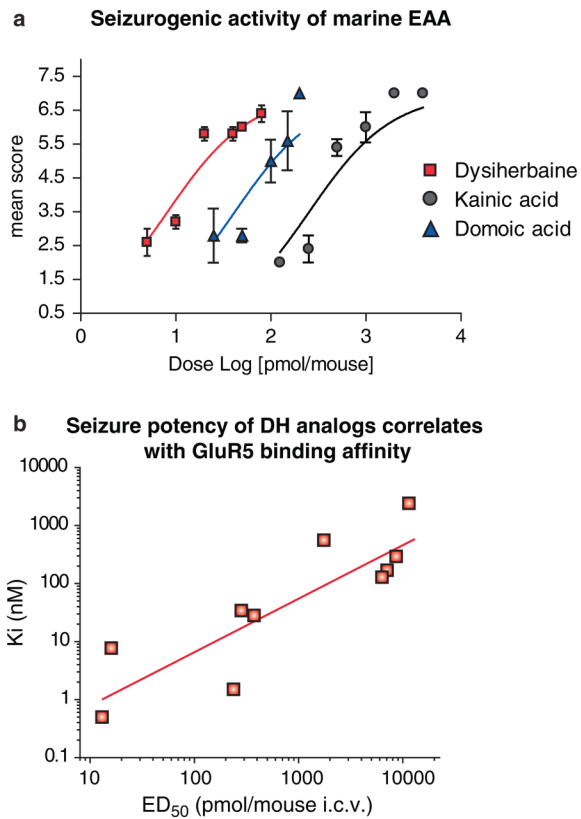


Fig. 5. Seizure activity of marine excitatory amino acids and synthetic analogs of neodysiherbaine A. **(a)** Seizure behaviors induced by i.c.v. injection of dysiherbaine, kainic acid, and domoic acid in mice were graded using a seven-point scale (Sakai et al. 2001b). Values, the mean scores \pm S.E.M., were fit on a sigmoidal curve using PrismTM software. **(b)** Binding affinity at GluR5-2a subunits correlates with seizure potency ($r = 0.86$; $p < 0.01$). Linear correlation graph is plotted as K_i (nanomolar) versus ED_{50} (picomoles per mouse) after i.c.v. injection of the following compounds: DH, neoDH, MSVII19, 8-deoxy-neoDH, 9-deoxy-neoDH, 8-epi-neoDH, 9-epi-neoDH, 9-F-8-epineoDH, 2,4-epi-neoDH, and 4-epi-neoDH (Lash et al. 2007)

Table 1

Convulsant activities of marine excitatory amino acids

ED₅₀ compound	i.c.v. (pmol/mouse)	i.p. mg/kg
Dysiherbaine ^a	6	0.97
Neodysiherbaine A ^b	15	
Kainic acid ^a	280	
Domoic acid ^a	34	5.7
<i>t</i> -HPIS ^c	20	
Cribronic acid ^c	29	
AMPA ^a	240	
NMDA ^a	430	

^aSakai et al. (2001b)^bSakai et al. (2001a)^cSakai et al. (2003)