

Tobias Langenhan
Torsten Schöneberg *Editors*

Adhesion G Protein-coupled Receptors

Molecular, Physiological and
Pharmacological Principles in Health
and Disease

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Editors

Adhesion G Protein-coupled Receptors

Molecular, Physiological and
Pharmacological Principles in
Health and Disease

 Springer

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Preface

The very first monograph that was dedicated to a general overview on the adhesion family of G protein-coupled receptors (aGPCRs) was published just in 2010 (Adhesion-GPCRs: Structure to Function. Yona and Stacey, Ed., Landes Bioscience and Springer). It was the earliest attempt by a small group of researchers to cast the scarce information on these enigmatic molecules into a general concept on what they do and how they do it.

The absence of such public face for the biology of aGPCRs was painfully felt by all colleagues who were actively researching aGPCRs in these days. Scepticism was high from many neighbouring fields why aGPCRs rise to such grotesque dimensions with thousands of residues dedicated to their extracellular tails alone. Also how their exotic functions during the development of organs could be accounted for by their peculiar bipartite adhesive/receptive structure was a constant source of doubt (and motivation for further investigation). Not least, whether aGPCRs are 'true' GPCRs and can thus be attacked by the immense technological armoury that has accumulated during the decades of research on other members of the GPCR superfamily was possibly the most pressing question we were confronted with. Next to the simple matter: what do these receptors sense, after all?

While many of these points could not be satisfactorily answered yet back then, the 2010 book project brought them on the map for the first time in a collective effort. Therefore, this venture from a group of adhesion GPCR aficionados was an incontestable sign of a growing community of researchers that had formed to pursue the inherent questions on aGPCRs with seriousness and persistence.

The roster of colleagues that have contributed their expertise, time and dedication to the current monograph bears testimony to that spirit, and we are immensely grateful for their support. We also wish to thank the Editorial Board of the *Handbook of Experimental Pharmacology* for allotting us an entire volume of this eminent book series to document our knowledge on aGPCRs. We are indebted to Susanne Dathe, Wilma McHugh, Rahila Nahid and Sumathy Thanigaivelu from *Springer Nature* for excellent editorial and technical support, and for generous funding from the Deutsche Forschungsgemeinschaft (DFG) to several chapter authors through a Research Unit Grant (FOR 2149), a first award of its kind to a coordinated scientific initiative dedicated to the study of aGPCRs.

The chapters of this volume are authored by renowned experts in the aGPCR field and chart the current state of aGPCR research. Following their contributions, the reader will learn that some of the pressing molecular issues of 2010 have begun to find answers:

- aGPCRs can signal via canonical signaling outlets and a credible mechanism on how they get activated has been recently devised (Liebscher et al., *Tethered agonism: a common activation mechanism of adhesion GPCRs*; Kishore et al., *Versatile signaling activity of adhesion GPCRs*).
- In some cases, the receptors' structural peculiarities have been experimentally matched with highly intriguing biochemical and biological phenomena such as in the case of the GAIN domain and other extracellular protein folds (Araç et al., *Understanding the structural basis of adhesion GPCR functions*).
- One such class of events regards the extensive proteolytic processing of aGPCRs and is discussed by Nieberler et al. (*Control of adhesion GPCR function through proteolytic processing*). Knapp et al. explore the central position of *adhesion GPCRs-related protein networks*, roles that are mainly relayed through their intracellular domains.
- Other vital components of their architecture such as the structure of the heptahelical transmembrane domain of aGPCRs have remained locked to our efforts, but it is clear that in the near future the focus will shift evermore into their direction and offer new vantage points to interfere with their activity. Nijmeijer et al. explored these possibilities in their chapter on *7TM domain structure of adhesion GPCRs*.
- Kovacs et al. review *the relevance of genomic signatures at adhesion GPCR loci* (specifically of human homologs), informing us about their role in phenotypic variation and disease aetiology, an overdue endeavour in the omics era that is aided by the novel harmonised nomenclature and classification system of the aGPCR family introduced by Krishnan et al. (*Classification, nomenclature and structural aspects of adhesion GPCRs*).

The second part of this book is dedicated to physiological and pathological aspects of aGPCRs:

- Scholz et al. describe the emerging concept of *adhesion GPCRs as a putative class of metabotropic mechanosensors*, which distinguishes them from the rest of the GPCR superfamily.
- Several chapters relate to this discovery with specialist focus on its implications in the nervous system (Harty et al., *Adhesion GPCRs as novel actors in neural and glial cell functions: from synaptogenesis to myelination*), in skeletal muscle (White et al., *Control of skeletal muscle cell growth and size through adhesion GPCRs*) and lung physiology (Ludwig et al., *Adhesion GPCR function in pulmonary development and disease*) and in the immune system (Hamann et al., *Adhesion GPCRs as modulators of immune cell function*). Musa et al. describe that *heart development, angiogenesis and blood-brain barrier*

function are modulated by adhesion GPCRs, adding further organ systems that require those receptors for their respective setups and daily operations.

- Finally, Strutt et al. discuss that *adhesion GPCRs govern polarity of epithelia and cell migration*, while the chapter of Aust et al. review the current state of knowledge on *adhesion GPCRs in tumorigenesis*.

We are certain that the research described in this book marks several milestones in the maturation of our understanding on how aGPCRs impact biology. It is to be hoped that the concepts on several aspects of aGPCRs unveiled in the last years are stepping stones to grasp their roles in human disease and therapeutic intervention. We are much looking forward to witness and participate in the exciting developments of this thriving area of biomedical research.

The book will start though with look back at the *History of the adhesion GPCR field* (Hamann and Petrenko), to record the path of our community and remark its scientific course throughout the last 20 years.

Würzburg, Germany
Leipzig, Germany

Tobias Langenhan
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Contents

Introduction: History of the Adhesion GPCR Field	1
Jörg Hamann and Alexander G. Petrenko	
Part I Molecular and Pharmacological Properties of Adhesion GPCRs	
Classification, Nomenclature, and Structural Aspects of Adhesion GPCRs	15
Arunkumar Krishnan, Saskia Nijmeijer, Chris de Graaf, and Helgi B. Schiöth	
7TM Domain Structure of Adhesion GPCRs	43
Chris de Graaf, Saskia Nijmeijer, Steffen Wolf, and Oliver P. Ernst	
Understanding the Structural Basis of Adhesion GPCR Functions	67
Demet Araç, Norbert Sträter, and Elena Seiradake	
Control of Adhesion GPCR Function Through Proteolytic Processing	83
Matthias Nieberler, Robert J. Kittel, Alexander G. Petrenko, Hsi-Hsien Lin, and Tobias Langenhan	
Tethered Agonism: A Common Activation Mechanism of Adhesion GPCRs	111
Ines Liebscher and Torsten Schöneberg	
Versatile Signaling Activity of Adhesion GPCRs	127
Ayush Kishore and Randy A. Hall	
Adhesion GPCR-Related Protein Networks	147
Barbara Knapp and Uwe Wolfrum	
The Relevance of Genomic Signatures at Adhesion GPCR Loci in Humans	179
Peter Kovacs and Torsten Schöneberg	

Part II Adhesion GPCRs as Pharmakotargets in Organ Function and Development	
Adhesion GPCRs as a Putative Class of Metabotropic Mechanosensors	221
Nicole Scholz, Kelly R. Monk, Robert J. Kittel, and Tobias Langenhan	
Adhesion GPCRs Govern Polarity of Epithelia and Cell Migration	249
David Strutt, Ralf Schnabel, Franziska Fiedler, and Simone Prömel	
Adhesion GPCRs as Novel Actors in Neural and Glial Cell Functions: From Synaptogenesis to Myelination	275
S��verine M. Sigoillot, Kelly R. Monk, Xianhua Piao, Fekrije Selimi, and Breanne L. Harty	
Control of Skeletal Muscle Cell Growth and Size Through Adhesion GPCRs	299
James P. White	
Adhesion GPCR Function in Pulmonary Development and Disease	309
Marie-Gabrielle Ludwig, Klaus Seuwen, and James P. Bridges	
Adhesion GPCRs as Modulators of Immune Cell Function	329
J��rg Hamann, Cheng-Chih Hsiao, Chang Sup Lee, Kodi S. Ravichandran, and Hsi-Hsien Lin	
Heart Development, Angiogenesis, and Blood-Brain Barrier Function Is Modulated by Adhesion GPCRs	351
Gentian Musa, Felix B. Engel, and Colin Niaudet	
Adhesion GPCRs in Tumorigenesis	369
Gabriela Aust, Dan Zhu, Erwin G. Van Meir, and Lei Xu	
Index	397

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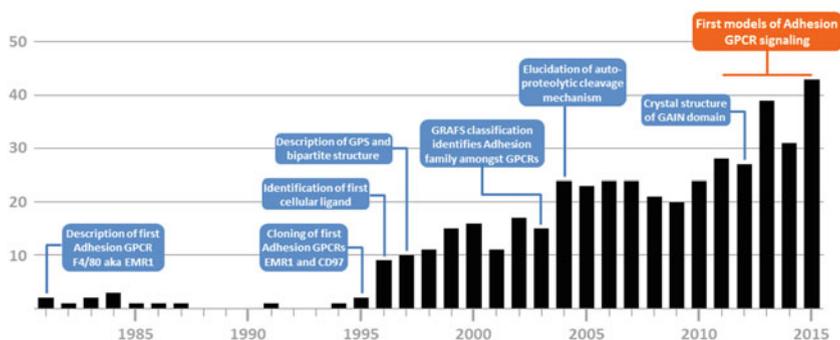
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Introduction: History of the Adhesion GPCR Field

Jörg Hamann and Alexander G. Petrenko

Graphical Abstract



Development of the aGPCR scientific field based on PubMed-listed research articles and selected key findings

Contents

1 A Novel Type of Seven-Transmembrane Receptors	2
2 Receptor Biology Convenes a New Research Field	4
3 From Molecular Structure to Pharmacology	7
References	9

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Abstract

Since the discovery of adhesion G-protein-coupled receptors (aGPCRs) 20 years ago, reverse genetics approaches have dominated the elucidation of their function and work mechanisms. Seminal findings in this field comprise the description of aGPCRs as seven-transmembrane (7TM) molecules with an extended extracellular region, the identification of matricellular ligands that bind to distinct protein folds at the N-terminus, the clarification of an autoproteolytic cleavage event at a juxtamembranous GPCR proteolysis site (GPS), the elucidation of the crystal structure of the GPCR autoproteolysis-inducing (GAIN) domain that embeds the GPS and connects the receptor fragments, the demonstration that a short N-terminal sequence of the seven-transmembrane (7TM) region can serve as a tethered agonist, and, recently, the notification that aGPCRs can serve as mechanosensors. We here discuss how these discoveries have moved forward aGPCR research and, finally, linked the field to the GPCR field. We argue that crucial questions remain to be addressed before we can fully appreciate the biological nature of these fascinating receptors.

Keywords

Adhesion GPCRs • History • Biology • Structure • Signaling • Pharmacology

1 A Novel Type of Seven-Transmembrane Receptors

After the discovery of hormones as “first messenger” and cyclic adenosine monophosphate (cAMP) as a “second messenger” in the twentieth century, the search for molecules that transduce the “message” through the cell membrane led to the discovery of the first G proteins and then G-protein-coupled receptors (GPCRs). Forward biological approaches, searching for membrane-bound cognate receptors for biocative molecules, subsequently resulted in the identification of many GPCRs and the finding that seven-transmembrane (7TM) receptors possess the largest receptor family in nature. Yet, in contrast to rhodopsin, secretin, glutamate, and Frizzled GPCRs, members of the fifth GPCR family, the adhesion (a) GPCRs, were not discovered via their ligand molecules. Their identification about 20 years ago was the result of genetic approaches that became available through the development of cDNA cloning techniques in the late 1980s (Fig. 1). In 1995, the primary structure of the leukocyte surface molecules CD97 and EMR1 (EGF module-containing, mucin-like hormone receptor 1; in the mouse known as F4/80) was described [1, 2]. The mature proteins were found to comprise a 7TM region, the hallmark of all GPCRs. Most notable was the extended extracellular part, possessing several tandem epidermal growth factor (EGF)-like domains at the N-terminus. With reference to the binary molecule structure, the name EGF-TM7 was coined for these novel receptors [3].

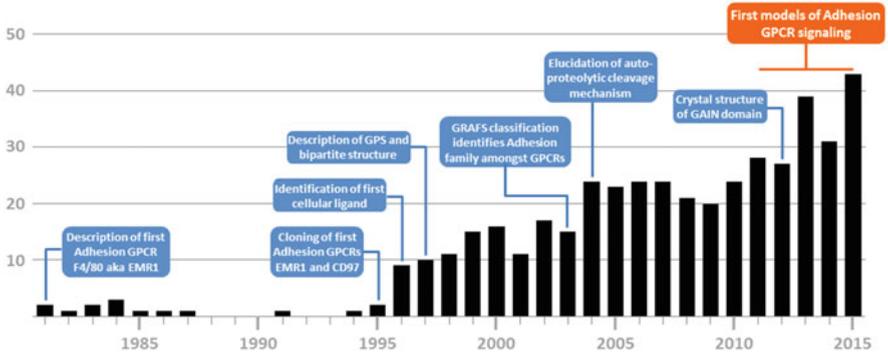


Fig. 1 Development of the aGPCR scientific field. PubMed-listed research articles reporting on aGPCRs indicated per year throughout the last 35 years. Selected key findings are highlighted

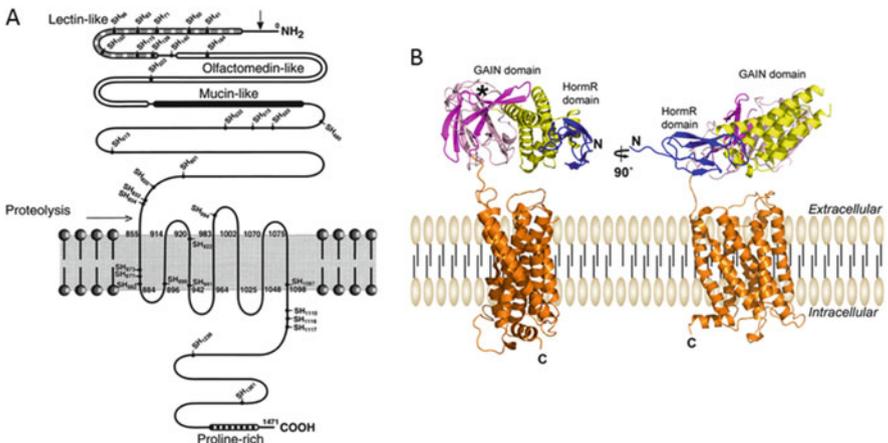


Fig. 2 Progress in the structural understanding of aGPCRs. (a) Protein structure of CIRL-1/latrophilin 1 predicted in 1997 from the deciphered amino acid sequence of the mature polypeptide, with indicated the 7TM region, the extended extracellular region with several protein domains, and the juxtamembranous proteolysis site (reproduced from [4]). (b) Model of CIRL-1/latrophilin 1 suggested in 2012 based on crystal structures of the GAIN and hormone receptor domain and modeling of the 7TM moiety (reproduced from [6])

Soon after, CIRL-1 (calcium-independent receptor of α -latrotoxin 1)/latrophilin 1, a neuronal receptor for the black widow spider poison α -latrotoxin, was shown to possess a similar structure and strong homology to the 7TM cores of EGF-TM7 receptors [4, 5] (Fig. 2). However, instead of repetitive EGF-like domains, CIRL-1/latrophilin 1 contains singular lectin-like, olfactomedin, and hormone receptor motif domains in its extracellular part. Subsequent description of other homologous 7TM receptors, including latrophilins, EMRs, CELSRs (cadherin EGF LAG seven-pass G-type receptors), BAIs (brain-specific angiogenesis inhibitors), HE6 (human

epididymal 6), and VLGR1 (very large GPCR 1), confirmed the existence of a novel type of GPCR with a large extracellular part, differently composed of structural modules that are typically found in cell adhesion proteins, suggesting their role in coupling cell-to-cell interaction to intracellular signaling.

Right at the beginning, it became clear that these chimeric GPCRs undergo intensive posttranslational modifications and that CD97, C1RL-1/latrophilin 1, and several of their relatives consist of two noncovalently attached fragments that arise from cleavage of the full-length precursor molecules at a juxtamembranous GPCR proteolysis site (GPS) [4, 7, 8]. By pulse-and-chase labeling, it was shown that the cleavage at the GPS site takes place in the endoplasmic reticulum, rendering it fundamentally different from other proteolytic steps, such as furin processing, which occurs in the Golgi apparatus. In 2004, Hsi-Hsien Lin and colleagues showed that the cleavage is an autocatalytic event commonly employed by N-terminal nucleophile hydrolases [9]. The GPS motif appeared to be highly conserved in the aGPCRs family, representing essentially the eighth region of homology within the family. N-terminal to the GPS, larger regions with no sequence homology were found, linking the cell adhesion-like domains. Why the N-terminal protein adhesion-like domains in many aGPCRs are separated from the 7TM part by a large spacer sequence remained unclear for many more years.

Deciphering of the human genome finally disclosed the existence of 33 related receptors that, based on phylogenetic comparison of the 7TM part, assemble a distinct family of GPCRs. The original interest in these proteins was based primarily on their potential of linking cell-to-cell interactions to intracellular signaling. Helgi Schiöth and coworkers thus called them aGPCRs and subdivided them into nine subfamilies [10]. Their unique molecular design clearly sets the aGPCRs apart from other GPCR families, including the secretin GPCRs [11]. It is of note that in spite of their intricate structure, aGPCRs seem to be ancestral to most other GPCR families and have been found even in the most ancient metazoan phyla [12].

As aGPCRs increasingly received attention from a wide spectrum of biomedical fields, the Adhesion GPCR Consortium, together with the International Union of Basic and Clinical Pharmacology Committee on Receptor Nomenclature and Drug Classification (NC-IUPHAR), recently proposed a unified nomenclature [13]. The new names carry ADGR as a common dominator, followed by a letter and a number to denote each subfamily and subtype, respectively.

2 Receptor Biology Convenes a New Research Field

In line with the discovery of aGPCRs through genomic approaches, an interest in these molecules developed concurrently in different biomedical areas. In particular, immunologists, neuroscientists, and developmental biologists were among the first who studied these intriguing receptors. Far before any molecular structures were disclosed, Jon Austyn and Siamon Gordon had described in 1981 a monoclonal antibody directed against an antigen on mouse macrophages, called F4/80 [14]. This antigen, currently known as EMR1 (ADGRE1), has become widely

used as a macrophage marker, expressed during development and throughout adult life in a range of inflammatory, infectious, tumor, and other disease models. Other ADGREs (EMRs) are expressed in specific granulocyte populations [15]. More recently, also ADGRBs (BAIs) and ADGRGs have been identified in immune cells, and BAI1 (ADGRB1) attracted interest as a macrophage receptor for danger-associated molecular patterns [16, 17].

A link between aGPCRs and neuronal function was first established by the finding that α -latrotoxin evokes massive neurotransmitter release and hormone secretion upon binding to C1RL-1/latrophilin 1 (ADGRL1) [5, 18]. More recently, involvement of several ADGRLs (latrophilins) in high-affinity transsynaptic interactions has been reported, suggesting involvement in synaptic functions [19–21]. Another highly intriguing observation was the discovery that defects in the ADGRG subfamily member GPR56 (ADGRG1) cause a cortical malformation, known as bilateral frontoparietal polymicrogyria (BFPP) [22]. GPR56-associated BFPP, also studied in mouse models, has become a prime example for a monogenic disorder arising from aGPCR dysfunction. More recently, additional roles for GPR56 in gyral patterning and in neocortex evolution as well as in oligodendrocyte development have been described [23–25]. Furthermore, elegant studies in zebrafish and mice have linked GPR126 (ADGRG6) and GPR56 on Schwann cells and oligodendrocytes to myelination of peripheral and central nervous axons, respectively [24, 26, 27].

Investigation of invertebrate aGPCRs has helped to understand fundamental developmental processes in health and disease. The *Drosophila* CELSR (ADGRC) homolog Flamingo/Starry night governs planar cell polarity (PCP) through facilitating the asymmetric distribution of Frizzled and Disheveled [28–30], and chicken CELSR1 (ADGRC1) facilitates core-PCP signaling-mediated closure of the neural tube [31]. In a similar way, the latrophilin homolog LAT-1 organizes cell division planes across the anterior–posterior axis of the *C. elegans* embryo, acting in parallel with noncanonical Wnt/Frizzled signaling [32]. Moreover, CELSR homologs in *C. elegans* and mice regulate axon guidance and neural circuit development [33, 34]. Finally, CELSR1 and VLGR1 (ADGRV1) are required for the development of sensory epithelia; mutations in the latter are associated with the human Usher syndrome, a severe sensory-neuronal disorder that affects vision and hearing [35].

Next to developmental effects in several organ systems, including the reproductive tract, the role of aGPCRs in tumorigenesis evoked interest in the clinical implication of the receptors. Gabriela Aust was the first who showed that expression of CD97 (ADGRE5) correlates with dedifferentiation and invasiveness in various carcinomas [36, 37]. Inversely, GPR56 controls melanoma growth and metastasis [38].

The examples of aGPCR research provided here are far from complete. However, they illustrate a research field that developed in parallel and fairly separated within different biomedical areas, resulting in a steadily growing number of publications (Fig. 1). It was Siamon Gordon who organized in 2002 a 1-day workshop for immunologists and tumor biologists working on EGF-TM7 receptors

Table 1 Biennial adhesion GPCR workshops

Date	Place	Organizers	Talks	Scientific highlights
April 4, 2002	Oxford	Siamon Gordon	16	Identification of cellular ligands
March 19, 2004	Leipzig	Gabriela Aust	19	Autoproteolytic cleavage at the GPS
March 24, 2006	Amsterdam	Jörg Hamann	22	Interaction between receptor fragments
March 29, 2008	Oxford	Martin Stacey	15	Adhesion GPCRs in development
May 1, 2010	Leipzig	Gabriela Aust	19	In vivo models for Adhesion GPCRs
September 6–8, 2012	Würzburg	Tobias Langenhan	23	Crystal structure of the GAIN domain; Autonomous signaling by the CTF; Tethered vs inverse agonist models
June 5–7, 2014	Boston	Xianhua Piao	33	Stachel mechanism of receptor activation; Receptor triggering by mechanosensation
June 2–4, 2016	Leipzig	Torsten Schöneberg; Tobias Langenhan	38	TBD

CTF C-terminal fragment, *GAIN* GPCR autoproteolysis-inducing, *GPCR* G-protein-coupled receptor, *GPS* GPCR proteolysis site, *TBD* to be determined

in Oxford (Table 1). During the following events in Leipzig (2004), Amsterdam (2006), Oxford (2008), and Leipzig (2010), aGPCRs expressed outside the immune system, such as C1RL-1/lathrophilin 1, GPR64 (ADGRG2), and VLGR1, slowly entered the stage. The more recent events in Würzburg (2012) and Boston (2014) dealt with all aspects of aGPCR biology and saw a strongly expanding audience [39, 40]. Yet, despite the transformation into 3-day events, the aGPCR Workshops are still informal gatherings, at which novel, unpublished work is presented, and open questions are discussed in an intimate setting. By catalyzing cross talk and collaboration between aGPCR researchers with a different scientific background, the aGPCR Workshops had a tremendous impact on the field. Currently, the community is looking forward to the next event in Leipzig in 2016.

A decisive step in the development of the field was the founding of the aGPCR Consortium (AGC; www.adhesiongpcr.org) in 2012. As an international, open network of academic and nonacademic laboratories interested in aGPCRs, the AGC currently connects more than 60 scientists from 15 countries. The AGC has become a meeting place for everyone interested in aGPCRs and organizes, currently, the biennial workshops. Moreover, the AGC provides information and visibility for the aGPCR community, works on terminology and nomenclature issues, and serves as a starting ground for collaborative research initiatives. The latter has led to the establishment of the Research Unit 2149—*Elucidation of*

Adhesion GPCR signaling—in 2015, which is supported by the Deutsche Forschungsgemeinschaft (www.adhesiongpcr.de).

3 From Molecular Structure to Pharmacology

While work on aGPCRs transcended different biomedical areas, the central question on the mechanism by which these receptors signal remained hard to answer for a long time. The existence of numerous protein domains implied that aGPCRs might engage in cell–cell interactions. A similar function of receptor tyrosine kinases has been very well described, with its importance in cancer biology and development. In 1996, Jörg Hamann demonstrated that CD97 binds decay-accelerating factor/CD55, a molecule associated with regulation of the complement cascade [41]. Since then, interacting partners, often matricellular molecules, have been identified for about ten aGPCRs. However, no comprehensive picture arose that would fit the concept of agonistic ligands as these have identified for other GPCR families [42].

Recently, the juxtamembrane part of the aGPCRs containing the GPS motif has been implicated in the receptor signaling. Demet Araç showed that the GPS is an integral part of a much larger domain that was termed GPCR autoproteolysis-inducing (GAIN) domain [6]. Crystal structures of GAIN domains from C1RL-1/latrophilin 1 and BAI3 (ADGRB3) revealed a conserved, novel fold that fine-tunes the chemical environment at the GPS to catalyze peptide bond hydrolysis (Fig. 2). Another key finding by the groups of Randy Hall and Lei Xu was the observation that the C-terminal fragment (CTF) of some aGPCRs shows intense metabotropic and biological activity, implying that the N-terminal fragment (NTF) controls receptor signaling [43, 44], and that the ectodomain of aGPCRs may act as a tethered ligand for their 7TM domain [45].

Building forth on these studies, the laboratories of Ines Liebscher, Torsten Schöneberg, and Gregory Tall have proposed a tethered agonist mechanism according to which displacement of the NTF exposes a short N-terminal sequence of the 7TM domain, designated *Stachel* (German for stinger), that is hidden within the GAIN domain [46, 47]. Synthetic peptides, comprising these *Stachel* sequences, have been shown to potently trigger various aGPCRs, in vitro and also in vivo. Finally, work from the groups of Bruce Spiegelman, Kelly Monk, and Tobias Langenhan uncovered that mechanical cues trigger the activity of aGPCRs under physiological conditions, adding mechanosensation to the sensory canon of the GPCR superfamily [27, 48, 49].

The ability to activate aGPCRs enabled studies aiming at identifying downstream signaling modes. The demonstration that the receptors can couple to all subclasses of G proteins [46, 50] led to the recognition as bona fide GPCRs [55]. Consequently, established GPCR conferences currently discuss developments in aGPCR research. Yet, uncertainties remain (Table 2). Information concerning the ability of aGPCR binding partners to trigger G proteins is very scarce so far [27, 51], and we do not know whether the functioning of the receptors is confined to

Table 2 Certainties and uncertainties about GPCRs

What do we know	What we are not sure of
<ul style="list-style-type: none"> • GPCRs are bipartite molecules with a large extracellular region that is connected through a GAIN domain to a 7TM moiety 	<ul style="list-style-type: none"> • A functional link between adhesive capacity and receptor signaling remains to be established
<ul style="list-style-type: none"> • The majority of aGPCRs undergo autocatalytic processing at a GPS embedded within the GAIN domain 	<ul style="list-style-type: none"> • Lack of cleavage of some aGPCRs suggests that a bipartite structure is not a prerequisite for receptor function
<ul style="list-style-type: none"> • aGPCRs can be activated through a tethered agonist (<i>Stachel</i> sequence) 	<ul style="list-style-type: none"> • Mechanisms allowing exposure of the <i>Stachel</i> need to be determined, in particular for solid tissues and non-cleavable receptors
<ul style="list-style-type: none"> • aGPCRs are widely distributed and cause distinct biological phenotypes 	<ul style="list-style-type: none"> • It is not clear whether aGPCRs display cell type-specific or general cellular functions

7TM seven-transmembrane, *aGPCR* adhesion GPCR, *GAIN* GPCR autoproteolysis-inducing, *GPCR* G-protein-coupled receptor, *GPS* GPCR proteolysis site

G-protein signaling. Early studies on PCP in *Drosophila* showed that the CELSR homolog Flamingo arranges in *trans* and in *cis* with other transmembrane molecules to execute its functions [28–30], possibly presenting another major working mechanism. In addition, CD97 has been shown to heterodimerize with the lysophosphatidic acid (LPA) receptor to amplify LPA-initiated Rho-dependent signaling and invasion in prostate cancer cells [52].

Another interesting possibility exists that the large NTF of aGPCRs may serve autonomously by interacting as a ligand with other receptors. In the original discovery of BAI1, its ectodomain soluble fragment had a role in the inhibition of brain-specific angiogenesis [53]. Also, the presence of a specifically cleaved soluble fragment of C1RL-1/lathophilin 1 was detected in the brain, comprising about 5 % of the total amount of the receptor expressed [54]. Finally, a genetic study uncovered a specific role of the N-terminal fragment of GPR126 in axon sorting [27].

Based on the anecdotal identification of most of its members, the aGPCR cohort is one of the prime examples of genome-sequencing effort-driven identification and definition of an entire molecule class. As a consequence, research on aGPCRs grows out of a “molecule-centered” rather than “biology-centered” history since almost two decades. This situation has recently changed with the advent of molecular models on the signaling paradigm of aGPCRs and their physiological mode of activation. The field has now entered a highly intriguing stage, and we predict that the pharmacological insight and tools that are currently developed will boost novel attempts to understand the biological functions of aGPCRs in health and disease.

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Part I

**Molecular and Pharmacological Properties of
Adhesion GPCRs**

Classification, Nomenclature, and Structural Aspects of Adhesion GPCRs

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and Helgi B. Schiöth

Contents

1	Introduction	17
2	Classification of aGPCRs	18
2.1	Human aGPCR Subfamilies	18
2.2	aGPCRs in Mammals and Other Vertebrates	19
2.3	aGPCRs in Invertebrates	20
3	Recommended Nomenclature of aGPCRs	21
4	Structural Aspects of aGPCRs	22
4.1	General Structural Features of aGPCRs	24
4.2	aGPCR Subfamily-Specific Structural Features and Protein Interactions of NTF ...	26
5	Summary	32
	References	33

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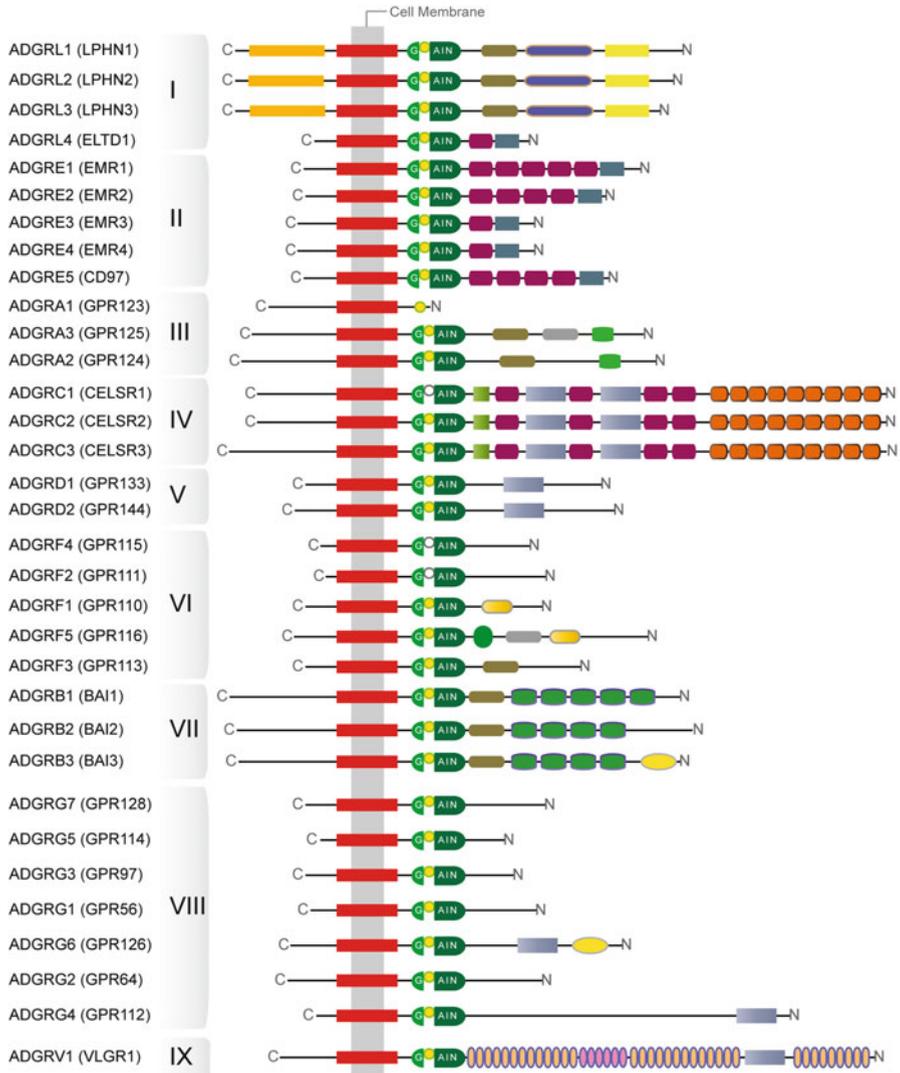
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Graphical Abstract



Representation of the nine distinct aGPCR subfamilies and their unique N-terminal domain architecture. The illustration also shows the extracellular structural feature shared by all aGPCRs (except ADGRA1), known as the GPCR autoproteolysis-inducing (GAIN) domain, that mediates autoproteolysis and subsequent attachment of the cleaved NTF and CTF fragments

Abstract

The adhesion family of G protein-coupled receptors (aGPCRs) is unique among all GPCR families with long N-termini and multiple domains that are implicated in cell–cell and cell–matrix interactions. Initially, aGPCRs in the human genome were phylogenetically classified into nine distinct subfamilies based on their 7TM sequence similarity. This phylogenetic grouping of genes into subfamilies was found to be in congruence in closely related mammals and other vertebrates as well. Over the years, aGPCR repertoires have been mapped in many species including model organisms, and, currently, there is a growing interest in exploring the pharmacological aspects of aGPCRs. Nonetheless, the aGPCR nomenclature has been highly diverse because experts in the field have used different names for different family members based on their characteristics (e.g., epidermal growth factor-seven-span transmembrane (EGF-TM7)), but without harmonization with regard to nomenclature efforts. In order to facilitate naming of orthologs and other genetic variants in different species in the future, the Adhesion-GPCR Consortium, together with the International Union of Basic and Clinical Pharmacology Committee on Receptor Nomenclature and Drug Classification, proposed a unified nomenclature for aGPCRs. Here, we review the classification and the most recent/current nomenclature of aGPCRs and as well discuss the structural topology of the extracellular domain (ECD)/N-terminal fragment (NTF) that is comparable with this 7TM subfamily classification. Of note, we systematically describe the structural domains in the ECD of aGPCR subfamilies and highlight their role in aGPCR-protein interactions.

Keywords

Adhesion GPCRs • Nomenclature • Classification • Pharmacology • Drug targets • Homologs • Mammals • Vertebrates • Model organisms • GAIN domain

1 Introduction

The G protein-coupled receptor (GPCR) superfamily is the largest family of cell surface receptors and is grouped into five major families: glutamate, rhodopsin, adhesion, frizzled, and secretin [1, 2]. Among all classes, the adhesion GPCRs (aGPCRs) comprise the second largest family with 33 members in the human genome [1, 2]. Prior to the release of the human genome, aGPCRs were not considered as a separate family of GPCRs. Indeed, at that time, only a few genes were identified that constituted a long extracellular region and a seven transmembrane segment (7TM) characteristic to GPCRs. One of the first aGPCRs cloned was the epidermal growth factor (EGF)-like molecule containing mucin-like hormone receptor 1 and later similar molecules were identified [3–6]. This paved the way for the recognition of these molecules as EGF-TM7-like receptors because of the presence of EGF-like domains in their extracellular region [6]. Similarly, other names that were initially termed for aGPCRs include LN-7TM [7] (for the presence of long N-terminal regions), LNB-7TM [8] (for their similarity to family B secretin-

like GPCRs), or family B2 receptors [9]. Shortly after the release of the human genome, several novel genes were identified, and subsequent gene mining showed that at least 30 GPCR-like sequences exist with a long extracellular region and GPCR proteolysis site (GPS) motif that induce autocatalytic processing [10]. Some of these receptors were often initially denoted or thought as secretin-like GPCRs and were placed in proximity to family B receptors [9]. Nonetheless, the large-scale effort to comprehensively classify the GPCRs in the human genome showed convincing phylogenetic evidence that aGPCRs constitute a separate family of GPCRs [1]. This made clearer that adhesion and secretin families are indeed distinct from each other, although these molecules share vague similarities and are often placed together as family B GPCRs [9]. This view is strengthened as the largest of differences were observed in their extracellular region and in particular aGPCRs are also distinct from secretin GPCRs in molecular function. For example, most aGPCRs contain the GPS motif, which is found in close proximity to the 7TM region (for review see [11]). Moreover, it is currently understood that the GPS motif is a part of a much larger GPCR autoproteolysis-inducing (GAIN) domain, which induces the autocatalytic processing of aGPCRs into an N-terminal fragment (NTF) and a C-terminal fragment (CTF) [12]. In addition, the NTF of aGPCRs contains numerous protein domains implicated in cell and matrix interactions [11, 13], and, thus, the established name of “adhesion” family GPCRs was initially coined to refer this feature. Conversely, the secretin GPCRs do not undergo such autocatalytic processing in their N-termini, however, contains a hormone-binding domain (HBD) to mediate hormonal responses [13, 14]. In this chapter, we review the classification of aGPCRs into nine families in the human genome and briefly discuss the classification and potential homologs of these families in other vertebrate and invertebrate genomes. Of note, we address the recently recommended nomenclature of aGPCRs [15] that aim to provide a coherent and systematic naming system independent of the species and subfamily names. Also, we discuss the similarities between aGPCR subclasses with respect to the organization of their structural topology (e.g., olfactomedin, cadherin, EGF-like and thrombospondin type 1 domain). The analysis nevertheless indicates remarkable differences that demonstrate the structural diversity of aGPCRs, but could also hint at potential interaction partners for orphan aGPCRs or provide information on NTF–CTF interactions. We therefore systematically describe the unique (sub) family-specific structural features and their protein interactions.

2 Classification of aGPCRs

2.1 Human aGPCR Subfamilies

Based on phylogenetic criteria, the human aGPCR repertoire is categorized into nine distinct subfamilies (considering ADGRV1 (VLGR1) as subfamily IX) according to the molecular signature of their 7TM region [1]. The number of genes belonging to the subfamilies I to VIII vary from two genes in “subfamily