Receptor-wide Determinants of G Protein Coupling Selectivity in Aminergic GPCRs

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Abstract

G protein-coupled receptors (GPCRs) induce signal transduction pathways through coupling to four main subtypes of G proteins (G_s, G_i, G_q, $G_{12/13}$), selectively. However, G protein selective activation mechanisms and residual determinants in GPCRs have remained obscure. Here, we identified conserved G protein selective activation mechanisms determining receptors' ability to couple to a type of G protein. Herein, we performed an extensive phylogenetic analysis and identified specifically conserved residues for the receptors having similar coupling profiles in each aminergic receptor. By integrating our methodology of differential evolutionary conservation of G protein-specific amino acids with structural analyses, we identified selective activation networks for G_s, G_{i1}, G_o, and G_q. We found that G protein selectivity is determined by not only the G protein interaction site but also other parts of the receptor including the ligand binding pocket. To validate our findings, we further studied an amino acid residue that we revealed as a selectivity-determining in G_s coupling and performed molecular dynamics (MD) simulations. We showed that previously uncharacterized Glycine at position 7x41 plays an important role in both receptor activation and G_s coupling. Finally, we gathered our results into a comprehensive model of G protein selectivity called "sequential switches of activation" describing three main molecular switches controlling GPCR activation: ligand binding, G protein selective activation mechanisms and G protein contact. We believe that our work provides a broader view on receptor-level determinants of G protein coupling selectivity.

Introduction

G protein-coupled receptors (GPCRs) constitute a significant group of membrane-bound receptors that contain five different classes (Fredriksson, Lagerström, Lundin, & Schiöth, 2003; Rosenbaum, Rasmussen, & Kobilka, 2009). The aminergic subfamily of receptors are present in class A and include receptors for dopamine, serotonin, epinephrine, histamine, trace amine, and acetylcholine (Vass et al., 2019). With a large amount of known coupling profiles, experimental structures, and mutagenesis experiments available, aminergic receptors are by far the most studied subfamily of GPCRs. These receptors can couple with different heterotrimeric G proteins which induce distinct downstream signaling pathways (Wettschureck & Offermanns, 2005). Disruption of the proper receptor activation is likely to be the cause of diseases such as coronary heart disease (Jialu Wang, Gareri, & Rockman, 2018) or major depression (Catapano & Manji, 2007; Senese, Rasenick, & Traynor, 2018) . Therefore,

understanding the molecular mechanisms of coupling selectivity is crucial for developing better therapeutics and diagnostics.

With the advancement of new methodologies, two recent studies have revealed the G protein-coupling profiles of a large set of receptors. Inoue et al. (Inoue et al., 2019) have used a shedding assay-based method to measure chimeric G protein activity for 11 different G protein subtypes and 148 human GPCRs. Because they have not managed to find an evident conserved motif determining G protein selectivity between receptors, they have built a machine learning-based prediction tool to identify sequence-based important features for each G protein. Similarly, Avet et al. (Avet et al., 2020) have used a BRET-based method detecting the recruitment of the G protein subunits to the receptor to reveal coupling profiles for 100 different receptors. The main strength of this study is that it does not require a modified G protein. Although both high-throughput studies largely agree with each other for certain G proteins, there are inconsistencies between the datasets. Thus, these valuable resources should be analyzed together in detail to gain more power in identifying the selectivity-determining factors in G protein coupling.

Several attempts have been made to identify molecular determinants of G protein coupling. Most of these (Chung et al., 2011; Du et al., 2019; Liu et al., 2019; Okashah et al., 2019; Semack, Sandhu, Malik, Vaidehi, & Sivaramakrishnan, 2016) have focused on the G protein-coupling interface by analyzing contacts between receptor and the G protein. The others (Kang et al., 2018; Rose et al., 2014; Van Eps et al., 2018; Jinan Wang & Miao, 2019) have highlighted the structural differences between receptors that couple to different G proteins. Flock et al. (Flock et al., 2017) have analyzed the evolutionary conserved positions of orthologous and paralogous G proteins and proposed the “lock and key” model. According to their model, G proteins (locks) have evolved with subtype-specific conserved barcodes that have been recognized by different subfamilies of receptors (keys). Because receptors with distinct evolutionary backgrounds can couple to the same G protein, receptors also must have evolved to recognize the existing barcodes. Although the model has explained the selectivity determining interactions between G protein and receptors, we still lack subfamily specific receptor signaling mechanisms that involves but not limited to the G protein coupling interface.

Despite the extensive research carried out to identify the determinants of G protein selectivity, selectivity determining positions within receptors have remained underexplored. Here, we developed a novel methodology to identify a set of specifically conserved residues for the aminergic subfamily of receptors that determines the G protein selectivity through evolutionary identification of orthologous receptors. Moreover, structural analyses of these positions revealed G protein specific activation pathways that allow receptors to transduce signal from ligand binding pocket to the G protein-coupling interface, induce the necessary conformational changes to get coupled by the relevant G protein subtype.

Results

After a gene duplication event, paralogous clades might diverge from each other with respect to their functions. Therefore, evolutionary pressure against paralogous genes might differ. To perform a precise conservation analysis, we aimed to identify the gene duplication nodes in aminergic receptor evolution. We identified receptor subfamilies (orthologous and paralogous sequences) through a meticulous phylogenetic analysis. As we previously proposed (Adebali, Reznik, Ory, & Zhulin, 2016), the variations that observed in a paralog protein of interest may not be tolerated in the orthologous proteins. In our analyses, we only used detected orthologous receptors to define a subfamily of interest, members of which are likely to retain the same function. This approach greatly improved the sensitivity of conserved residue assignment for each human GPCR.

To identify distinctly conserved residues between two receptor clades, we revealed differentially conserved amino acids **(Figure 1a)**. For the residues that play a role in common receptor functions we expect both clades to retain the amino acid residues with similar physicochemical properties. On the other hand, the positions that serve receptor-specific functions, in our case the coupling selectivity, we expect to see differential conservation (Figure 1a). Therefore, we grouped the receptors based on their known coupling profiles for nine different G proteins **(Figure 1b)**. We termed these groups as couplers (e.g., G_s coupler receptors) and non-couplers, and performed a two-step enrichment method (Figure 1b) to distinguish specifically conserved residues in couplers from non-couplers. Initially, we used a specific approach to identify evident differentially conserved amino acid residues with high confidence. According to the specific approach, residues were labeled as specifically conserved when there was a variation between coupler and non-coupler receptors but not within coupler receptors (Figure 1b. red

and blue arrows). This approach depends solely on the coupling profile datasets (Avet et al., 2020; Inoue et al., 2019) and thus, they may contain false-positive couplings. To tolerate the insensitivity introduced by potential false positive couplings, we developed and employed a sensitive approach enabling to obtain a more complete set of residues for each G protein subtype by allowing minor variations within the coupler receptors. With this method, we used a single comprehensive multiple sequence alignment that combined all coupler receptors and their orthologs (Figure 1b. orange arrows), allowed minor variations within a group. Finally, we compared each aminergic receptor and identified positions that were conserved across all aminergic receptors to link the specifically conserved residues with the general mechanism of receptor activation. In total, we identified 51 specifically conserved and 22 consensus residues. The distribution of the specific residues is presented in **Figure 1c**. Hierarchical clustering based on the residues associated with a specific G protein coupling resulted in distinct groupings of G_{α} subtypes belonging to $G_{\alpha q}$, $G_{\alpha i}$ and $G_{\alpha 12/13}$.

We aimed to validate the functional importance of potentially deleterious variants that we discovered. Thus, we used a dataset (Jones et al., 2020) containing G_s activity scores at EC100 for each possible mutation of ADRB2. 31 residues were identified for G_s and the activity scores of non-coupler variants were plotted **(Figure 1d)**. Non-coupler variants that we identified predominantly decrease G_s activity when compared to wild-type reference. Because the substituted amino acids are indeed found in non-coupler receptors, we argue that these positions do not necessarily halt the general activation mechanism or protein folding but disrupt the specific G protein (G_s in this example) activity. Additional to the G_s coupling dataset, Kim et al. (Kim et al., 2020) mutated two of the residues we identified for G_q coupling (8x47 and 6x37) to alanine and showed a decrease in G_q activity compared to wild-type 5HT2A receptor which validates our findings further.

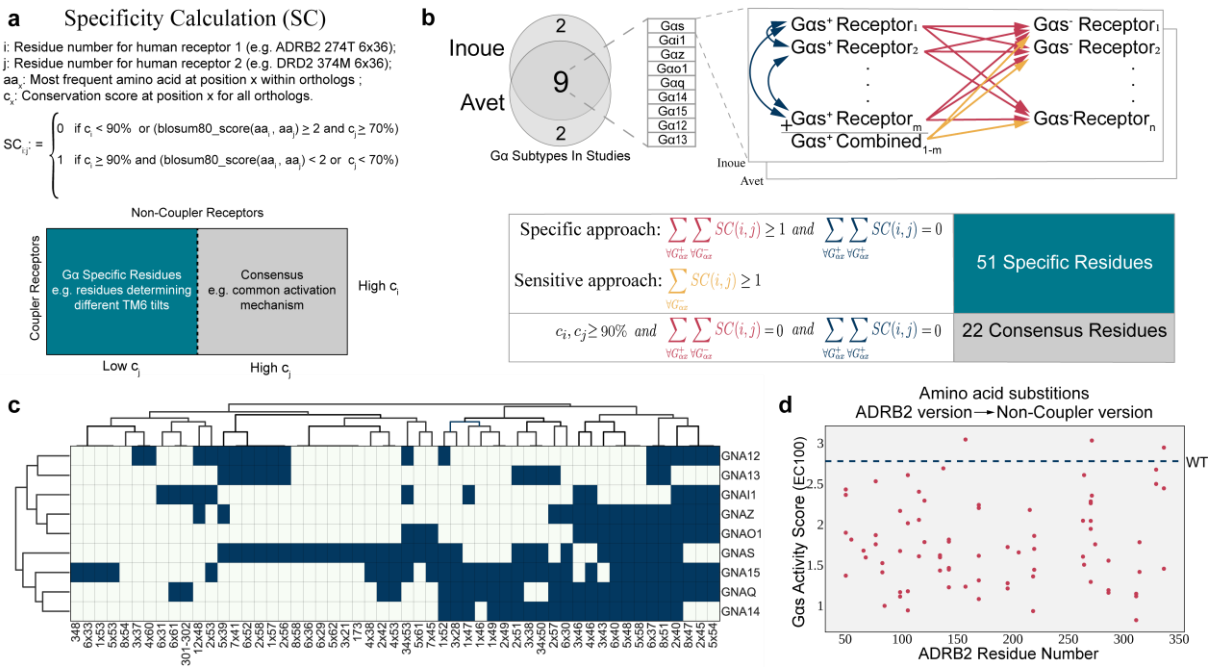

Figure 1: Selectivity determining residues for each Gα subtype. **(a)** The formula for specific residue identification. **(b)** The schema describes the comparisons between paralogous human receptors to find the specifically conserved residues for each Gα. Arrows represent a single comparison. **(c)** The distribution of specifically conserved residues for each Gα subtype. **(d)** Possible variants of G_s specific residues that are observed in non-coupler receptors are compared with the wild-type activity score.

After identifying residues belonging to each G_α subtype, we investigated how these residues determine the selectivity. Hence, we assigned each residue into functional clusters such as coupling interface and ligand binding. For example, our method identified positions that are at the G protein coupling interface such as 8x47 (Kim et al., 2020; Maeda, Qu, Robertson, Skiniotis, & Kobilka, 2019; Zhuang, Xu, et al., 2021) and 6x36 (Rasmussen et al., 2011; Xiao et al., 2021; Yang et al., 2020) without any requirement of structural information. The residues that are in the coupling interface validate the model that Flock et al. proposed. For the residues that we could not directly assign a role in G protein coupling activity, we explored the contact changes upon activation. We used an algorithm that is called Residue-Residue Contact Score (RRCS) which has been proposed to discover the common activation mechanism in class A GPCRs (Zhou et al., 2019). We calculated ΔRRCS for each interacting residue pairs by subtracting contact scores of the active structure from the inactive structure. All the active structures we used contained a heteromeric G protein machinery coupled to receptor. We filtered out residue pairs with |ΔRRCS| <= 0.2 and only kept residues that are in our pool of conserved residues (73 residues in total).

We analyzed structures of eight different receptors with four different G proteins **(Figure 2a)**. The structures we used were experimentally characterized except for one state of a single receptor. As we aimed to use the 10 active-state $G_{\alpha s}$ coupled structures of DRD1, which lacks an experimental inactive structure, we used a model inactive DRD1 structure (Pándy-Szekeres et al., 2018) retrieved from GPCRdb (Kooistra et al., 2021).

In total, we analyzed 41 pairs of active and inactive structures and identified ΔRRCS values of activation networks. We analyzed each network and detected edges observed at least 36 times regardless the sign of ΔRRCS value to build a network that would represent all 41 networks. By using this network, we identified the most frequently used signal transduction paths **(Figure 2b)**, connecting ligand binding pocket to G protein-coupling interface and create a basis for selective coupling. We divided the receptor into five layers based on sequential nature of interactions and illustrated the direction of signal transduction between layers. Additional to the 4 layers (1-4) that were previously proposed in the common activation mechanism (Zhou et al., 2019) we defined “Layer 0” which is related to ligand binding. Though the most of the signaling paths pass through important motifs such as Na^+ binding pocket and PIF (Katritch et al., 2014), it is remarkable that the novel path starting with a 3x37 does not require the involvement of any of these important motifs (highlighted in Fig 2b). For selective coupling, the signal is transmitted from ligand binding pocket to the G protein interface by using mainly TM2, TM3, and TM4.

To determine the contribution of each layer for G_s, G_{i1}, G_o and G_q, we calculated the distribution of specific residues to different layers (Figure 2c). Layer 0 and Layer 1 is more involved in the coupling for G_s and G_q relative to G_{i1} and G_o. For G_o, 86% of the coupling-related residues are positioned in the layers (2, 3 and 4) closer to the G protein binding site. Differences in these distributions indicate mechanistic differences between distinct coupling events.

a

Receptor Name	G- Protein Subtype	# of Active Structures	# of Inactive Structures
ADRB2	Gs	2	4
DRD1	Gs	10	1*
DRD2	Gi1	2	3
DRD3	Gi1	2	1
5HT1B	Go	1	4
ACM2	Go	1	6
5HT2A	Gq	1	4
HRH1	Gq	1	1

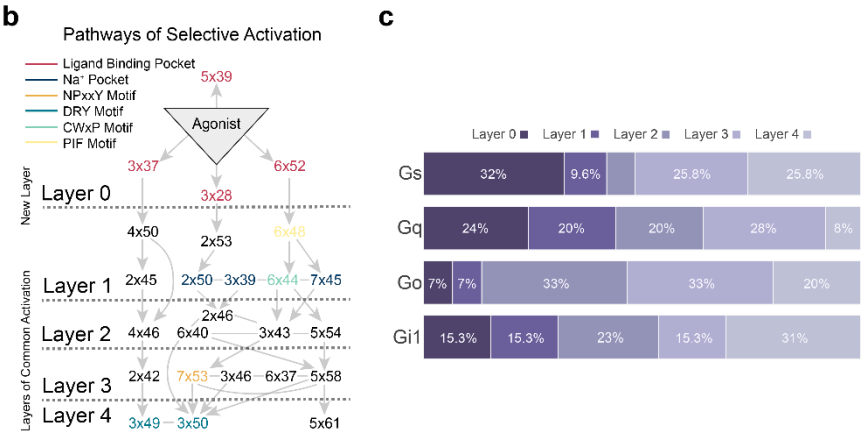

Figure 2: Structural analysis of molecular pathways that are observed upon coupling with heteromeric G-protein complex. **(a)** Table for the structures that were used to perform the structural analysis. * : GPCRdb model of DRD1 was used. **(b)** The most common molecular signal transduction pathways from ligand binding pocket to G-protein coupling interface. The network is summarized and divided into different layers based on their functional relevance. **(c)** The distribution of specifically conserved residues for each analyzed Gα subtype.

To distinguish G protein specific activation pathways, we grouped ΔRRCS for each G protein and receptor for each residue pair. Then two sample t-test was applied to identify interaction changes (ΔΔRRCS) within the receptors that are significantly different ($p<0.01$) and specific for G_s, G_{i1}, G_o, and G_q. We evaluated these contact changes in receptors based on two main principles; they can either be the cause of the selectivity by enabling G protein specific conformational changes or arise due to the physical interaction between G protein and receptor. Moreover, because interactions at the upper layers sequentially trigger the interactions at lower layers, they are more likely to lead the G protein specific activation mechanisms. By taking these factors that may influence contact changes within receptors into consideration, we aimed to reveal G protein specific molecular mechanisms underlying the coupling selectivity. Previously, it was shown that receptors coupled to G_s achieve a larger TM6 tilt (Rose et al., 2014; Van Eps et al., 2018). Superimposition of the active structures **(Figure 3a)** also validates the previous findings. An exception to this is the TM6 position of 5HT1B (García-Nafría, Nehmé, Edwards, & Tate, 2018) that is coupled to G_o (Figure 3a, blue structure), because it achieved a slightly larger tilt. Thus, we performed an additional t-test by excluding the samples for 5HT1B and revealed the 6x52-6x48 interaction which is on TM6 ($p=0.0023$).

In **Figure 3b**, we demonstrated the specific activation network for G_s. We projected a small portion of this network which we associated with the differential TM6 movement onto experimental active (red, 3SN6) and inactive (blue, 2RH1) ADRB2 structures. More specifically, we hypothesize that the network containing 6x52 and 7x41 triggers this structural difference. In agreement with our hypothesis, deep mutational scanning of ADRB2 (Jones et al., 2020), has revealed that 7x41 is the second and 6x48 is the fourth most intolerant residue and, to our knowledge, no previous study has identified the functional role of 7x41 until now. Furthermore, it is reasonable to expect that a mutation that disrupts the G_s signal to be one of the most intolerant residues. **Figure 3 d-f** shows the networks we identified for the other three G proteins. Further experimental research is required to validate the significance of these networks.

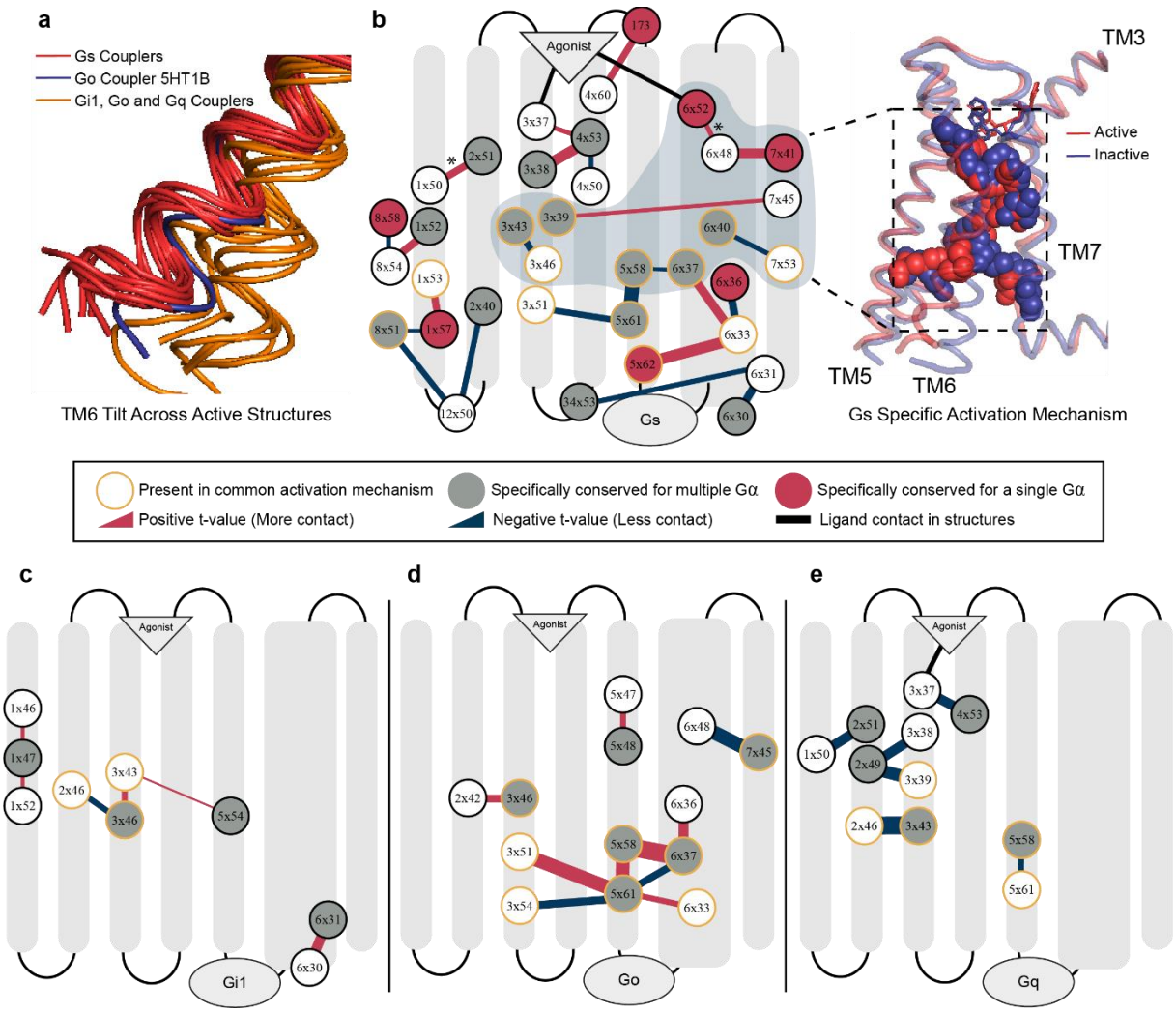

Figure 3: Specific Activation Networks for G_s, G_{i1}, G_o and G_q. **(a)** TM6 tilt comparison between the active receptors we used. Red: G_s couplers, Orange: G_o, G_{i1} and G_q, Blue:5HT1B G_o coupler as an exception. **(b)**

Interactions within the receptor that are specific ($p<0.01$) to G_s. Red: increasing contact, blue: decreasing contact, orange circle: present in common activation mechanism, red fill: uniquely identified specific residue for G_s, grey fill: G_α specific residue. Width of the lines correlate with statistical significance. Group of residues that possibly facilitate in TM6 movement for G_s coupling were shown on inactive (blue) and active (red) structures. (**c-e)** Specific interaction networks for G_{i1}, G_o and G_q. $p<0.1$ is used for G_{i1}. *: This interaction is identified only if 5HT1B is neglected from the comparison due to its larger TM6 movement.

To validate our methodology and further understand the mechanistic insight of the relevance of core transmembrane region in G protein coupling, we studied the glycine at position 7x41 as a test case and performed molecular dynamics (MD) simulations to understand its molecular contribution to receptor activation and G_s coupling mechanism. We applied three different mutations, G315C, G315Q, and G315L, on monomeric active and inactive-state ADRB2 (Figure 4a). We particularly selected these variants because they exist in other aminergic receptors at the same position. We used two main metrics to assess the molecular impact of these three mutations. First, the comparison active/inactive states based on GPCRdb distances (see methods) revealed that wild-type receptor keeps its active state more than the variants (Figure 4b) and leucine residue was the most inactivating mutation. The significant inactivation through integration of leucine mutation is parallel to pre-existing experiments (Arakawa et al., 2011; Jones et al., 2020). Then, to identify the molecular changes in absence of glycine, we looked at the significant contact differences (ΔRRCS) between WT and mutated MD simulation trajectories.

To represent a whole trajectory, we selected 11 frames from each simulation with 50 ns time gap (in total 500 ns). Thus, we compared residue-residue contact scores of 77 mutated and 77 WT frames for active-state simulations, while we compared 22 mutated and 22 WT frames for inactive-state simulations by using two-sided t-test. For each mutation and activation state, we identified significant contact changes ($p<0.01$) and intersected common changes that we observed for all of mutated systems. As a result, we identified 135 residue pairs for active and 83 residue pairs for inactive simulations. When we projected these residue pairs (135 residue pairs) as a contact network, we identified a conserved and highly affected pathway (Figure 4c) connecting ligand binding pocket to NPxxY motif which showed changes towards inactivation of the receptor. Then, we projected the identified molecular pathway onto average cluster structures that were produced by using the trajectories from all 7 replicates (35000 frames in total) for each mutation (Figure 4d-e). This led us to propose a pathway (Figure 4c) which

explains the importance of G315: An increase bulkiness of the amino acid at 7x41 (by non-glycine amino acids) leads to increased contact with 7x42 and 6x51 while 7x41 physically impairs the interaction between 6x48 and 7x42. When 6x48 loses its contact with 7x42 (Figure 4d), it increases its contact residues at TM3 3x43 and 3x39 (Figure 4e). Increased interactions between TM6 and TM3 loosens TM3-TM7 packing which is an important initiator of the TM6 tilt in class-A GPCRs (Zhou et al., 2019). Additionally, it loosens the contacts between TM6 and TM7 through 6x48-7x42, 6x44-7x49, and 6x52-7x45, which explains the increased distance between 7x53 and 3x43 (Figure 4e). Moreover, the simulations of cysteine and leucine variants exhibited an increased contact between 3x43 and 6x40 ($p<0.01$) inhibiting the receptor activation through restricting outward TM6 movement. When we evaluated the inactive trajectories, we observed similar contact changes between 6x48, 6x51, 7x41 and 7x42 ($p<0.01$) proving that the simulation results are not biased to active-state simulations. Because residues 6x48, 6x51, 7x41, and 7x53 play an important role in G_s selective activation mechanism, it is not surprising that they were identified within top-6 mutational intolerant residues for G_s coupling (Jones et al., 2020). The identified changes suggest that glycine at 7x41 plays an important role in receptor activation and larger tilt of TM6 which we observe in G_s coupled receptors.

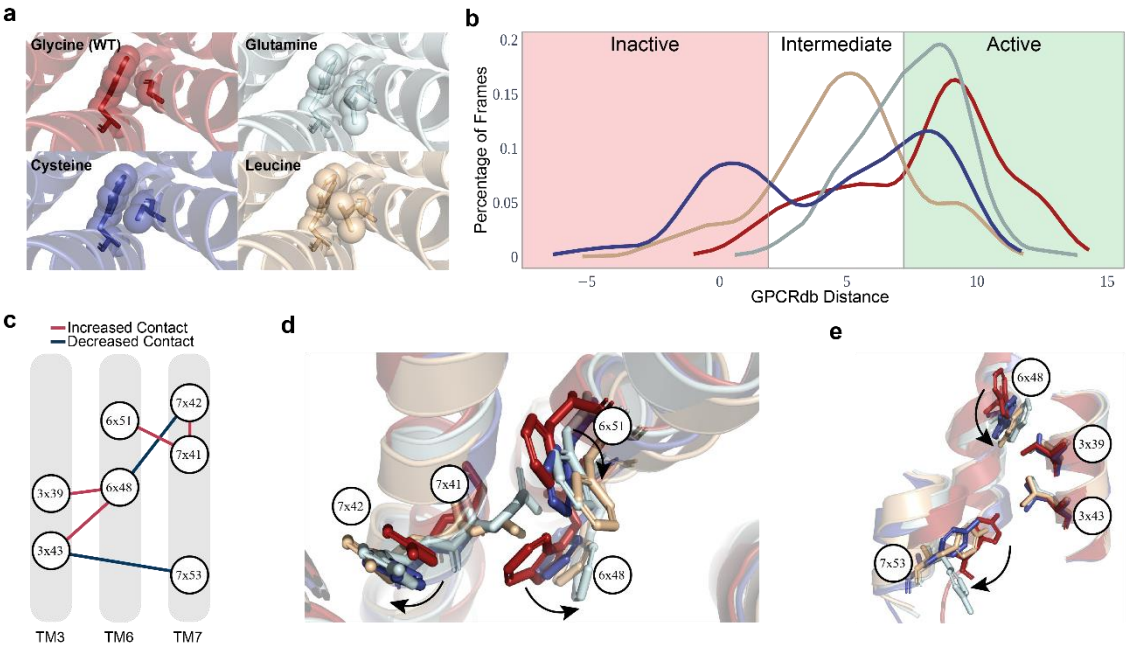

Figure 4: Analysis of molecular dynamics simulations reveal functional importance of glycine at 7x41. (a) 4 different MD simulation systems were shown in their initial conformation. **(b)** For each simulation distribution of frames with respect to their state of activation were shown, distance in Angstrom. **(c)** The common pathway representing impact of the mutations at 7x41. **(d-e)** The common pathway was represented on average structures

that were obtained in all MD trajectories for every mutation and WT. The movements of residues were represented with arrows.

Discussion

The G protein selectivity model we propose involves a series of action. As pilots turn on switches in a pre-determined order before the takeoff, GPCRs must turn on their molecular switches for a specific type of G-protein coupling to occur. If pilots fail to turn on all the switches properly due to an error, there will be no permission for them to depart. Similarly, all molecular switches must be turned on for receptors to engage with a G protein and induce downstream signaling pathways. For these reasons, we named our model **"sequential switches of activation".** We propose the existence of three main switches within a GPCR structure. The first switch checks for binding of the proper agonist which induces conformational changes in lower layers of the receptors. If an agonist makes the proper contacts with the receptor the first switch turns on. Then as a next step, receptors should be activated through G protein selective activation mechanisms which includes multiple micro-switches to turn of the second main switch. Micro-switches represent the arrangement of inner contacts that are specific for G protein subtypes. When inner contacts are established properly the second switch turns on as well. As a third and last check point, receptors should contain the set of residues that can recognize the ridges on G proteins according to the "key and lock" model that Flock et al suggested. When required contact between G protein and receptor is established, the third switch turns on and the receptor is successfully coupled by a subtype of G proteins. Mutations inducing constitutional activity can be considered as a "short circuit" because they can bypass switches. On the other hand, mutations that halt receptor's ability to turn on a particular switch can prevent coupling. It is important to note that our model is both complementary and inclusive to the model Flock et al. suggested. Combination of these two models gives us a more complete perspective on receptor-level determinants of coupling selectivity.

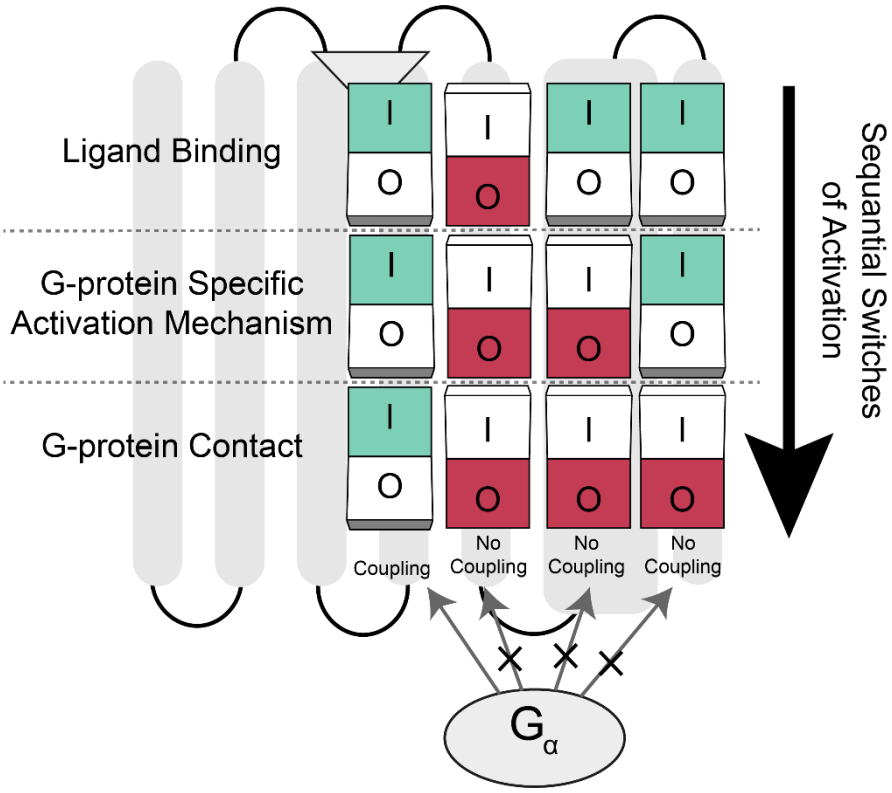

Figure 5: Sequential switches of activation model for G protein selectivity. The model describes that all switches in different layers of receptors must be turned off for receptor activation and coupling of the G protein. If switches at upper layers are halted due to a mutation, following switches become turned off which inhibits G protein coupling eventually.

In our study, we used a novel phylogenetic approach and combined it with structural analysis through novel applications of residue-residue contact score (RRCS) algorithm. We identified G protein specific activation mechanisms within aminergic subfamily of receptors and identified the role a previously uncharacterized residue (Jones et al., 2020). The identified results are limited aminergic receptors only because there has been no supporting evidence for a common selective mechanism that might present for all class A GPCRs. Therefore, we propose that it is necessary to handle each GPCR subfamily separately to identify subfamily specific selectivity determinants. With such an effort, it may be possible to discover commonalities and differences between different subfamilies of GPCRs. Although different subfamilies of receptors couple to a G protein by having similar structural conformations, underlying mechanisms for achieving a conformation might vary. Moreover, there are also receptor specific variations within a subfamily affecting the coupling selectivity for individual receptors. As the number of

solved G protein-coupled receptor structures increase in the protein data bank, it is inevitable that similar mechanisms will be discovered in near future.

Acknowledgements

This work is supported by EMBO Installation Grant (to OA 4163) that is funded by TUBITAK. The molecular dynamics simulations reported in this paper were fully performed at TUBITAK ULAKBIM, High Performance and Grid Computing Center (TRUBA resources).

Methods

Sequence Selection

Sequence selection is the very first step of this study. We used the BLAST+ (Camacho et al., 2009) algorithm to obtain homologous protein sequences from other organisms. We blasted a human target protein to find its homologs. The UniProt ("UniProt: a worldwide hub of protein knowledge," 2019) database is used as a source for the sequences. We retrieved all the sequences until the third human protein from the blast output.

Multiple Sequence Alignment (MSA) #1

After sequence selection, the next step is performing multiple sequence alignment for obtained sequences. For this purpose, we used MAFFT (Katoh & Standley, 2013) “einsi” option which allows large gaps. This option allows us to align multiple homologous regions of different receptors.

Maximum Likelihood (ML) Tree #1

The MSA was used to produce a maximum likelihood (ML) tree. ML trees helped us to find relationships between different proteins. ML Tree 1 was used to identify the clade which contains our protein of interest. For ML tree construction we use the IQ-Tree version 2.0.6 (Minh et al., 2020) We used 1000 Ultra-fast bootstraps and JTT+I+G4+F substitution model. IQ-Tree is used at this step for mainly its high speed in bootstrapping.

Obtaining Gene Clade

For making modifications on the ML trees we use a Python based tool ETE3 (Huerta-Cepas, Serra, & Bork, 2016). To analyze a tree, we first need to root it properly. We chose the third human protein from our BLAST results, as an outgroup. Then, we traversed from our target human leaf node to root until we reached a clade containing another human protein. After each move, we analyzed the species content of the clades we are observing. When a clade contained species that were not observed in previous moves, we included all of the leaf nodes to our analysis. On the other hand, when a clade contains a previously observed species, we exclude that clade from our analysis,. because seeing a species at a lower phylogenetic levels is an indication of a differential gene loss event. We continued with the remaining sequences and produced a multiple sequence alignment with them.

Multiple Sequence Alignment Trimming

MSA trimming is needed to remove some of the noise from the alignment and it speeds up tree reconstruction. MSA trimming removes positions that are misleading for tree production. For example, positions having too many gaps can be removed from the alignment. We used trimAl (Capella-Gutiérrez, Silla-Martínez, & Gabaldón, 2009) with automated1 option which is stated to be the best option for constructing maximum likelihood trees.

Maximum Likelihood Tree #2

ML tree 2 was used to identify the paralogous sequences that we have in our analysis. For ML tree construction we used the RaxML-NG version 0.9.0 (Kozlov, Darriba, Flouri, Morel, & Stamatakis, 2019) --search option with JTT+I+G4+F substitution model.

Paralog Trimming

Paralog trimming is a key part of our approach. After gene duplication, one of the paralogous clade tends to diverge more than the other. Unless the diverged clade is removed from our analyses (MSA), it might introduce false divergence signals in conservation calculation. For this reason, we need to exclude diverged paralogs from our analyses. We used the second ML tree for detection of the diverged paralogs.

We first calculated the global alignment scores (BLOSUM62 is used) of every sequence on the ML tree 2 with respect to our human target sequence. We assessed each internode having two child clades based on the number of leaf nodes and species they contain. When two child clades contained at least one identical species, we looked for significant divergence between the clades in terms of global alignment scores to label one clade as paralogous. Also, we need those clades to be evolutionarily comparable, thus we compared the taxonomic level of the organisms between two clades. If the clades are comparable to each other, we applied two-sample t test for by using the global alignment scores. If one clade has significantly lower similarity scores ($p<=0.1$) that clade is labeled as a diverged paralogous clade. We applied the same approach for detecting the taxonomic level of the organisms and common lineage numbers with *Homo sapiens* was used this time ($p<=0.1$). If the clades are evolutionarily comparable and one clade had a significantly lower global alignment score, all of the sequences belonging to that clade were eliminated.

When two of the clades contained less than three sequences each, it was hard to obtain a significance. Therefore, for those cases we compared the average global alignment scores and eliminated the clade with lower average. For the remaining situations we don't remove any of the clades.

Conservation Calculation

After obtaining orthologs we used them to calculate the conservation scores for each receptor.
The conservation percentage for a certain residue is calculated as follows:

1. Find the most frequent amino acid for a certain position in the multiple sequence alignment (MSA).
2. After finding the most frequent amino acid, we compared it with other alternatives in that position. When comparing amino acids, we calculated BLOSUM80 score for each of them. If the BLOSUM80 score is higher than 2 we accept it as an "allowed" substitution because it means that these amino acids replace each other frequently and have similar properties.
3. The gaps are not included while calculating the conservation percentage.
4. If gaps are more than %50 percent, we categorized that position as a gap.
5. The conservation score is equal to the number of most frequently observed and "allowed" amino acids over number of all non-gap positions

Specificity Calculation (SC)

For a position to be specific or consensus the criteria is the following:

1. First, we need one alignment of two proteins with their orthologs. Then we split the alignment into two alignments with the same length.
2. We label a position as **consensus,** when both alignments are conserved more than consensus threshold (90%) at that particular position and the most frequent amino acids are similar (BLOSUM80 score is more than 1) to each other.
3. We calculated conservation percentages for each alignment. There are two different scenarios in this case. The first one is when the most frequent amino acids of the two of the alignments are not similar (BLOSUM80 score is lower than 2) to each other. If this is the case and conservation percentage for any alignment is above the specificity threshold (90%) we label that position as **specifically conserved** for that alignment. The second case is where the most frequently observed amino acids are similar to each other. In this case, for a position to be specific for one alignment first it should satisfy the specificity threshold and secondly the conservation percentage of the other alignment should be lower than our lower threshold (70%).

For the steps above we choose 90 percent for both specificity and consensus thresholds. 70 percent is selected for lower specificity threshold.

Enrichment of Specifically Conserved Residues

We identified specifically conserved residues with two different approaches:

Specific Approach:

1. We divided receptors into two as couplers vs non-couplers. Let's assume that we have n number of couplers and m number of non-couplers.
2. We compare coupler receptors with non-couplers in a pairwise manner. In these comparisons we count the number of being specific for every residue. In total there are n times m comparisons. We divide the obtained counts to the total number of comparisons in order to get the frequency of a residue being specific for the couplers' group.
3. To examine if a residue is generally variable or specific to the coupling event, we compared couplers with themselves. We applied STEP 2 for couplers - couplers comparison as well.

This time, we have n*(n-1) comparisons in total. We again calculated the frequencies accordingly.

4. For the specific approach, we don't allow any inside variation and this makes the result of STEP 3 zero. On the other hand, for a residue to be labeled as specific, we expect the STEP 2 more than zero. When these two conditions are satisfied, we label that residue as specifically conserved

Sensitive Approach:

1. We built a comprehensive multiple sequence alignment for the coupler receptors and their orthologs.
2. We compared this alignment with non-coupler receptor's MSAs similarly to the STEP 2 of the Specific Approach.
3. We added newly discovered positions to our analysis as specifically conserved.

Building the phylogenetic tree for aminergic receptors

1. We blasted (Camacho et al., 2009) aminergic receptors and obtained first 50 sequences to generate a fasta file
2. From that fasta file we selected representative sequences by using cd-hit default options
3. MAFFT (Katoh & Standley, 2013) einsi algorithm was used to align representative sequences
4. IQTree version 2.0.5 (Minh et al., 2020) was used to create the phylogenetic tree with options: -m JTT+G+I+F -b 100 --tbe

Residue-Residue Contact Score (RRCS) and Network Analysis

We calculated the RRCS score for 20 active (ADRB2: 3SN6,7DHI; DRD1: 7CKW, 7CKX, 7CKZ, 7CKY, 7CRH, 7JV5, 7JVP, 7JVQ, 7LJC, 7LJD; DRD2: 6VMS, 7JVR; DRD3: 7CMU, 7CMV; 5HT1B: 6G79 ; ACM2: 6OIK; 5HT2A: 6WHA ; HRH1: 7DFL)(García-Nafría et al., 2018; Kim et al., 2020; Maeda et al., 2019; Rasmussen et al., 2011; Xia et al., 2021; Xiao et al., 2021; Xu et al., 2021; Yang et al., 2020; J. Yin et al., 2020; Zhuang, Krumm, et al., 2021; Zhuang, Xu, et al., 2021) and 24 inactive structures (ADRB2: 2RH1, 6PS2, 6PS3, 5D5A; DRD1: GPCRdb inactive model; DRD2: 6CM4, 6LUQ, 7DFP; DRD3: 3PBL; 5HT1B: 4IAQ, 4IAR, 5V54, 7C61; ACM2: 3UON, 5YC8, 5ZK3, 5ZKB, 5ZKC; 5HT2A: 6A93, 6A94, 6WH4, 6WGT; H RH1: 3RZE)(Cherezov et al., 2007; Chien et al., 2010; Fan et al., 2020; Haga et al., 2012; C.-Y. Huang et al., 2016; Im et al., 2020; Ishchenko et al., 2019; Kim et al., 2020;

Kimura et al., 2019; Miyagi et al., 2020; Shimamura et al., 2011; Suno et al., 2018; C. Wang et al., 2013; S. Wang et al., 2018; W. Yin et al., 2018) . For each receptor we substracted inactive RRCS from activeRRCS to obtain ΔRRCS values for each residue pairs. We wrote a custom python code to obtain files with ΔRRCS scores. We combined all of the networks that contain information about the contact changes upon activation to produce the most common molecular signal transduction pathways. (Supplementary File). For the details of the RRCS algorithm please read the corresponding article (Zhou et al., 2019).

Identification of G protein Specific Activation Networks

After obtaining ΔRRCS networks for each active-inactive structure pairs we grouped ΔRRCS values based on the G protein subtype coupling the receptors. Then we compared ΔRRCS values of individual groups (e.g. G_s: ADRB2 and DRD1) with the rest of the groups (e.g. Non-G_s: DRD2, DRD3, 5HT1B, ACM2, 5HT2A, HRH1) by using two-sample t-test. While $p<=0.01$ is used for G_s, G_q, and G_o, $p<=0.1$ is used for G_{i1}. We obtained significant contact changes upon coupling to a particular G protein.

Molecular Dynamics Simulations

We downloaded inactive and active structures of Beta2 Adrenergic receptor (β_2AR) from PDB (PDB ID: 4GBR, and 3SN6, respectively)(Rasmussen et al., 2011; Zou, Weis, & Kobilka, 2012) .Three thermostabilizing mutations, T96M^{2x66}, T98M^{23x49}, and E187N^{ECL2,} were mutated back to the wild-type (WT) in both sequences. Since used inactive structure of the β_2AR has a short ICL3 that links the TM5 and TM6, we did not introduce additional residues to the ICL3, and used the crystal structure as it is. However, active structure of the β_2AR lacks ICL3, and we modeled a short loop with GalaxyLoop code (Park, Lee, Heo, & Seok, 2014). We inserted FHVSKF between ARG239 and CYS265. We introduced three changes at 315^{7x41} position, and one WT and obtained three mutants (namely; G315C, G315L, and G315Q). We used PyMOL to place mutations (PyMOL(TM) Molecular Graphics System, Version 2.1.0.). Orientations of proteins in biological membranes were calculated with OPM server (Lomize, Pogozheva, Joo, Mosberg, & Lomize, 2012) and We used CHARMM-GUI web server (Jo, Kim, Iyer, & Im, 2008; Lee et al., 2016; Wu et al., 2014) to create input files for the molecular dynamics simulations for Gromacs. Since, inactive and active structures start with ASP29^{1x28} and GLU30^{1x30}; end with LEU342^{Cterm} and CYS341^{8x59}, respectively, we introduced acetylated N-terminus and methylamidated C-terminus to the N and C-terminal ends. Two disulfide bridges between CYS106^{3x25}-CYS191^{ECL2}, and

CYS184^{ECL2}-CYS190^{ECL2} were introduced. Each lipid leaflet contains 92 (1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine) POPC biological lipid type (total 192 POPC molecules in system). Systems were neutralized with 0.15 M NaCl ions (50 Na^+ and 55 Cl^- ions in total). We used TIP3P water model for water molecules (MacKerell et al., 1998), and CHARMM36m force field for the protein, lipids and ions (J. Huang et al., 2017). One minimization and six equilibration steps were applied to the systems, before production runs (for the equilibration phases 5 ns, 5 ns, 10 ns, 10 ns, 10 ns, and 10 ns MD simulations were run, in total 50 ns). In equilibration phases, both Berendsen thermostat and barostat were used (Berendsen, Postma, Van Gunsteren, Dinola, & Haak, 1984). In production runs, we applied Noose-Hoover thermostat (Hoover, 1986; Nosé & Klein, 1983) and Parrinello-Rahman barostat (Parrinello & Rahman, 1980). 500 ns production simulations were run with Gromacs v2020 (Abraham et al., 2015) and repeated 7 times to increase sampling (in total for each system we simulated 3.5 µs). 5000 frames collected for each run, and for instance for the WT system, we concatenated 35000 frames to calculate GPCRdb distance distributions (*gmx distance* tool was utilized for this purpose) and find average structures (Visual Molecular Dynamics code utilized to find average structure (Humphrey, Dalke, & Schulten, 1996)). To calculate the GPCRdb distance in Class A GPCR structures, CYS125^{3x44}-ILE325^{7x52} distance subtracted from TYR70^{2x41}-GLY276^{6x38} distance. If calculated distance is higher than 7.15 Å, lower than 2 Å, and between 2-7.15 Å state of the receptors labelled as active, inactive, and intermediate, respectively (Isberg et al., 2015; Shahraki et al., 2021). All figures were generated with PyMOL v2.1.0.

Analysis of Contact Changes Within Molecular Dynamics Simulation Trajectories

Frames of MD simulation trajectories were selected from 0ns to 500ns with 50ns gaps for each trajectory and replicate for a mutation. Including the frame at t=0ns, for a replicate we obtained 11 frames to represent the whole trajectory. We have applied the same strategy for all 7 active-state replicates and obtained 77 frames for WT and mutated MD trajectories. For each frame, we calculated RRCSs for every residue pair and identified statistically significant ($p<0.05$) differences between WT and mutated trajectories by applying a two-sided t-test. For the inactive simulations, we had only two replicates, therefore we compared 22 mutated frames with 22 WT frames.

After applying t-test, we intersected the significant contact changes we observed for each mutational state to observe the common change due to the absence of glycine. In total, we identified 135 common changes for active-state simulations and 83 common changes for inactive-state simulations. We used Cytoscape (Shannon et al., 2003) to visualize the changes as a network. PyMOL was used to visualize the identified pathway on protein structures.

Data and Materials Availability

The open-source code and supplementary data are available at our GitHub repository: https://github.com/CompGenomeLab/GPCR-coupling-selectivity

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