

Molecular pharmacology of histamine H₄ receptors

Saskia Nijmeijer¹, Chris de Graaf¹, Rob Leurs¹, Henry F. Vischer¹

¹VU University Amsterdam, Leiden-Amsterdam Center for Drug Research, De Boelelaan 1083, 1081HV Amsterdam, The Netherlands

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1. ABSTRACT

The histamine H₄ receptor (H₄R) is the youngest member of the histamine receptor family. Based on its predominant expression pattern in hematopoietic cells, the H₄R is considered to be an interesting drug target for inflammatory disorders such as allergy and asthma. Since the identification and cloning of the H₄R in 2000, drug discovery programs boosted the development of various H₄R (specific) ligands. Differences between H₄R orthologs in combination with available three-dimensional G protein-coupled receptor (GPCR) models have guided site-directed mutagenesis studies to gain insight in ligand binding and receptor activation. In addition, ongoing characterization of H₄R-mediated signaling in transfected and native cells contributes to further unravel the (patho-) physiological functions of H₄Rs.

2. INTRODUCTION / HISTORY

The small biogenic amine histamine was identified as an important mediator in a variety of physiological processes in the beginning of the 20th century (1-3). Histamine is produced *de novo* by L-histidinedecarboxylase (HDC)-catalyzed decarboxylation of the amino acid L-histidine, and is stored in cytoplasmic granules in immune cells (e.g. eosinophils and mast cells), enterochromaffin-like cells in the stomach and in neurons. Contact of eosinophils or mast cells with an allergen results in immunoglobulin cross-linking and release of stored histamine from the granules (4). Histamine causes the well-known allergic responses, such as sneezing, coughing, rhinorrhea and vasoconstriction. Drugs inhibiting these allergic symptoms were initially classified as

antihistamines and are now known to act through a receptor protein called histamine H1 receptor (H₁R).

In the stomach, histamine stimulation increases gastric acid secretion. The different pharmacology that was found for some histaminergic ligands in airway smooth muscle, heart, uterus and stomach, indicated that histamine affects at least two distinct receptors, namely the H₁R and histamine H2 receptor (H₂R) (5). Unambiguous evidence for the existence of two different receptors arose from the development of the first (H₂R-) selective antagonists burimamide and metiamide by Sir James Black and colleagues (6). These compounds prevented the histamine-induced release of HCl in the stomach, but did not affect the responses supposed to be mediated by the H₁R. Consequently, in the following years a plethora of selective drugs was developed against either H₁R or H₂R to relief either allergic symptoms or inhibit abundant gastric acid release in the stomach, respectively. These H₁R (antihistamines) and H₂R antagonists became worldwide blockbuster drugs that are now readily available from the local drugstore without a prescription. The sedative effects of the first generation antihistamines revealed the presence of H₁R receptors in the brain. To prevent drowsiness as side effect, a second generation of H₁R antihistamines was developed, that could not pass the blood brain barrier. At the same time, brain-penetrating antihistamines were marketed and even newly developed as sleep aid.

In the eighties, a new histamine receptor that could not be inhibited according to the known pharmacology of the H₁R or H₂R antagonists was identified in rat brain (7). This new receptor was classified as the histamine H3 receptor (H₃R) and is now known to be involved in the regulation of e.g. sleep/wake cycle and cognitive processes, by presynaptically inhibiting the release of histamine, but also other neurotransmitters like dopamine, noradrenaline, acetylcholine and serotonin. The H₃R is seen as a potential target in central nervous system (CNS) disorders such as Alzheimer's disease, schizophrenia and attention deficit hyperactivity disorder (ADHD) (8, 9).

In addition to the "classical" techniques such as *ex vivo* organ-based studies to pharmacologically define histamine-induced effects, new molecular biology techniques became available in the late twentieth century, eventually leading to the sequencing of complete genomes. Thanks to these developments, histamine receptors can now be recombinantly expressed in convenient host cell lines and biochemically and pharmacologically characterized. Moreover, using site-directed mutagenesis the role of specific amino acids in protein function can be studied. In 1991, both H₁R- and H₂R-encoding genes were readily cloned, but it lasted until 1999 before the gene of the H₃R was identified (10). The histamine receptor proteins are all classified as G protein-coupled receptors (GPCRs), which are characterized by seven transmembrane (TM) alpha-helices. In a quest for new GPCRs that show homology to the H₃R gene, a deduced sequence was found that shares considerable amino acid similarity. Several groups cloned this new gene at the same time, and the corresponding protein was named histamine H4 receptor (H₄R) (11-16).

In this essay we will give a broad overview of past and present H₄R research, as well as highlight some of the emerging developments in the H₄R field.

3. H₄R GENE

The protein encoded by the human histamine H₄R gene (i.e. HRH4) shows very low (~19%) amino acid sequence homology to the histamine H1 and H2 receptors and shares ~37% identity with the H₃R. The HRH4 is 16.98kb in size and is mapped by radiation hybrid experiments on chromosome 18q11.2 as a single copy (17). Increased copy numbers of HRH4 are associated with the occurrence of the autoimmune disorder systemic lupus erythematosus (SLE), arthritis, and proteinuria, due to elevated H₄R expression levels (18). On the other hand, lower copy numbers are associated with decreased proteinuria (18).

Transcription of HRH4 results in a mRNA molecule of 3.7kb. The open reading frame is 1173bp in size and encodes 390 amino acids. The HRH4 contains two introns of 7867 bp and >17500 bp, dividing the actual coding region into three exons (amino acids 1-65, 66-119 and 120-390) (Figure. 1). The HRH3 and HRH4 share a similar intron/exon distribution (19), suggesting that they have evolved from a common ancestral gene. In contrast, HRH1 and HRH2 are intron-less in their coding region (20, 21). Four alternative splicing variants of HRH4 have been identified so far, namely H₄R (302), H₄R (67) (Figure. 2) and H₄bR and H₄cR. The H₄R (302) splice variant contains TM1, part of TM2 and TM5-7, whereas H₄R (67) is truncated due to a frame shift and only contains TM1 and the first half of TM2 (22). Both these HRH4 splice variants are predominantly located intracellularly and are not able to activate signaling pathways. However, these splice variants act as dominant negative partners for the full length H₄R (see 5.1). The splice variants H₄bR and H₄cR were cloned from human spleen cDNA by Merck (patent WO 03/020907 A2). The H₄bR is identically spliced as H₄R (67), whereas H₄cR contains exon 2 and recognizes an alternative acceptor site in exon 3, which causes a 33 amino acid deletion. In contrast to H₄R (302) and H₄R (67), both splice variants are reported in a patent to bind [³H]-histamine and to activate downstream pathways like cAMP inhibition, Ca²⁺ release and MAPK activation (22), but this has so far not been confirmed.

The promoter region of HRH4 contains several binding motifs for transcription factors (TF), such as nuclear factor kappa B, nuclear factor to interleukin 6, interferon regulatory factor and interferon-stimulated response element (17), but lacks TATA or CAAT box sequences. This suggests that HRH4 expression could be induced by inflammatory factors like interferon, TNF α or IL-6.

Numerous single nucleotide polymorphisms (SNPs) have been identified in the HRH4. Most SNPs are located in non-coding regions with 37 SNPs in intron 1, 45 in intron 2 and 21 in the 3' untranslated region. However, four SNPs were identified in the coding region, resulting in

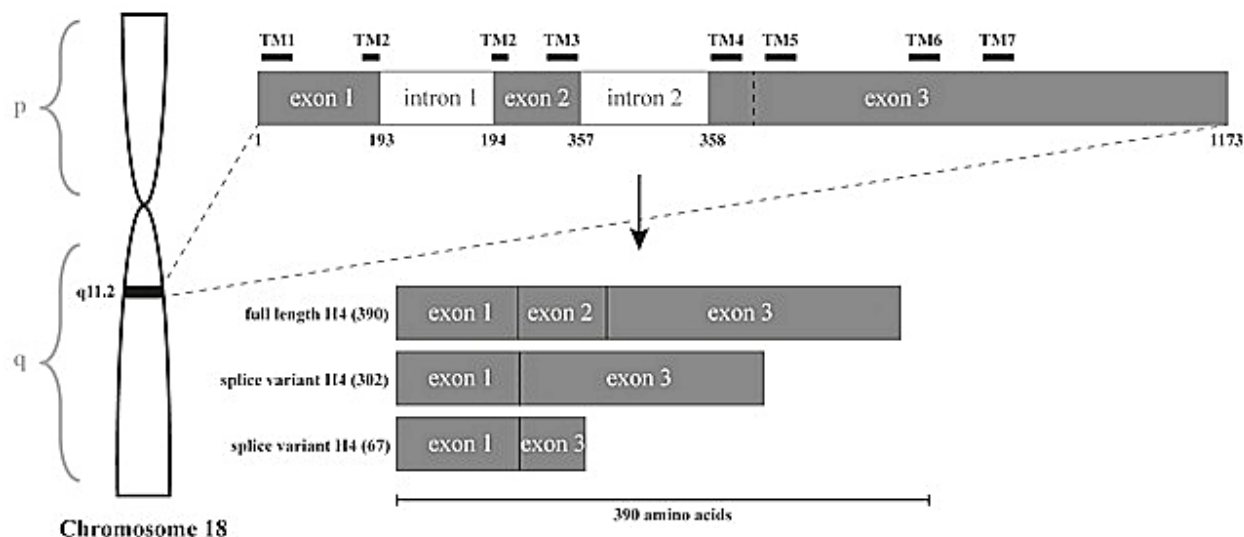


Figure 1. Schematic representation of the H₄R gene location on chromosome 18 and an overview of the exon/intron distribution of the different splice variants. The gene is located on position q11.2 and consists of three exons and two introns. The regions that encode the typical 7 TM domains of the full length H₄R (390) are shown above the sequence. The splice variant H₄R (302) does not contain exon-2 and recognizes an alternative acceptor site (dotted vertical line) in between the TM4 and TM5 coding sequence. The H₄R (67) variant passes over exon-2, continues at the normal acceptor site of exon-3, which subsequently results in a frame shift and premature stop codon.

Val^{4.48}Ala, Arg^{5.70}His, Cys^{6.16}Ser or a frame shift at Leu^{7.75}. The first two changes give rise to the differences between the HRH4 sequences as published by Oda *et al* (12) and other research groups. Recently, three SNPs (i.e. ss142022671, ss142022677 and ss142022679) were associated with atopic dermatitis (23). The SNP ss142022671 is located inside a consensus transcription factor binding motif in intron 1, resulting in increased transcription. On the other hand, the SNPs ss142022677 and ss142022679 are located in exon 3, resulting in the substitution of the Lys^{7.71}-encoding sequence by a stopcodon or mutation of Lys^{7.71} to Ile, respectively. Moreover, when both these SNPs are present Lys^{7.71} is changed to Leu (23). Unfortunately, the effects of these SNPs on H₄R pharmacology are not yet resolved.

Soon after the identification of the human HRH4, corresponding orthologs were cloned from mouse, rat, guinea pig, pig, monkey and dog (24, 25). The amino acid similarity between monkey and human H₄R is the highest with 93%, but decreases when comparing with rodent or pig H₄R proteins (65-72%, respectively) (Figure. 2) (24, 26-28). Unraveling sequence differences between species is an interesting study for evolutionary scientists. However, it has proven to be a very useful tool to delineate ligand-binding sites as well (see 7.1).

4. H₄R EXPRESSION PROFILE

The HRH4 is expressed in a variety of tissues such as bone marrow, spleen, peripheral blood, thymus, small intestine, colon, heart and lung, as revealed by quantitative polymerase chain reactions (qPCR), Northern blot analysis, microarray analysis or *in situ* hybridization

(29-33). However, HRH4 seems to be predominantly expressed on cells of hematopoietic origin, e.g. eosinophils, mast cells, basophils, neutrophils, dendritic cells, monocytes and T cells (Figure. 3). HRH4 mRNA of the splice variants could be detected in pre-monocytes and eosinophils (22). In addition, HRH4 expression was also detected in subsets of endocrine cells in the gastrointestinal tract (34), dermal fibroblasts and in the central nervous system (35). There is evidence of HRH4 expression in the mouse brain (14), but human data is still contradictory (13, 15, 17, 24, 36). Although the above-mentioned techniques detect HRH4 expression, they obviously do not give an indication regarding H₄R protein levels.

A useful tool to detect H₄R proteins on cells and tissues is a H₄R specific antibody such as the polyclonal anti-H₄R antibody developed against the last 17 amino acids of the C-tail (32). H₄R proteins have been detected by antibody-based immunofluorescent staining in human monocyte-derived dendritic cells (MoDC) (29) as well as on primary Langerhans cells from murine and human skin samples (37). Moreover, it was observed that H₄R are upregulated during the differentiation from monocytes into MoDC (38). More recently, this anti-hH₄R receptor antibody was used to localize human and mouse H₄R protein in the CNS (35). Histamine H₄R are expressed in distinct deep laminae (particularly layer VI) in the human cortex and mouse thalamus, hippocampal CA4 stratum lucidum and layer IV of the cerebral cortex. In contrast, very low H₄R expression was observed in the striatum and the remaining subfields of the hippocampus (35). The antibody data were confirmed by H₄R-mediated electrophysiology responses in layer VI somatosensory cortex neurons in mice (35). In addition, H₄R protein was

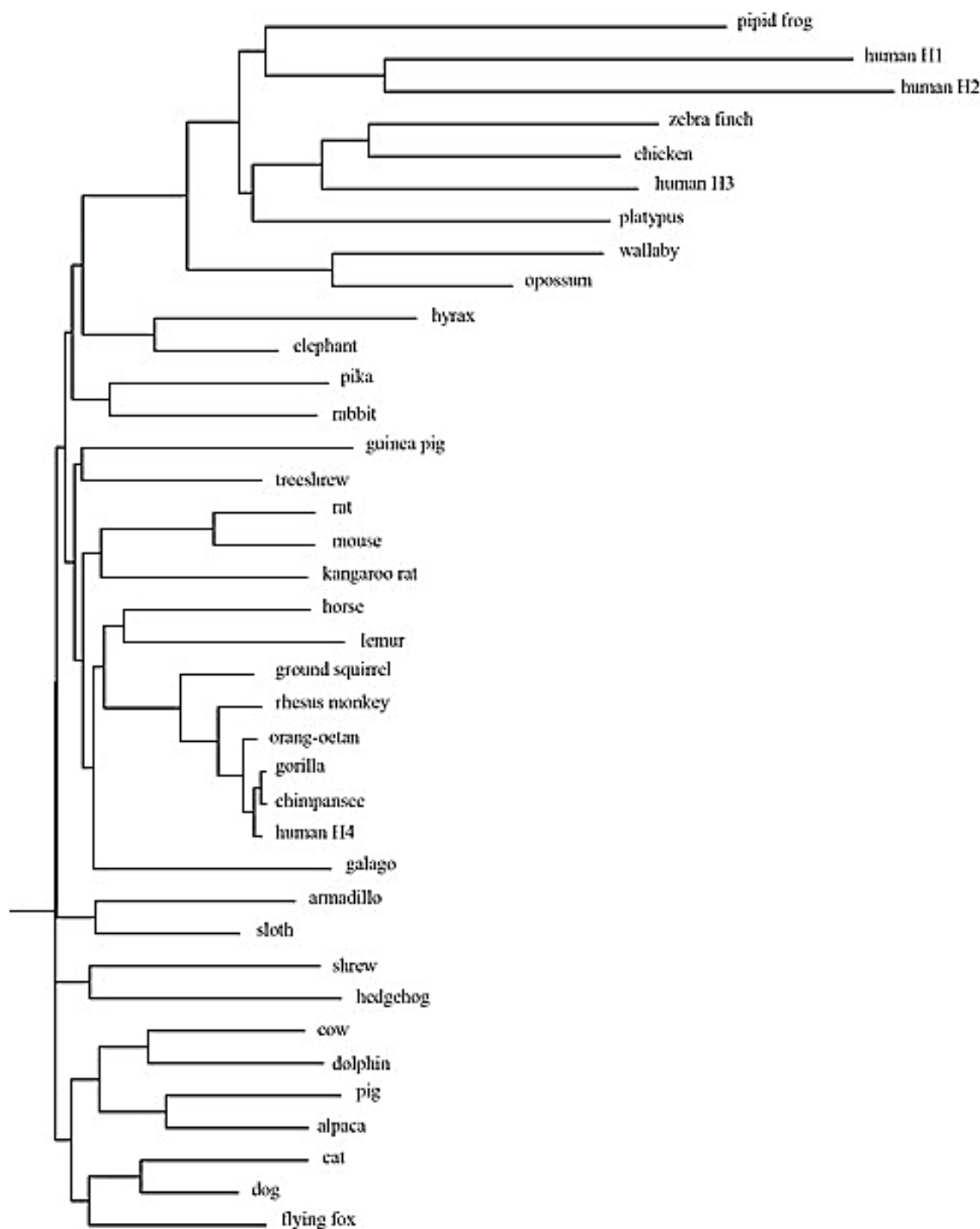


Figure 2. Phylogenetic tree of the human histamine receptors and H₄R orthologs. Sequences are downloaded from NCBI website, and the graph was created with ClustalW. Alignment parameters from the Gonnet series were used.

also detected on mouse spinal cords motor neurons (39). On nerves of human nasal mucosa, H₄R proteins were found to colocalize with both H₁R and H₃R (40). H₁R, H₂R, and H₄R proteins are expressed in human intestinal tissue (41). Interestingly, both H₁R and H₄R expression was significantly decreased in colorectal tumors (41).

5. H₄R PROTEIN STRUCTURE AND POST-TRANSLATIONAL MODIFICATIONS

Histamine receptors belong to the family of GPCRs. These receptor proteins consist of seven cell membrane-spanning alpha-helices that are connected by three extracellular loops (ELs) and three intracellular loops

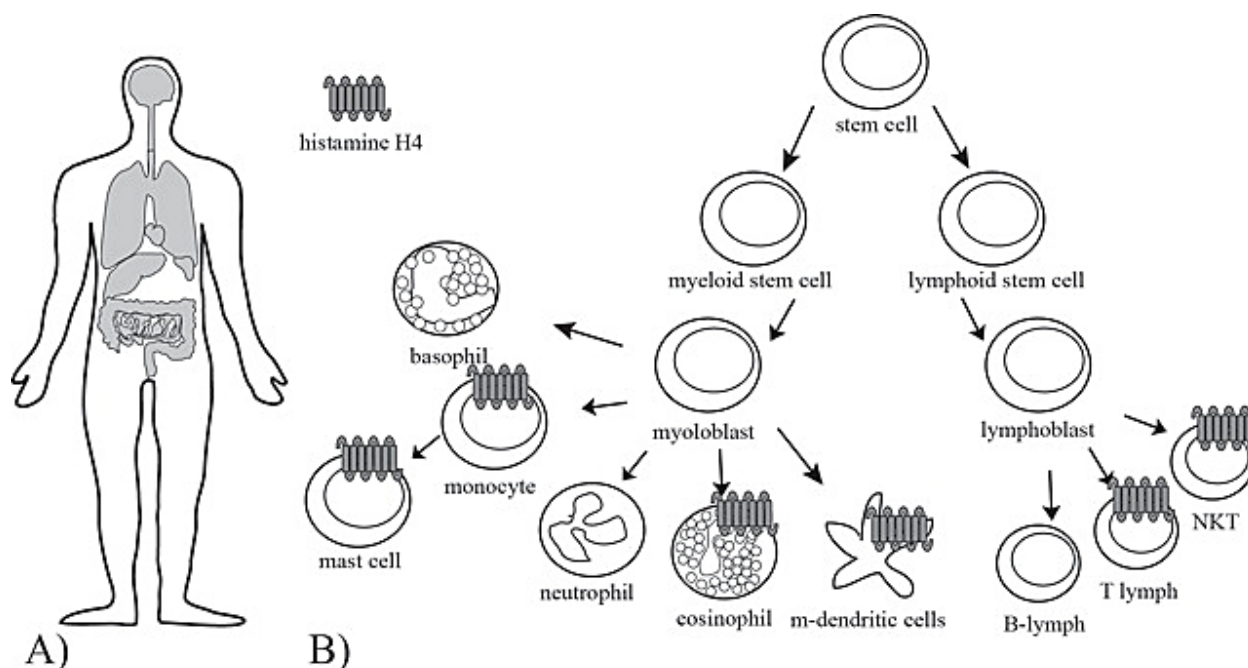


Figure 3. H₄R distribution in the human body. A) Organs and tissues that express H₄R are drawn and colored gray. B) H₄R are predominantly expressed in hematopoietic cells. Data were either obtained from mRNA detection via micro-array and qPCR or protein detection via H₄R specific antibodies.

(ILs). The N-terminal tail is located extracellular and the C-tail intracellular (Figure. 4). The histamine receptors have several conserved structural motifs that are common to the class A (rhodopsin-like) GPCRs, including the highly conserved residues Asn^{1.50}, Asp^{2.50}, Arg^{3.50}, Trp^{4.50}, Pro^{5.50}, Pro^{6.50} and Pro^{7.50} (43). Like in most other GPCRs, (42) TM3 and the EL2 of H₄R are presumably connected by a disulphide bridge between Cys^{3.25} and Cys^{45.50}. The extracellular N-terminal tail contains two asparagines (Asn^{1.21} and Asn^{1.25}) that are predicted to be involved in post-translational glycosylation, whereas the intracellular C-tail is possibly anchored to the cell membrane through palmitoylation of the Cys^{7.69} residue (Figure. 4). In addition, like most GPCRs, H₄R has an additional helix 8 that is located intracellularly and does not span the cell membrane.

5.1. H₄R assembly in the cell membrane

In the era of the first two histamine receptors it was generally believed that GPCRs function as monomeric entities. However the last two decades, a substantial amount of literature was published showing the existence of higher order structures consisting of two or more GPCRs (Figure. 5). One of the most striking examples was given by two class C GPCRs, the GABA_{B1} and GABA_{B2} receptors. The GABA_B proteins are obligatory heterodimers, not able to reach the cell surface or signal in the absence of one another (44-47). Although there is increasing evidence of GPCRs interacting with each other, the functional consequences of class A GPCR di- or oligomerization are less clear. Hence the quaternary organization for this class of GPCRs is not indisputably accepted (48).

All four histamine receptors form higher order assemblies (49-52). H₄R dimers were detected in native cells (e.g. human phytohaemagglutinin (PHA) blasts and spleen lysates) using a selective anti-H₄R antibody in co-immunoprecipitation experiments (32). However, co-immunoprecipitation experiments are disputable because of a-specific aggregation after disruption of the cellular environment. Therefore, supporting evidence for dimerization was obtained in transfected living cells (e.g. HEK293 and COS7 cells) that express H₄R proteins at physiological relevant (~300 fmol/mg membrane protein) (32). Both homo- and heteromeric complexes were identified for the H₄R using biophysical (bioluminescence & time-resolved fluorescence resonance energy transfer) techniques (32, 53). Moreover, H₄R dimers are localized at the cell surface, as demonstrated by antibody-based time-resolved fluorescence resonance energy transfer (trFRET) measurement, that only allows detection of cell surface complexes.

H₄R oligomers are formed constitutively and their formation is not modulated by (inverse) agonists or antagonists. H₄R oligomerization does not require posttranslational N-glycosylation, although a possible role for glycosylation in stabilization of the complex was suggested, based on a decrease in the dimeric population upon deglycosylation (32). H₁R-H₄R heteromeric complexes are only detected at very high expression levels, and are most likely the consequence of random interactions.

The HRH4 splice variants H₄R (67) and H₄R (302) form complexes with the full length H₄R, and retain

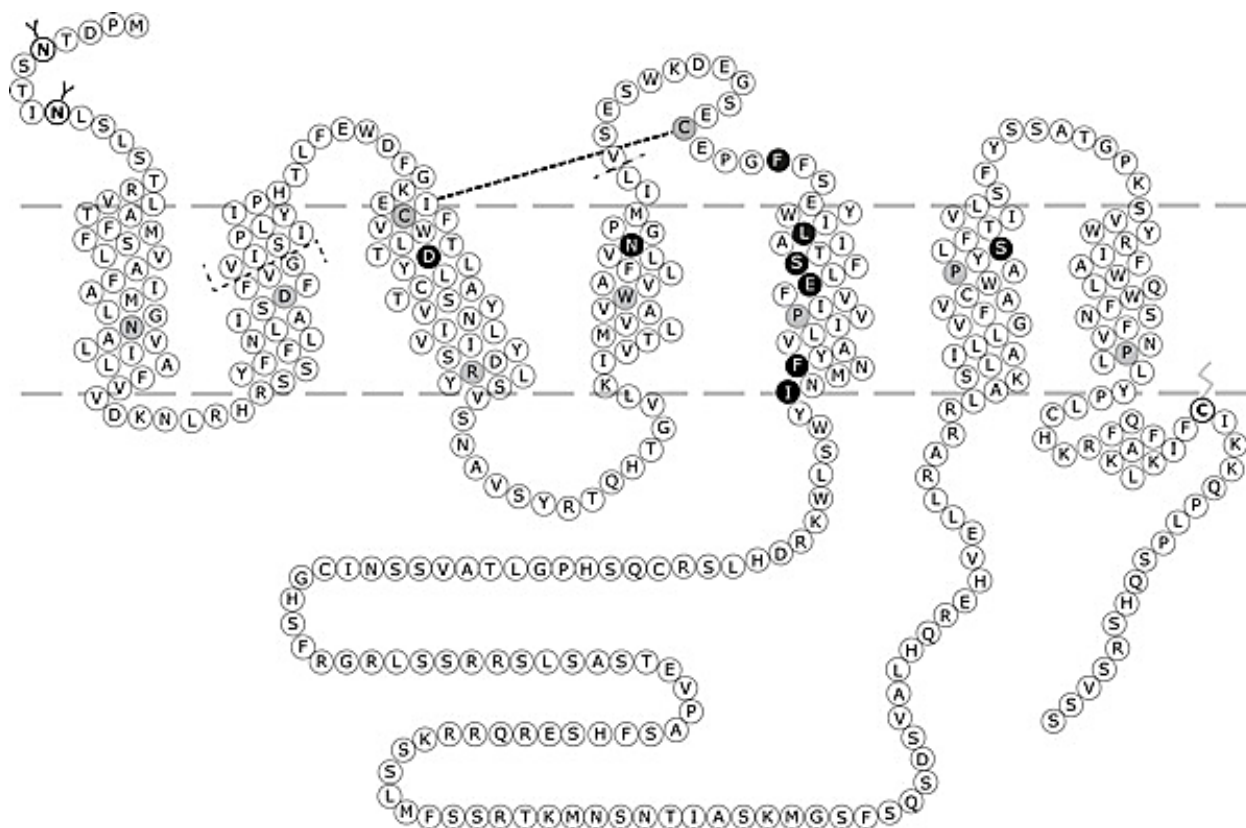


Figure 4. Snake plot of the human H₄R protein. The cell membrane-associated H₄R has 7TM helices and several conserved structural motifs that are common to class A (rhodopsin-like) GPCRs. A disulphide bridge between the conserved Cys^{3.25} and Cys^{45.50} (gray circles) connects the first EL/TM3 and the second EL. The N-terminal extracellular tail contains two asparagines (Asn^{1.21} and Asn^{1.25}) (bold) that are possibly involved in post-translational glycosylation. The intracellular C-tail is presumably anchored to the cell membrane through palmitoylation of the Cys^{7.69} residue (bold). Residues that have been shown to be important in ligand binding and/or receptor activation as well to be responsible for observed differences in ligand binding between species are shown in black circles with white text.

the latter intracellularly in a dominant negative manner (22). Hypothetically, since the mRNA of these splice variants is differentially expressed in different cell types, it could well be that they have a role in the regulation of H₄R expression at the cell surface (22).

6. H₄R LIGANDS

Since the discovery of the H₄R, numerous ligands have been identified that bind the receptor and affect downstream signaling pathways. Several efforts have been made to design and synthesize H₄R selective (inverse) agonists and antagonists. Considering the amino acid similarity to the H₃R, especially in the ligand binding pocket that is formed by the TM domain, it is not surprising that the majority of imidazole-containing H₃R ligands have affinity for the H₄R as well (54) (Figure 6). Examples include R- α -methylhistamine (RAMH), imnepip (both 40-fold selective for H₃R), immetridine and methimepip (300 and 2000-fold H₃R selective, respectively). Small changes in ligand structure result in great differences in histamine receptor subtype specificity. Even so remarkable is the change in efficacy for some compounds on the distinct

histamine receptor subtypes. The H₃R antagonist clobenpropit, for example, acts as a high affinity partial agonist at the H₄R.

Besides H₃R cross reactivity, some H₄R ligands are able to bind H₁R or H₂R (Figure. 6) (55). The majority of these shared ligands contain the characteristic imidazole heterocycle, with the exception of clozapine (analogues) (56). Interestingly, clozapine binds promiscuously to several GPCRs, but only acts as an agonist on H₄R (36).

6.1. H₄R agonists

Optimization of the dibenzodiazepine clozapine resulted in the rigid structure VUF6884, a H₁R antagonist and H₄R agonist (57). Another non-imidazole H₄R agonist is the dimaprit analog VUF8430 (54, 58). The latter is a full agonist with high affinity for the H₄R and 30-fold selectivity over the H₃R. In contrast to the H₃R, H₄R agonists are thus not limited to imidazole containing structures. Ligand optimization studies and evaluation of other histamine receptor compounds resulted in more selective H₄R agonists. OUP-16 (59) and 4-methylhistamine (54), display respectively 40-fold and

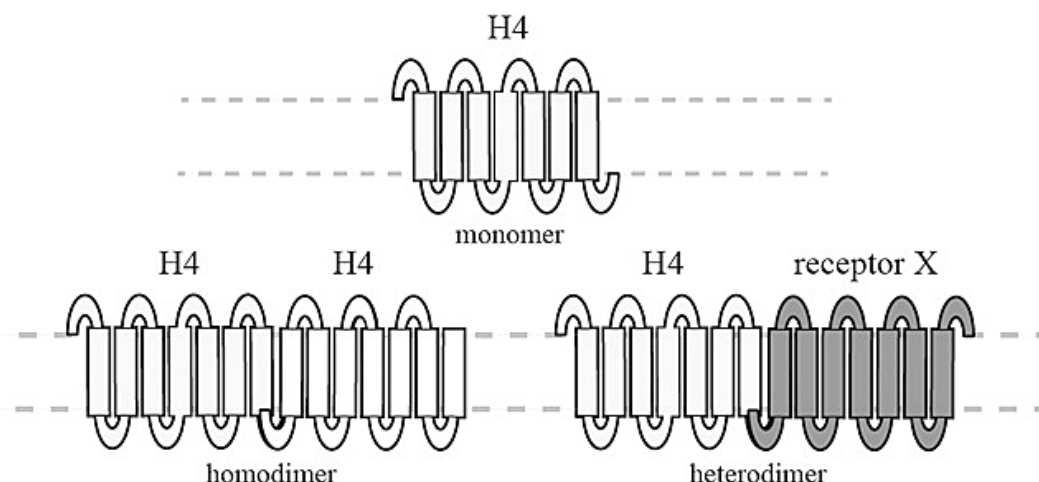


Figure 5. H₄R organization in the cell membrane. H₄Rs were shown with biochemical and biophysical methods to constitutively dimerize both in native cells and transfected cells. H₄R can form homodimers consisting of two H₄R proteins or heterodimers consisting of H₄R and another GPCR.

100-fold H₄R selectivity over the other histamine receptor subtypes.

In more recent years new classes of H₄R agonists were discovered, each with their advantages and disadvantages. The acylguanidine agonists were developed as H₃R/H₄R interacting compounds and can be useful to study H₄R pharmacology in absence of H₃R (e.g. in some immune cells). Exchange of the acyl group with a cyano group resulting in the cyanoguanidines, improves H₄R selectivity (60). UR-PI376 shows 30-fold binding selectivity over H₃R, but shows a drop in potency on mouse H₄Rs. An interesting aspect of this H₄R agonist is that it is unable to activate any other histamine receptor subtype (61).

Recently, Johnson and Johnson (J&J) published their newest class of H₄R agonists, the oxime analogues of JNJ 7777120 (see below) and JNJ 10191584 (VUF6002) (62). They show low affinity for the other histamine receptor subtypes and very promising, maintain their efficacy on H₄R species orthologs (except for dog H₄R) (62). Another interesting class of H₄R agonists is the 2-arylbenzimidazoles. They were also developed by J&J and the best compound of this series has subnanomolar affinity for H₄R. This compound is highly selective by showing more than 600-fold selectivity over the other histamine receptor subtypes, but is unfortunately less potent on the mouse H₄R. Interestingly, minor changes in this 2-arylbenzimidazoles series lead to an efficacy shift from agonist into antagonists (63).

6.2. H₄R antagonists/inverse agonists

One of the first identified antagonists (later discovered to be inverse agonist) was thioperamide, but this compound is equiactive on both H₃R and H₄R receptors (64–67). The first H₄R-selective (non-imidazole) neutral antagonist JNJ 7777120 (>1000 fold selective over other histamine receptor subtypes) was discovered by J&J following a high throughput screen. This compound has

equal affinity for human, mouse and rat H₄Rs (68, 69) initially making it a valuable compound to extend the *in vitro* pharmacology to *in vivo* studies. Intriguingly, the more research is performed on this compound, the more “active” it becomes. It was reported that in a steady-state GTPase assay JNJ 7777120 acts as a partial inverse agonist on the human H₄R. In the same assay, however, it behaves as a partial agonist on mouse, rat and dog H₄Rs (70). Very recently JNJ 7777120 was identified as partial biased agonist, able to recruit beta-arrestin in a G protein-independent manner (71) (see 8.4). Hence, the usefulness of this compound as reference neutral H₄R antagonist is currently under debate. JNJ 7777120 has a poor half-life (2h) upon oral administration to rats (72, 73), which should be taken into account when using it for *in vivo* H₄R targeting.

Another class of H₄R antagonists that has gained enormous interest from industry is the aminopyrimidines. According to filed patents, Bayer Healthcare AG, Palau Pharma, Pfizer and J&J all have their current research programs based on these structures. Also Abbott Laboratories followed this series of pyrimidines, eventually leading to the anti-inflammatory A-987306 (K_i H₄R = 5.8 nM) with very good pharmacokinetic properties and an *in vivo* half-life up to 3.7 hours (74).

The new class of quinoxalinone H₄R ligands was found in a fragment-based drug discovery project at the VU University Amsterdam as well as at J&J, where they originated from 5-HT₃ ligand discovery projects (75). The VU University Amsterdam developed these quinoxalines by combining clozapine and JNJ 7777120 in a pharmacophore model. These compounds were shown to have anti-inflammatory properties in a carrageenan-induced paw-edema model in rats (76). Subsequent scaffold hopping resulted in the discovery of inverse agonists quinoxalines (56). Interestingly those structures can be extended with a sulfonamide group (resulting in the inverse agonists quinoxaline sulfonamides) with a variety of

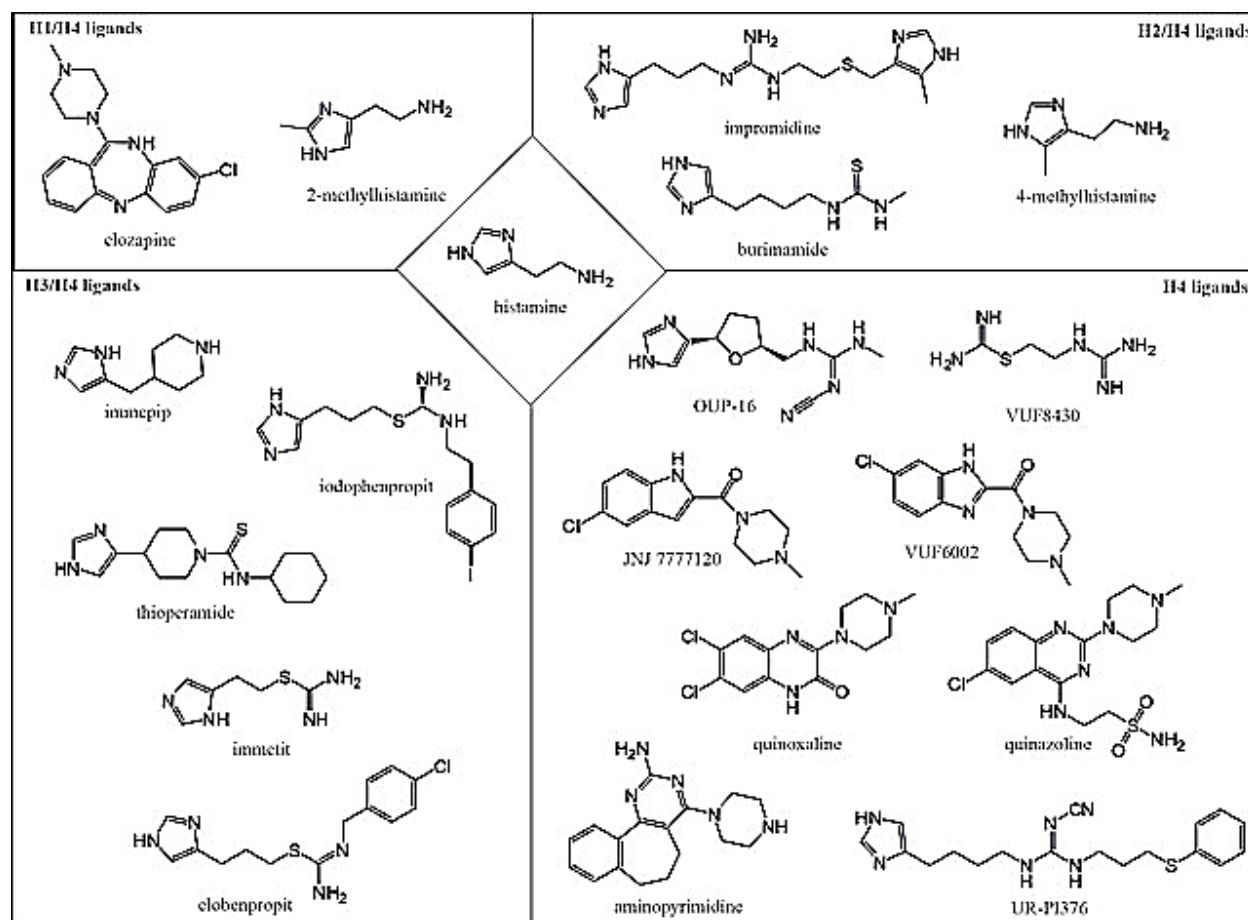


Figure 6. Chemical structures of H₄R ligands and their binding to other histamine receptor subtypes.

substituents without losing affinity for the H₄R (77). H₄R ligands and their clinical applications have been extensively discussed in recent reviews by Smits *et al.* (78) and Engelhardt *et al.* (79).

6.3. H₄R radioligands

The agonists histamine and UR-PI294 (61) can be readily labeled with tritium and used as radioligand in ligand/receptor binding studies. Since histamine and UR-PI294 interact with high affinity to other histamine receptor subtypes (i.e. H₃Rs), only 4-methylhistamine is a H₄R-selective radioligand.

The only available H₄R antagonist radioligand is [³H]-JNJ 7777120 (69), which is particularly useful when studying mutant H₄Rs that are unable to bind histamine.

7. ELUCIDATION OF LIGAND BINDING MODES IN H₄R

By relating distinct pharmacology of H₄R orthologs to their sequence divergence, information can be obtained on ligand binding modes (Figure. 7) and receptor activation. To this end, chimeras between H₄R of human and other species have been constructed and evaluated, subsequently followed by site-directed mutagenesis to pinpoint the specific amino acid (s) involved in ligand interaction.

7.1. Species differences

Recently, an extensive study was performed in which H₄Rs of several species were characterized (28). These H₄R orthologs were heterologously expressed and binding affinities of several well-known ligands were determined. Histamine and 4-methylhistamine show an equal trend when comparing their H₄R binding affinities between species. VUF8430 (58) shows a different pattern with a decreased affinity for pig, dog, and guinea pig H₄R, in comparison to other H₄R orthologs. Clozapine loses affinity for the pig, dog, mouse and rat, compared to the human H₄R. Interestingly, monkey and guinea pig show higher affinity for this tricyclic compound (28). Clobenpropit has lower affinity for pig and dog H₄R, but similar affinities for the other tested H₄R species variants, whereas the inverse agonist thioperamide has equipotent affinity for all H₄R orthologs. Both antagonists JNJ 7777120 and VUF6002 show significant lower affinity for monkey, pig, dog and guinea pig receptors as compared to the other tested species.

Most of the tested ligands show significant differences in affinity at the different species variants (24). Therefore, careful *in vitro* pharmacological characterization of H₄R orthologs is of major importance as several animal models are used to study H₄R (ligands) function *in vivo*.

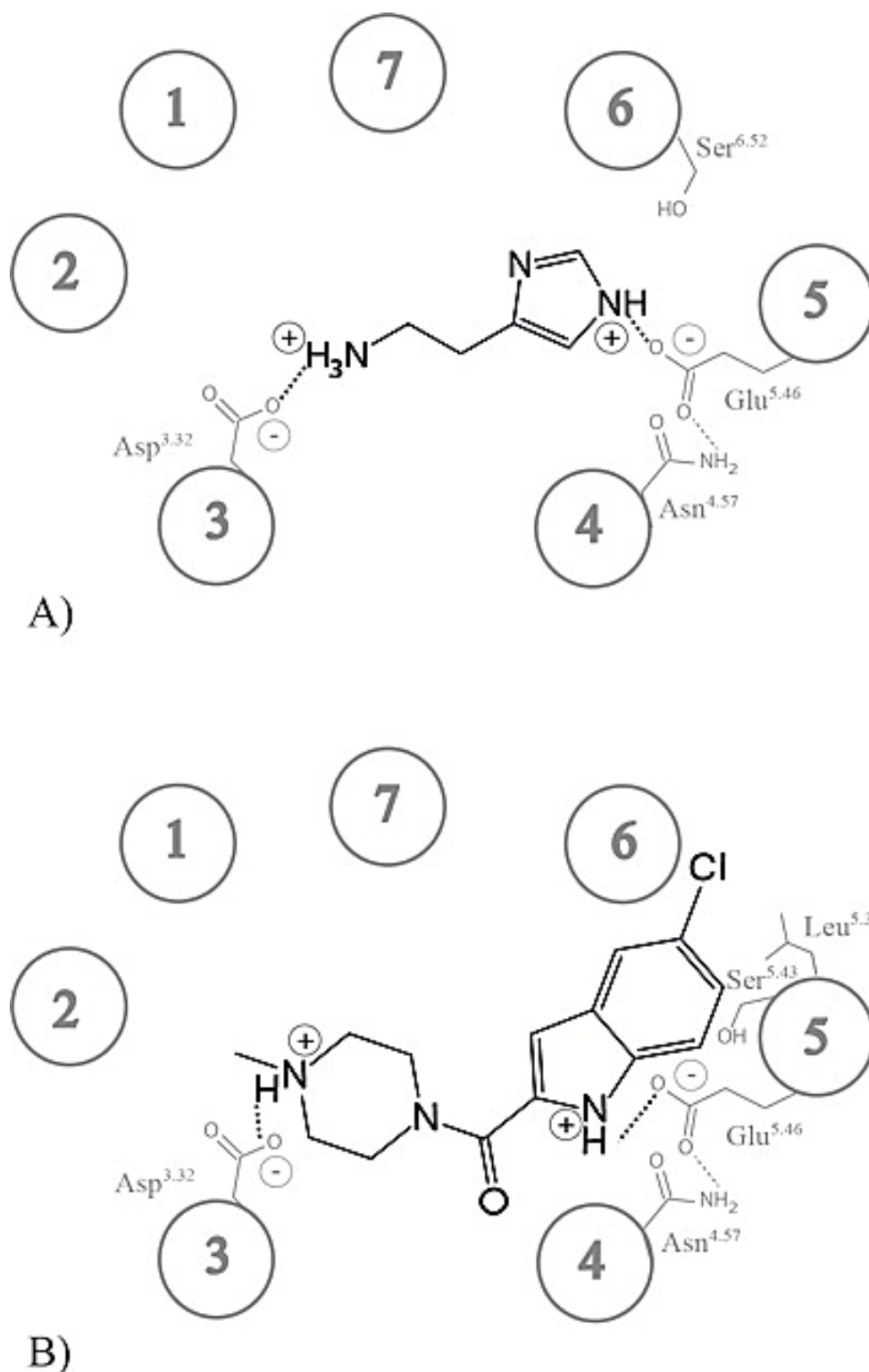


Figure 7. a) Schematic 2D representation of histamine and its interactions with H₄R residues. Based on side-directed mutagenesis (SDM) studies D^{3.32} and E^{5.46} are identified as the key interacting residues (83, 84). Ser^{6.52} and Asn^{4.57} are not crucial for binding but mutations at these positions have an effect on histamine-induced receptor activation (28). b) Schematic 2D representation of JNJ 777120 and its interactions with H₄R residues. In SDM studies D^{3.32} was identified as the major anchor point for JNJ 777120. E^{5.46} plays a less pronounced role compared to histamine binding and L^{5.39} is important for the position of the chlorinated ring (28).

Considering the H₄R differences between animals, caution should be taken in selecting appropriate species to evaluate specific ligands. JNJ 7777120 is currently the most commonly used reference compound to block H₄Rs in animal models (55). However, recent developments request re-evaluation whether JNJ 7777120 should still be used as reference antagonist (see sections 6.2 and 8.4).

Chimeras between human and pig H₄Rs, followed by site-directed mutagenesis, identified residues at positions 45.55, 4.57, 5.39 and 5.43 responsible for the observed species differences in ligand affinity (28). Residue 5.39 was shown to be also responsible for the differences in ligand binding between human and monkey (28), whereas Phe^{45.55} in EL2 (Figure 4) of the human H₄R was identified to be responsible for the increase in agonist affinity compared to mouse H₄R (80).

7.2. Binding pockets in H₄R

H₄R ligands bind the receptor in the common binding pocket located in the cavities formed by the TM helices. This binding pocket consists of two subpockets, which are designated i and ii (81). Pocket i is located between TM domains 2, 3 and 7, whereas pocket ii is located between TMs 3, 4, 5 and 6. Besides these general pockets, two hydrophobic subpockets exist in pocket ii. The first hydrophobic subpocket is located between TM3, TM4, TM5 and TM6 in the vicinity of Trp^{6.48}. The second hydrophobic subpocket is situated between TM3, TM5, TM6 and EL2 (and EL3) towards the extracellular side of the receptor (82). Compound classes such as the aminopyrimidines, quinoxalines and quinazolines are proposed to occupy these subpockets with their hydrophobic moieties (82).

7.3. Binding mode of histamine

Although the similarity with the other histamine receptor family members is relatively low (55), earlier identified key residues in ligand binding to the H₁R-H₃R, are also present in the H₄R (83). The amine group of histamine interacts with Asp^{3.32} (83, 84) in subpocket i of H₄Rs and the protonated nitrogen of the basic imidazole ring is forming a hydrogen bond with Glu^{5.46} in subpocket ii (Figure. 7) (83, 85). Interestingly, both in H₃R and H₄R a Glu residue is present at position 5.46, compared to Asn in H₁R and Thr in H₂R. The importance of Glu^{5.46} is also shown by the inability or decrease in binding of [³H]-histamine to H₄Rs in which Glu^{5.46} is substituted with Ala or Gln, respectively (83, 84). It is hypothesized that the presence of this negatively charged residue is the reason for increased binding affinity of histamine to H₃R and H₄R as compared to H₁R and H₂R (83). Asn^{4.57} and Ser^{6.52} were also suggested to be important residues in histamine-induced activation of H₄R (84), but do not play a direct critical role in histamine binding (28). The non-imidazole small molecule agonist VUF8430 is believed to bind in a similar binding mode as histamine (83). In contrast, for the tricyclic agonist clozapine the interaction with residue Glu^{5.46} is less pronounced, as illustrated by its ability to bind the mutated H₄R-Glu^{5.46} (83, 86, 87).

7.4. Binding mode JNJ 7777120

Although JNJ 7777120 binds in the same binding cavity as histamine, the actual binding mode is proposed to be different. This is supported by the fact that [³H]-histamine binding is almost lost in an E^{4.56}Q mutant, but [³H]-JNJ 7777120 is still able to interact with this mutant receptor. The positively charged piperidine nitrogen atom is believed to form a hydrogen bond with Asp^{3.32} (83). The indole nitrogen atom donates a hydrogen bond to the carboxylate group of Glu^{5.46}. Considering the drop in affinity for JNJ 7777120 on the L^{5.39}V mutant compared to a increase in affinity for clozapine for the same H₄R mutant, the chlorinated aromatic ring of JNJ 7777120 is believed to be positioned in the vicinity of this residue (Figure. 7) (86).

The binding mode of a variety of H₄R ligands has recently been extensively reviewed by Istyastono *et al.* (86).

8. SIGNALING OF H4R

Although H₄R signaling has been studied in cells endogenously expressing H₄Rs, determination of the exact mechanisms of H₄R functioning as well as ligand characterization is predominantly performed in H₄R transfected cells. In HEK293T cells, transfected with H₄R and a cAMP-response element (CRE) reporter gene construct, H₄R activation inhibits forskolin-induced cAMP production by adenylyl cyclase (AC) and subsequent CRE-driven gene transcription in a pertussis toxin (PTX)-sensitive manner, indicating the involvement of Galpha_{i/o} proteins (14, 16, 36). Interestingly, no changes in cAMP levels were observed in H₄R-expressing HEK293 cells in response to histamine, even though other Galpha-mediated responses (mitogen-activated protein kinase (MAPK) phosphorylation and PTX sensitivity) could be measured (15). In addition, in the presence of chimeric Galpha_{q11/2}, Galpha_{q13} or Galpha₁₆ proteins H₄R stimulation resulted in increased calcium mobilization in transfected CHO, COS-7 and HEK293 cells (15).

Furthermore, H₄R stimulation resulted in an increase in [³⁵S]-GTPgammaS binding in SK-N-MC and HEK293 cells. Interestingly, increased basal levels are observed in this assay when comparing H₄R expressing cells with control cells. Thioperamide inhibits this basal signaling. The same phenomenon is seen in Sf9 insect cells co-expressing mammalian Galpha_{i2} and Gbeta₁gamma₂ proteins (88). This indicates that H₄Rs are constitutively active (i.e. signal in absence of a ligand) and thioperamide is acting as inverse agonist (54). Constitutive activity has been demonstrated for other histamine receptor family members (89-92) but in the steady state GTPase assay, the H₄R shows the highest amount of constitutive activity compared with H₁R-H₃R (88).

8.1. Calcium mobilization

Histamine induces calcium release from intracellular calcium stores in both mast cells and eosinophils (65), which was antagonized by thioperamide

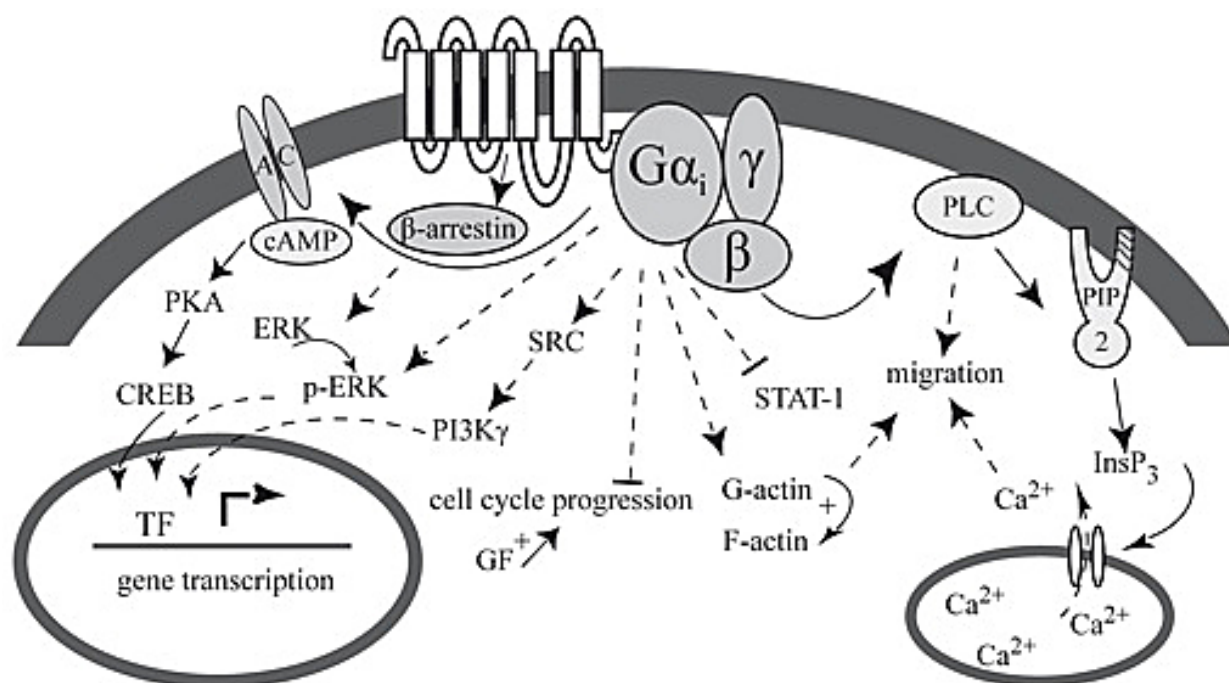


Figure 8. Overview of H₄R signaling pathways in both endogenous and transfected cells. H₄R can signal constitutively, but can also be regulated by agonists, inverse agonists and antagonists. The H₄R activates Galpha_{i/o} and/or beta-arrestin proteins and their downstream signaling pathways.

indicating a role for H₄R (64). Direct proof of H₄R-mediated calcium mobilization came from experiments with H₄R knock out mice, as mast cells isolated from these mice failed to mobilize calcium in response to 30 mM histamine (65). Upon histamine binding, H₄R couples to PTX-sensitive Galpha_{i/o} proteins which subsequently can activate phospholipase C (PLC) via their Gbetagamma subunits. PLC hydrolyzes phosphatidylinositol 4,5-bisphosphate (PIP₂) to diacylglycerol and inositol 1,4,5-triphosphate (InsP₃). InsP₃ can bind to its receptor on the endoplasmic reticulum (ER) membrane, thereby stimulating the release of calcium, which can on its turn induce chemotaxis towards histamine (65) (Figure. 8).

8.2. Migration

More than 25 years before the identification of H₄R, Clark and colleagues already observed that low concentrations of histamine induced chemotaxis of eosinophils (93). Soon after the introduction of the newest member of the histamine receptor family a role for H₄R in this eosinophil migration was discovered (94). More recently, the chemotactic properties of isolated human eosinophils were tested in the presence of several H₁R/H₃R agonists, but only histamine could provoke a response. Interestingly, only H₃R/H₄R antagonists were able to block this effect. Since eosinophils do not express H₃R, the H₄R is responsible for the histamine-induced migration of eosinophils (94-96).

The actin cytoskeleton determines both cell morphology and cell movement. The real “moving” is occurring because the G actin monomers are rearranged to

form F actin polymers. An imaging approach was used to show that stimulation of H₄R-expressing eosinophils induces maximal actin polymerization to F actin already after 5-10 seconds (64, 96). Histamine-induced actin polymerization was inhibited by JNJ 777120 and H₃R/H₄R inverse agonist thioperamide, confirming an exclusive role for H₄R (96). H₄R agonists also induced F-actin polymerization via H₄R in MoDC as shown by the observation that clobenpropit-induced polymerization could be blocked by JNJ 777120 (38).

In addition, H₄R agonists induce a rapid PTX-sensitive shape change in eosinophils, which was blocked by H₄R antagonists, but not by antagonists of other histamine receptors (64). In comparison to the chemokine eotaxin (CCL11)-induced eosinophil migration, histamine was found to be a relative weak chemotactic factor in a whole blood migration assay (95). Of concern is the observation that histamine failed to stimulate guinea-pig eosinophils in a variety of these shape change or chemotaxis assays (64). This again emphasizes the importance of understanding the species differences in H₄R pharmacology.

Histamine stimulation of the H₄R also induces mast cell migration *in vitro*. Investigation of the signaling components proved that both Galpha_{i/o} and PLC are involved in the downstream signaling events. Histamine inhalation led to an increase in the total number of mast cells and sub-epithelial mast cells in trachea of mice, which could be inhibited by JNJ 777120 (69), thereby ruling out H₁R and H₂R-mediated effects.

In an *ex vivo* migration assay, skin dendritic cells isolated from mice and guinea pig were able to enhance chemotaxis upon stimulation with histamine or H₃R/H₄R ligand clobenpropit. These observations were confirmed in *in vitro* migration experiments with bone marrow derived dendritic cells from human and mice (29). This histamine/clobenpropit-induced effect was fully inhibited by JNJ 7777120. However, the histamine-induced chemotaxis could also be fully inhibited by H₁R antagonist diphenhydramine (29), suggesting crosstalk between these two histamine receptor subtypes.

In a human epidermis and murine *in vivo* assay it was shown that Langerhans cell migration from the epidermis was increased upon H₄R activation. In addition, a downregulation of the production of CCL2 was observed (37).

More recently the effect of histamine on migration of human fetal lung fibroblasts to human plasma fibronectin (HFn) *in vitro* was examined (97). Histamine did not induce migration of these cells, but appeared to potentiate the migration to Hfn in a bell shaped relation. Addition of JNJ 7777120 inhibited this effect, as did PTX, indicating an H₄R/G $\alpha_{i/o}$ -mediated process (Figure. 8) (97).

8.3. Modulation of protein expression and physiological effects regulated by H₄R

Leukocyte chemoattractants affect the function and cell surface expression of adhesion molecules, which play an important role in the interaction of leukocytes with the microvascular endothelium. Histamine is also able to upregulate adhesion molecules (e.g. CD11b/CD18 and CD54) in eosinophils. This upregulation occurs already within 10 min after stimulation (95). Upregulation of CD11b could be inhibited by preincubation with thioperamide (64) indicating a role for the H₄R. In addition, pre-stimulation with histamine increased the amount of eosinophils to migrate towards CCL11, which could also be inhibited by thioperamide (64).

A potentiation is also observed for CXCL12 chemotactic activity on the precursor mast cell population upon stimulation with histamine or supernatants from IgE-activated mast cells. Small interfering RNA (siRNA) was used to specifically block each histamine receptor subtype. This resulted in the identification of the H₄R as the one responsible for the observed synergy. In addition, JNJ 7777120 was able to completely block this potentiation. Interestingly, CXCR4 (receptor for CXCL12) protein levels did not change. An explanation was put forward, in which the authors speculated on a shared signaling pathway between H₄R and CXCR4 downstream of the G $\alpha_{i/o}$ protein (98).

Histamine suppresses polyIC-induced IL-12p70 production of MoDC via different pathways activated by H₂R and H₄R. H₄R activates the MAPK pathway, resulting in the activation of AP-1 (Figure. 8). Interestingly, this was independent of ERK1/2 phosphorylation. AP-1 induction by clobenpropit could be blocked by JNJ 7777120,

demonstrating that AP-1 is indeed induced by H₄R stimulation. The H₂R-mediated IL-12p70 suppression involves cAMP production (38).

A recent study in peripheral blood mononuclear cell (PBMC) cultures from non-atopic human volunteers showed a possible role for the H₄R in modulating signaling pathways via STAT1. It was already shown that H₄R might play a role in lymphocyte signaling and in Th2 differentiation (69, 99, 100). JNJ 7777120 stimulated the production of STAT1 α and its downstream phosphorylation in the non-atopic group. JNJ 7777120 could also enhance the binding of STAT1 to DNA. A model was proposed, in which histamine acts through the H₄R on T cells, thereby inhibiting STAT1 activation and thus helps to drive the Th2 polarization by inhibiting IFN- γ mediated events (101, 102).

Histamine-free histidine decarboxylase deficient mice (HDC^{-/-}) show a functional deficit in invariant natural killer (iNKT) cells. This is clearly demonstrated by decreased IL-4 and IFN- γ production. Addition of histamine induced a functional recovery that is mediated by the H₄R, since JNJ 7777120 could prevent this. To unambiguously state that the H₄R is involved, iNKT cells of H₄R knock out mice were also tested. These cells generate lower amounts of circulating cytokines than WT mice, clearly showing a role for H₄R in this process (103).

H₄R proteins were recently shown to be involved in the production of interleukin 6 (IL-6) from mouse bone marrow-derived mast cells. Both histamine and H₄R agonist JNJ 28610244 can induce the transient production of this cytokine. In turn, H₄R antagonists could inhibit this effect. Additionally, H₄R potentiates the prolonged lipopolysaccharide- (LPS) induced IL-6 production via MAPK (ERK) and Src/PI3K γ pathways, suggesting crosstalk between toll-like receptors (TLR) and H₄R signaling pathways (104).

Murine and human progenitor cell populations express functional H₄R. Upon activation of the receptor, the cells show a reduced growth factor-induced cell cycle progression. As a consequence, myeloid, erythroid and lymphoid colony formation is decreased, hence the cells show reduced proliferation. The H₄R thus prevents induction of cell cycle genes, presumably via its cAMP and subsequent protein kinase A (PKA) pathway (Figure. 8). A special role for the H₄R was confirmed with H₄R selective antagonists that restored cell cycle progression. Very interesting is the observation that the arrest of growth factor-induced G1/S phase transition (quiescence) protects the murine and human progenitor cells from the toxicity of the cell cycle dependent anticancer drug Ara-C *in vitro* and reduces aplasia in a murine model of chemotherapy (103). This opens a new possible role for H₄R targeting drugs (105).

The function of H₄R in the stomach was explored in ulcer models in both rat and mice. JNJ 7777120 (10-30 mg/kg sc) reduced the indomethacin-induced gastric mucosal damage by approximately 70% in the conscious

rat. In addition, JNJ 7777120 reduced indomethacin- and bethanechol-induced gastroresive effects in conscious mice. H₄R agonist VUF 10460 (4- (4-methylpiperazin-1-yl)-6-phenylpyrimidin-2-amine) reduced indomethacin-induced lesions in the rat, but not in mice (106).

8.4. Beta-arrestin recruitment to H₄R / Biased agonism

In addition to G protein coupling, both histamine and 4-methylhistamine induce beta-arrestin recruitment to H₄R as revealed in a protein-fragment complementation-based beta-arrestin recruitment assay (i.e. Tango assay Invitrogen). Histamine-induced beta-arrestin recruitment to the H₄R was recently confirmed by Rosethorne and Charlton in PathhunterTM U2OS-H4 / beta-arrestin cells (107). Interestingly, this recruitment was PTX insensitive, indicating a G_α_i-independent mechanism. Surprisingly, the antagonist JNJ 7777120 was shown to behave as a partial agonist by inducing G_α_i-independent beta-arrestin recruitment to the H₄R (71).

Moreover, in the same cell line both histamine and JNJ 7777120 stimulate phosphorylation of ERK in time frames that are characteristic for G protein-mediated (seconds) or beta-arrestin-mediated (~20min) signaling, respectively (Figure. 8) (71).

These recent findings indicate that the H₄R ligands may display distinct efficacies towards G protein-dependent and -independent pathways, with the reference antagonist JNJ 7777120 turning out to be a partial agonist with bias towards beta-arrestin driven pathways. Although this ligand-directed signaling is very exciting and opens the door for the development of pathway-selective compounds it also invites to re-assess the efficacies of known H₄R ligands towards G-protein-independent pathways (70, 71, 107).

9. FINAL REMARKS

There is substantial evidence that H₄R plays a role in inflammatory processes, based on their localization pattern on cells of hematopoietic origin and the medicinal in vivo studies so far. H₄R inhibitors can be interesting drugs to counteract allergic reactions, hence the interest of the pharmaceutical industry. However, recently also other expression patterns were identified, such as the brain. In addition, a link between H₄R and diseases as rheumatoid arthritis (108), colon (109, 110) and breast cancer (111) was postulated. This opens doors for even more possibilities than the initial anti-inflammatory properties.

New development programs for the search for novel H₄R ligands are ongoing. In parallel with the computational design of ligands, and our increased understanding of receptor-ligand binding interactions the ultimate goal is to develop H₄R-specific ligands with on forehand known efficacies and binding modes.

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Send correspondence to: Rob Leurs, VU University Amsterdam, Leiden, Amsterdam Center for Drug Research, De Boelelaan 1083, 1081HV Amsterdam, The Netherlands, Tel: 31205987579, Fax: 31205987610, E-mail: r.leurs@vu.nl