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# RECEPTORES CYS-LOOP: MECANISMOS MOLECULARES DE ACTIVACIÓN Y MODULACIÓN POR FÁRMACOS NEUROACTIVOS

## RESUMEN

Los receptores Cys-loop pertenecen a la familia de canales iónicos pentaméricos activados por ligandos (pLGICs). Se expresan ampliamente en el sistema nervioso, donde ejercen un rol vital en la comunicación neuronal. Están involucrados en los procesos de aprendizaje, memoria, movimiento, entre otros. Se han asociado alteraciones en la funcionalidad de estos receptores con una gran variedad de desórdenes neurológicos, tales como enfermedad de Alzheimer, enfermedad de Parkinson, epilepsia, síndromes miasténicos, esquizofrenia y depresión. Por ello, los receptores Cys-loop son importantes blancos farmacológicos. En consecuencia, consideramos que el conocimiento de los mecanismos moleculares que conducen a su activación y disfunción es de suma relevancia.

Los receptores Cys-loop están formados por un dominio extracelular, que contiene los sitios de unión de agonista, y un dominio transmembrana, que forma el poro iónico. La interfase entre ambos dominios, llamada región de acoplamiento, desempeña un rol clave en la propagación de los cambios conformacionales que se inician con la unión del agonista en la región extracelular y culminan con la apertura del poro iónico a nivel transmembranal.

En este trabajo de Tesis Doctoral estudiamos dos regiones claves en el proceso de activación de los receptores Cys-loop: el sitio de unión de agonista, donde comienza la respuesta, y la interfase entre los dominios extracelular y transmembrana o región de acoplamiento. Utilizamos receptores homopentaméricos que por estar compuestos por cinco subunidades iguales, poseen cinco sitios de unión de agonista y cinco regiones de acoplamiento idénticas. Los receptores homoméricos surgieron más tempranamente en la escala evolutiva por lo que presentan características estructurales y funcionales comunes a todos los miembros Cys-loop, y son, por lo tanto, modelos útiles para el estudio de los receptores de esta familia.

En el Capítulo I de esta Tesis determinamos el número de regiones de acoplamiento necesario para la activación de los receptores Cys-loop y su relación con los sitios de unión de agonista. Para ello, utilizamos como modelo de receptor homopentamérico al receptor quimérico  $\alpha 7$ -5HT<sub>3</sub>A, compuesto por secuencias del receptor  $\alpha 7$  en su dominio extracelular y secuencias del receptor 5-HT<sub>3</sub>A en su dominio transmembrana, el que ha sido ampliamente utilizado como modelo de  $\alpha 7$ .

Para conocer la contribución de cada una de las cinco regiones de acoplamiento a la estabilidad de canal abierto del receptor  $\alpha 7$ -5HT<sub>3</sub>A, empleamos nuestra estrategia experimental denominada *electrical fingerprinting*. Según esta estrategia, co-transfectamos células con una subunidad conteniendo la región de acoplamiento activa y otra subunidad conteniendo la región de acoplamiento inactiva, una de ellas conteniendo además mutaciones reporteras de conductancia. De esta forma, logramos expresar en membrana receptores con distinto número de regiones de acoplamiento funcionales que son identificados mediante registros de *patch-clamp* de canal único. Gracias a la presencia de las mutaciones reporteras de conductancia, la medición de la amplitud de cada apertura nos permitió conocer la estequiometría del receptor, es decir, el número de subunidades con región de acoplamiento funcional que tiene el receptor pentamérico que dio origen a esa apertura. Determinamos la duración de los eventos de apertura provenientes de receptores con distinto número de regiones de acoplamiento funcionales, que constituye una medida de la estabilidad de canal abierto. Encontramos que cada región de acoplamiento contribuye en forma independiente y simétrica a la estabilidad del canal abierto y que son necesarias las cinco regiones de acoplamiento funcionales para lograr la óptima activación del receptor. Demostramos además que la presencia de una sola región de acoplamiento funcional en el pentámero es suficiente para lograr la activación pero no permite mantener el canal abierto en su tiempo óptimo.

Además generamos receptores  $\alpha 7$ -5HT<sub>3</sub>A mutantes, que contenían distinto número de sitios de unión de agonista y regiones de acoplamiento funcionales. Esta estrategia nos permitió establecer los requisitos estructurales mínimos que logran la activación del receptor, así como también los requerimientos estructurales que conducen a la máxima estabilidad del estado abierto. Encontramos que el receptor es capaz de responder al agonista mediante la ocupación de un único sitio si este se encuentra formado por dos subunidades con regiones de acoplamiento funcionales. Sin embargo, para lograr la óptima activación y duración máxima del canal abierto, el receptor modelo utilizado requiere de tres sitios de unión de agonista funcionales y sus cinco regiones de acoplamiento intactas.

En el Capítulo II, estudiamos la activación del receptor neuronal  $\alpha 7$  en condiciones de sub-ocupación de sus cinco sitios de unión de agonista. Este receptor se localiza principalmente en sitios distantes a los sitios de síntesis y liberación de acetilcolina (ACh), por lo que la ACh, o su producto colina, deben difundir y unirse a receptores  $\alpha 7$  distantes. Este mecanismo colinérgico no sináptico predice que el grado de ocupación de los receptores  $\alpha 7$  sería bajo en condiciones fisiológicas.

Para estudiar la activación del receptor  $\alpha 7$  en condiciones de sub-ocupación de sus sitios de agonista, realizamos ensayos electrofisiológicos y medimos la duración del canal abierto de receptores individuales que presentan un único sitio de unión de agonista

funcional, y la comparamos con la de receptores que tienen sus cinco sitios funcionales. Para conocer el número de sitios de unión de agonista funcionales empleamos nuevamente la estrategia *electrical fingerprinting*. Esta estrategia requiere la medición exacta de la amplitud. Teniendo en cuenta que los receptores  $\alpha 7$  presentan aperturas de duración breve que no permiten la resolución de su máxima amplitud, los estudios electrofisiológicos se realizaron sobre receptores  $\alpha 7$  mutados o en presencia de potenciadores que aumentan la duración del canal abierto. En este trabajo, demostramos que la estabilidad del canal abierto de receptores  $\alpha 7$  que presentan un único sitio de unión de agonista funcional es la misma que la de los receptores que presentan sus cinco sitios disponibles.

Por otro lado, cuando reemplazamos el dominio transmembrana del receptor  $\alpha 7$  por el del receptor 5-HT<sub>3</sub>A, encontramos que la duración del canal abierto se incrementa al aumentar el número de sitios ocupados por agonista. Este resultado demuestra por primera vez que el dominio extracelular no es el único determinante de la relación entre ocupación y estabilidad del canal abierto.

Por lo tanto, en este trabajo demostramos la capacidad del receptor  $\alpha 7$  de activarse y producir respuestas máximas con la ocupación de un solo sitio de unión de agonista, propiedad que es única y exclusiva de este receptor dentro de todos los miembros de la familia de receptores Cys-loop. Este resultado posee además relevancia fisiológica dado que esta propiedad le permitiría al receptor adaptarse al mecanismo de transmisión no sináptico.

En su conjunto, los resultados que surgen de esta Tesis revelan una novedosa relación funcional entre dos dominios estructurales de estos receptores, el sitio de unión de agonista y la región de acoplamiento, y, además, contribuyen al conocimiento general del mecanismo de activación de los receptores de la familia Cys-loop.

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# CYS-LOOP RECEPTORS: MOLECULAR MECHANISMS OF ACTIVATION AND MODULATION BY NEUROACTIVE DRUGS

## SUMMARY

Cys-loop receptors belong to the family of pentameric ligand-gated ion channels (pLGICs). They are widely expressed in the nervous system, where they exert a vital role in neuronal communication. They are involved in learning, memory, movement processes, among others. Functional disorders of these receptors have been associated with several neurological disorders, such as Alzheimer's disease, Parkinson's disease, epilepsy, myasthenic syndromes, schizophrenia and depression. Because Cys-loop receptors are important pharmacological targets for the development of therapies, the knowledge of the molecular mechanisms leading to activation and dysfunction of these receptors is of great importance.

Cys-loop receptors contain an extracellular domain that carries the agonist binding sites and a transmembrane region that forms the ion pore. The interface between both domains, named as the coupling region, plays a key role in the propagation of the conformational changes from the binding site at the extracellular domain to the pore, located at the transmembrane region.

In this Thesis, we studied two key regions that are essential for the activation process of Cys-loop receptors: the agonist binding site, where the response begins, and the interface between the extracellular and transmembrane domains or coupling region. We used homopentameric receptors that contain five identical subunits, and therefore five identical agonist binding sites and coupling regions. Because homomeric receptors appeared earlier on the evolutionary scale, they present structural and functional features that are common to all Cys-loop members, and are therefore useful models for the study of this receptor family.

In Chapter I of this Thesis we studied the number of coupling regions necessary for Cys-loop receptor activation and evaluated the functional relationship of this domain with the agonist binding sites. To this end, we used a model of homopentameric receptor, the  $\alpha 7$ -5HT<sub>3</sub>A chimeric receptor, which contains  $\alpha 7$  sequences in the extracellular domain and 5-HT<sub>3</sub>A sequences in the transmembrane domain.

To determine the contribution of each of the five coupling regions to the stability of the open channel, we used our experimental strategy which is called electrical fingerprinting. For this strategy, cells were co-transfected with a subunit with an active coupling region and another subunit with an inactive coupling region, one of which carrying reporter

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conductance mutations, to generate receptors with different number of functional coupling regions. Next, we performed single-channel recordings to identify functional receptors using the patch-clamp technique. Due to the introduction of reporter conductance mutations, the measurement of the amplitude of each opening event allowed us to know receptor stoichiometry, i.e., the number of subunits with functional coupling region present in the pentameric receptor which originated the event. We measured open channel duration of receptors with different numbers of functional coupling regions, which indicates the open channel stability. We found that each coupling region contributes independently and symmetrically to open channel stability. We showed that five coupling regions are necessary to achieve optimal receptor activation and that the presence of only one functional coupling region is sufficient for receptor activation, but with reduced open channel duration.

Furthermore, we constructed  $\alpha 7$ -5HT<sub>3</sub>A mutant receptors, containing different number of agonist binding sites and functional coupling regions. This strategy allowed us to establish the minimum structural requirements for receptor activation as well as the structural requirements for maximal open channel stability. We found that  $\alpha 7$ -5HT<sub>3</sub>A receptors are capable of responding to agonist by occupying a single agonist binding site, only if this site is formed by two subunits carrying functional coupling regions. However, to achieve optimal activation and maximal open channel duration, the model receptor requires three functional agonist binding sites and five functional coupling regions.

In Chapter II, we studied  $\alpha 7$  neuronal receptor activation under sub-occupancy conditions of its five agonist binding sites. In the brain, this receptor is mainly located at distant sites from the sites of synthesis and release of acetylcholine (ACh), so ACh, or its product choline, diffuse to bind distant  $\alpha 7$  receptors. This non-synaptic cholinergic mechanism predicts that the degree of  $\alpha 7$  receptor occupancy is low under physiological conditions.

To study  $\alpha 7$  activation under sub-occupancy conditions we performed single-channel recordings and measured open channel duration of receptors with only one functional agonist binding site, and compared it with that of receptors containing their five intact agonist binding sites. To know the number of agonist binding sites, we employed again the electrical fingerprinting strategy. This strategy requires accurate measurement of open channel amplitude. Because the brief duration of  $\alpha 7$  opening events do not allow full amplitude resolution, single-channel recordings were performed in either  $\alpha 7$  mutant receptors or in the presence of potentiators that increase open channel duration. In this work, we demonstrated that open channel stability of receptors with a single agonist binding site is the same as that of receptors containing five functional sites.

Moreover, when we replaced the transmembrane domain of  $\alpha 7$  receptors by that of 5-HT<sub>3</sub>A receptor, we found that open channel lifetime increases as the number of sites

occupied by agonist increases. This result shows for the first time that the extracellular domain is not the only determinant of the relationship between occupancy and open channel stability.

Therefore, in this work we demonstrated the ability of  $\alpha 7$  receptor for activation and eliciting maximal responses with occupancy of only one agonist binding site, a property that is unique for  $\alpha 7$  among all members of the Cys-loop family. This result has a physiological relevance since this property would allow  $\alpha 7$  receptors to adapt to their non-synaptic mechanism.

Taken together, the results that emerge from this Thesis reveal a novel functional relationship between two structural domains, the agonist binding site and the coupling region, and contribute to the general knowledge of the activation mechanism of Cys-loop receptors.

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