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Chemical characterizations of Neurotransmission Receptors of human and plant to unfold the evolutionary relationships among them

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Abstract

Vertebrates have very well defined nervous system. It is established that plant also has an alternative sort of sensitive nervous system. Researchers find a close relationship of the neurotransmission mechanism of animal with the plant and suspects close relation in amino acid transport mechanism among both the organisms. Along with the abilities of determining protein structure and various functions, the chemical properties of amino acids also have great contribution in molecular evolution. Hence, in this present work it is aimed at making comparative study on the distribution of amino acids in the neurotransmission receptors associated to animals and plants, based on the chemical properties the amino acids contain. It is possible to classify 20 amino acids into 8 chemical groups and are identified by specific numeric value. The common pattern finding procedure in numerical representation of protein sequences find some conserved regions in the receptor protein sequences of both the species. The comparative study has been made on distributions of chemical properties in protein sequences of ionotropic glutamate receptor protein sequences and GABA receptor protein sequences of two species namely human, a vertebrate and Arabidopsis thaliana, a plant. Experiments have been carried out to calculate proximity between protein sequences based on the distribution of each chemical group (in percentage) in them and phylogenetic trees have been constructed to find evolutionary relationships of neurotransmission receptors of both the species.

Keywords: Ionotropic Glutamate Receptors, GABA A Receptors, ALMT, Arabidopsis thaliana, Human, Chemical Properties

1. Introduction

Neurotransmission refers to a process by which signaling molecules are released by the axon terminal of a neuron, and then react with the receptors on the dendrites of another neuron by binding with them. Thus, vertebrates have very well defined nervous system. Plants grow in silence. Reported research works established the fact that plant also has an alternative sort of sensitive nervous system. In both the species some receptors are there which play very vital role in neurotransmissions. In vertebrates Ionotropic glutamate Receptors are a kind of receptors which have the ability of synapses to modify their synaptic strength in response to activity. It is a fundamental property of the nervous system[1]. There are four classes of ionotropic glutamate receptors in animals, namely NMDA (N-methyl-D-aspartate) receptor, AMPA (-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid) receptor, Delta receptor and kainate receptors[2]. According to researchers, similar to ionotropic glutamate receptor (iGluR) gene family of animals, glutamate-like receptor (GLRs) gene family in plants also have some functions in neurotransmission[3]. In human, another type of receptors that respond to the neurotransmission is gamma-aminobutyric acid (GABA) receptor. It is the chief inhibitory neurotransmitter in the vertebrate central nervous system[4]. Two classes of GABA receptors are there, GABA A and GABA B. GABA A receptors are ligand-gated ion channels (also known as ionotropic glutamate receptors), whereas

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GABA B receptors are G protein-coupled receptors (also known as metabotropic receptors). Ionotropic receptors (IRs) are made up of some protein subunits that together form an ion-conducting pore in the center of the receptor. IRs are more ancient than ORs (Olfactory Receptors). GABA is synthesised in a pathway known as the GABA shunt, which operates not only in the animals, but in plants too. A plant 'GABA receptor' inhibits anion passage through the aluminium-activated malate transporter family of proteins (ALMTs). GABA regulation of aluminium activated malate transporter (ALMT) activity could function as a signal that modulates plant growth, development, and stress response.

Numerous works since Darwin [5] have proved the response of plants to various signals like light, touch, wounding, stimulating etc. Now it has been reported that glutamate receptors of vertebrate nervous system and similar receptors in the plant equivalent of nerve have so close similarities that they must have evolved from a common ancestor [6, 7, 8]. Authors have tried to establish evolutionary relationships between the iGLuR gene family of mammals and GLRs of plants like *Arabidopsis thaliana* [3, 9]. Characterization of an *Arabidopsis* GABA transaminase mutant (pop2) revealed that a GABA concentration gradient in the style is required to guide pollen tubes to the ovary [10]. Now, if specific protein sequences are there in plants which make control over such functionalities in neuro-transmission, then the next question arose that do the plants sleep and feel pain? Do they have consciousness? Do they have effects of anesthetics [11]? Numerous research papers are reported on it [12]. Till now reported research works indicate that plants lack the neural anatomy and all behaviors related to pain [13, 14]. Amino acids are the building block of a protein. Evidence suggests that along with the role of protein synthesis some of the canonical amino acids play significant roles in modulating neurotransmission in animals [15]. Like, glutamic acid (Glu) works with ionotropic glutamate receptors and acts as excitatory neurotransmitter in Central Nervous System [16, 17, 18]. Aspartic acid (Asp) plays both the roles of neurotransmitter and neuromodulator [19, 20]. Isoleucine, leucine and valine are called as Branched Chain Amino Acids (BCAAs) and act as precursors for Glutamate [21, 22]. Glycine (Gly), Serine (Ser) and Alanine play the role of co-agonist for NMDA receptors [23, 24, 25]. Arginine [26, 27], Lysine [28], Glutamine [29, 30] and Asparagine (asn) [31] act as precursors. Deficiencies in Asparagine can be responsible for the abnormalities in the brain. Proline (Pro) acts as a neuromodulator at receptors like NMDA, AMPA/Kainate and Glycine [32].

According to Jack C. Schultz [33] plant's behaviour is largely biochemical. Researchers find a close relationship of the neurotransmission mechanism of animal with the plant protein sequences and suspects close relation in AA transport mechanism among both the organism [34]. It is known that each of 20 standard canonical amino acids contain specific chemical properties. Thus, 20 amino acids can be classified into 8 groups based on 8 distinct chemical properties [35]. Hence, it is worth to make comparative study on the distribution of amino acids in the receptor protein sequences associated to animals and plants, based on the chemical properties the amino acids contain. The investigation may unfold information about evolutionary relationships (if any) among the two organisms. Thus, in this present work a comparative study has been made on distributions of chemical properties in protein sequences of ionotropic glutamate receptor protein sequences and GABA receptor protein sequences of two species namely human, a vertebrate and *Arabidopsis thaliana*, a plant. Experiments have been carried out to investigate evolutionary relationship among the neurotransmission receptors of both the species.

2. Methods and Materials

2.1. Collection of protein sequences

Table 1: Dataset Specification

Ionotropic receptor Gene Name	Accession No.	GABA receptor Gene Name	Accession No.
Arabidopsis		Arabidopsis	
AtGLR1.1	AAF26802.1	ALMT4	Q9C6L8
AtGLR1.2	BAA96960.1	ALMT5	Q93Z29
AtGLR1.3	BAA96961.2	ALMT6	Q9SHM1
AtGLR1.4	AAF02156.1	ALMT8	Q9SRM9
AtGLR2.1	AAB61068.1	ALMT9	Q9LS46
AtGLR2.2	AAD26895.1	ALMT10	O23086
AtGLR2.3	AAD26894.1	ALMT12	O49696
AtGLR2.4	CAA19752.1	ALMT14	Q9LS22
AtGLR2.5	CAB96656.1	Human	
AtGLR2.6	CAB96653.1	GABRA1	P14867
AtGLR2.7	AAC33239.1	GABRA2	P47869
AtGLR2.8	AAC33237.1	GABRA3	P34903
AtGLR2.9	AAC33236.1	GABRA4	P48169
AtGLR3.2	CAA18740.1	GABRA5	P31644
AtGLR3.3	AAG51316.1	GABRA6	Q16445
AtGLR3.4	AAB71458.1	GABRB1	P18505
AtGLR3.5	AAC69939.1	GABRB2	P47870
AtGLR3.6	CAB63012.1	GABRB3	P28472
AtGLR3.7	AAC69938.1	GABRD	O14764
Human		GABRE	P78334
GRIA1	P42261	GABRG1	Q8N1C3
GRIA2	P42262	GABRG2	P18507
GRIA3	P42263	GABRG3	Q99928
GRIA4	P48058	GABRP	O00591
GRID1	Q9ULK0	GABRQ	Q9UN88
GRID2	O43424	GABRR1	P24046
GRIK1	P39086	GABRR2	P28476
GRIK2	Q13002	GABRR3	A8MPY1
GRIK3	Q13003		
GRIK4	Q16099		
GRIK5	Q16478		
GRIN1	Q05586		
GRIN2A	Q12879		
GRIN2B	Q13224		
GRIN2C	Q14957		
GRIN2D	O15399		
GRIN3A	Q8TCU5		
GRIN3B	O60391		

To carry out the investigation two sets of protein sequences are considered for the species of human from animals and Arabidopsis thaliana from plant. To characterize ionotropic glutamate receptors 19 protein sequences from Arabidopsis thaliana and 18 protein sequences from human are collected from NCBI Genebank. The second set is Gamma-aminobutyric acid (GABA) receptors, where 8 Aluminum-activated Malate Transporters (ALMT) protein sequences are representing the Arabidopsis thaliana and 19 GABA A protein sequences of human. The details about the dataset taken are summarized in the Table 1.

2.2. Methods

2.2.1. Classification of Amino Acids with respect to their chemical properties

Along with the abilities of determining protein structure and various functions, the chemical properties of amino acids also have great contribution in molecular evolution. Hence, in this section it is aimed at making comparative study on the distribution of amino acids in the neurotransmission receptors associated to animals and plants, based on the chemical properties the amino acids contain. It is possible to classify 20 amino acids into 8 chemical groups as shown in Table 2.

Table 2: Classification of Amino Acids with respect to their chemical properties

Group No.	Group Name	Amino Acids
1	Acidic	Aspartate , Glutamate
2	Basic	Histidine,Arginine, Lysine
3	Aromatic	Tryptophan, Tyrosine, Phenylalanine
4	Aliphatic	Isoleucine, Glycine Leucine, Valine, Alanine,
5	Cyclic	Proline
6	Sulfur containing	Methionine, Cysteine
7	Hydroxyl containing	Threonine ,Serine
8	Acidic amide	Glutamine, Asparagine

2.2.2. Numerical Representation of protein sequences according to the chemical classification

Numerical representation of genomic sequences based on some predefined biological facts or properties simplifies the process of quantitative analysis of them [3, 35, 36]. In this subsection the amino acids of each protein sequences are converted into their corresponding group number of the chemical properties as specified in table 2. Thus here we find the numerical representation of all the protein sequences. Let $S = S_1, S_2, \dots, S_n$ is an arbitrary protein sequence, where for any S , S_i represents a single amino acid from the set, such that $S_i \in A, C, D, E, F, G, H, I, K, L, M, N, O, P, Q, R, S, T, V, W, Y$. Let's consider 20 amino acids are classified into a set of groups C , then it is possible to read each amino acid of a protein sequence by its corresponding chemical group, such that, $C_i \in 1, 2, 3, 4, 5, 6, 7, 8$. As an example, a string of amino acid sequence 'CLICK' will be represented as '64462' after encoding it into the numeric representation.

2.2.3. Percentage-wise analysis of Amino Acid group present in each protein sequences.

All 20 Amino acids can not be equally distributed throughout the entire sequence. Distribution of chemical properties throughout each sequences are calculated. Thus for each set of data a matrix will be generated, from which it is possible to measure the proximity among the protein sequences.

2.2.4. Finding common patterns and identifying conserved regions

Conservation of DNA or protein sequences across species refers to identical or similar pattern of DNA or amino acids occurring in same or different species over the generations. Sometimes for the functional and structural importance of those conserved regions, they carry very essential ingredients to study the evolutionary relationship between species. Here in this subsection it is aimed to search for firstly block of amino acids which are existing in all the protein sequences of ionotropic glutamate receptors and GABA receptors of both the species respectively. Secondly, common patterns length L (where, $2 \leq L \leq 8$), are searched in numeric representations of protein sequences to find the proximity of the sequences in terms of distribution of chemical properties. Given an input of pattern length L (where, $2 \leq L \leq 8$), every possible pattern (made up any combination of numeric value 1 to 8) of length L are investigated among the sequences. If the pattern is found in every sequences, then the pattern is stored along with its location, otherwise it is discarded. Thus, by varying pattern length L , it is possible to find patterns of different lengths along with their corresponding location.

2.2.5. Investigating evolutionary relationships between two species with respect to the chemical properties of the protein sequence

Investigating evolutionary relationships between species measuring proximity between genomic sequences based on specific biological properties and investigating evolutionary relationships among them is a quite accepted approach. Here in this section it is intended to calculate proximity between protein sequences based on the distribution of each chemical group (in percentage) in them. Consider, S_1 and S_2 are any two protein sequences and $P = (P_1, P_2, \dots, P_8)$ and $Q = (Q_1, Q_2, \dots, Q_8)$ are the percentage of occurrence of a eight chemical group in the given sequences respectively. Then it is possible to construct a distance matrix for a given set of sequences depending upon the distribution of chemical groups of each protein sequences, such that $P_i \in \{P_1, P_2, P_3, P_4, P_5, P_6, P_7, P_8\}$ and $Q_i \in \{Q_1, Q_2, Q_3, Q_4, Q_5, Q_6, Q_7, Q_8\}$.

The proximity of S_1 and S_2 with respect to the distribution of chemical properties can be calculated using the following equation,

$$\xi(S_1, S_2) = \sum_{n=1}^8 |P_i - Q_i| \quad (1)$$

3. Results

3.1. Percentage-wise measurement of amino acid compositions in all the protein sequences

Amino acid compositions in protein sequences are well conserved from species to species. The aim behind is to reduce the deleterious impact of mutations, to keep the function and structure of the protein relatively unaltered. In this subsection the amino acid composition of each protein sequence is measured (shown in Figure 1). It has been found that in all the protein sequences of ionotropic glutamate receptor protein sequences from both the species have majorly highest count of Leucine (Leu). Other most occurred amino acids are Glycine (Gly), Valine (Val), and Serine (Ser). The amino acid compositions of all GABA A receptor protein sequences of Human and ALMT receptor protein sequences of Arabidopsis thaliana also have some commonalities such that they all have huge amount of Leucine (Leu), Valine (Val), and Serine (Ser). The percentage-wise count of amino acids of all the protein sequences are shown in supplementary Table S7.

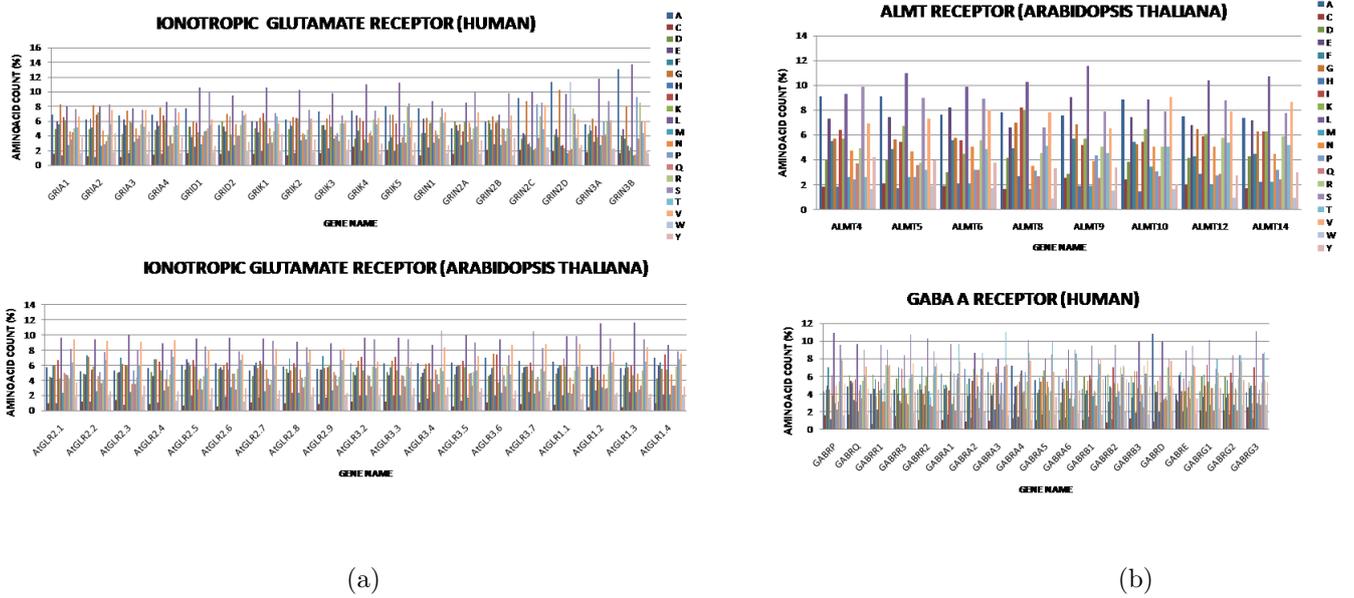


Figure 1: Percentage-wise measurement of amino acid compositions in all the protein sequences (a) ionotropic glutamate receptor protein sequences of both Arabidopsis thaliana and human. (b) ALMT protein sequences of Arabidopsis thaliana and GABA A protein sequences of Human.

3.2. Calculate Percentage of each Group of Amino Acids present in each protein sequences.

3.2.1. Percentage of each Group of Amino Acids present in each of ionotropic glutamate receptor protein sequences

Table 3: Percentage of each Group of Amino Acids present in each of ionotropic glutamate receptor protein sequences of human

AA GROUP	GRIA1	GRIA2	GRIA3	GRIA4	GRID1	GRID2	GRIK1	GRIK2	GRIK3
1	10.82	11.21	10.40	10.75	10.51	11.22	10.89	10.68	10.88
2	12.36	12.46	13.09	12.86	11.99	11.52	12.42	12.67	13.17
3	11.04	11.10	11.63	10.75	8.13	9.73	10.68	10.57	10.34
4	36.31	36.81	35.23	37.36	36.17	35.45	35.73	35.57	36.34
5	3.53	2.83	3.58	4.10	4.56	4.07	4.03	4.19	4.35
6	4.30	3.85	4.25	4.10	4.56	4.17	4.47	4.74	5.22
7	12.69	13.82	12.75	13.19	15.36	14.20	13.73	13.77	12.40
8	8.94	7.93	9.06	6.87	8.72	9.63	8.06	7.82	7.29
AA GROUP	GRIK4	GRIK5	GRIN1	GRIN2A	GRIN2B	GRIN2C	GRIN2D	GRIN3A	GRIN3B
1	10.36	10.10	10.66	11.41	11.79	7.95	9.06	9.69	8.82
2	11.61	12.76	14.61	13.66	13.88	12.00	12.57	12.83	13.42
3	9.21	8.16	8.74	9.63	9.77	8.84	8.76	9.06	7.19
4	37.13	37.86	35.61	30.87	31.87	39.25	40.19	35.07	42.86
5	4.71	5.71	4.16	5.12	4.85	8.27	11.30	6.01	9.30
6	5.54	5.10	4.37	4.78	4.78	4.22	3.52	4.48	2.97
7	12.97	13.47	13.54	15.30	14.69	13.46	10.63	14.80	10.35
8	8.47	6.84	8.32	9.22	8.36	6.00	3.97	8.07	5.08

Table 4: Percentage of each Group of Amino Acids present in each of ionotropic glutamate receptor protein sequences of Arabidopsis thaliana

AA GROUP	AtGLR2.1	AtGLR2.2	AtGLR2.3	AtGLR2.4	AtGLR2.5	AtGLR2.6	AtGLR2.7	AtGLR2.8	AtGLR2.9	AtGLR3.2
1	8.85	9.67	10.17	9.69	12.18	11.26	10.49	10.54	10.85	9.73
2	9.49	10.98	11.17	11.25	12.30	12.69	11.78	12.53	12.23	13.08
3	11.51	11.63	12.07	10.58	10.86	9.60	10.60	11.68	11.49	10.49
4	37.74	36.41	36.54	37.08	36.19	35.76	35.12	34.45	34.04	36.11
5	4.80	5.11	5.25	5.46	4.22	4.86	4.28	4.38	4.68	4.54
6	3.30	3.70	3.80	3.56	3.38	3.64	3.64	3.24	3.51	3.24
7	14.61	14.35	14.08	15.03	14.11	14.57	15.20	14.72	14.79	15.03
8	9.70	8.15	6.93	7.35	6.76	7.62	8.89	8.46	8.40	7.78
AA GROUP	AtGLR3.3	AtGLR3.4	AtGLR3.5	AtGLR3.6	AtGLR3.7	AtGLR1.1	AtGLR1.2	AtGLR1.3	AtGLR1.4	
1	9.73	9.46	10.61	9.34	10.75	10.40	10.38	10.23	10.14	
2	13.08	11.33	12.07	11.74	13.25	13.12	12.69	12.44	13.29	
3	10.49	10.50	11.40	9.82	10.10	9.65	10.03	10.35	11.42	
4	36.11	35.76	36.20	40.04	38.22	38.00	36.79	37.21	36.25	
5	4.54	4.78	5.03	4.62	4.45	2.23	2.88	2.79	3.26	
6	3.24	3.43	2.23	3.37	3.15	3.09	3.58	2.91	3.03	
7	15.03	15.80	14.30	12.13	13.46	15.72	15.92	15.93	14.57	
8	7.78	8.94	8.16	8.95	6.62	7.80	7.73	8.14	8.04	

3.2.2. Percentage of each Group of Amino Acids present in each of GABA A and ALMT Receptor protein sequences

Table 5: Percentage of each Group of Amino Acids present in each of GABA A Receptor protein sequences of human

AA GROUP	GABRP	GABRQ	GABRR1	GABRR3	GABRR2	GABRA1	GABRA2	GABRA3	GABRA4	GABRA5
1	9.55	11.71	10.86	9.85	9.68	9.65	8.87	9.16	7.76	8.66
2	10.45	12.03	13.99	13.49	15.05	14.04	12.42	12.60	13.18	12.77
3	13.86	11.55	12.32	13.28	13.55	11.18	12.20	10.77	9.57	11.26
4	33.64	32.75	30.06	30.41	31.40	32.89	33.04	34.15	32.13	31.60
5	2.27	5.06	5.22	3.00	3.66	6.36	4.88	5.28	6.50	4.76
6	4.55	3.80	5.22	6.21	5.38	3.95	4.43	3.86	5.42	4.98
7	17.50	15.19	16.08	16.92	15.91	16.01	15.52	18.09	18.77	18.40
8	8.18	7.91	6.26	6.85	5.38	5.92	8.65	6.10	6.68	7.58
AA GROUP	GABRA6	GABRB1	GABRB2	GABRB3	GABRD	GABRE	GABRG1	GABRG2	GABRG3	
1	8.39	9.92	9.38	9.52	9.29	9.29	9.68	9.64	10.06	
2	10.38	12.87	13.48	13.74	12.17	12.25	12.47	12.85	11.56	
3	11.92	11.81	12.50	11.84	10.84	11.86	13.33	13.92	13.06	
4	34.22	33.76	34.38	36.15	40.05	30.04	33.12	30.62	31.05	
5	5.96	4.22	4.30	4.02	3.76	5.53	4.73	4.50	4.50	
6	4.64	4.85	4.49	4.44	4.20	5.93	4.95	4.93	5.57	
7	17.66	15.40	13.48	12.68	12.83	16.80	14.84	16.70	17.34	
8	6.84	7.17	8.01	7.61	6.86	8.30	6.88	6.85	6.85	

Table 6: Percentage of each Group of Amino Acids present in each of ALMT Receptor protein sequences of Arabidopsis thaliana

AA GROUP	ALMT4	ALMT5	ALMT6	ALMT8	ALMT9	ALMT10	ALMT12	ALMT14
1	11.31	11.36	11.16	10.66	11.87	11.27	10.89	11.42
2	12.41	12.11	12.08	15.16	12.54	12.88	14.64	14.36
3	11.31	10.61	10.97	9.02	10.54	9.05	7.85	8.29
4	37.41	38.36	36.80	40.98	37.63	37.42	38.04	39.23
5	2.37	2.61	3.16	3.07	4.35	3.02	2.68	3.13
6	4.38	4.66	3.90	3.28	4.35	5.84	3.93	3.87
7	12.41	12.10	13.75	11.68	12.37	12.88	14.11	12.89
8	8.39	8.19	8.18	6.15	6.35	7.65	7.86	6.81

3.3. Common pattern finding in protein sequences

It has been observed that it is possible to classify 20 amino acids into 8 chemical groups and are identified by specific numeric value. The common pattern finding procedure of numerical representation of protein sequences find some conserved regions in the receptor protein sequences of both the species. The microscopic view of those common patterns are stated in the tables below. It has been found that all the ionotropic glutamate receptor protein sequences of human have a common pattern '3748444' of length 7 at 872th position, which encodes the string of amino acid "YTANLAA". The table 7 find common patterns (length of 2 AA and 3 AA) based on chemical groups of protein sequences of ionotropic glutamate receptor protein sequences and the table 8 states the common patterns ((length of 1 AA) found in the protein sequences in GABA receptor genes. It is to be noted that as in the protein sequences in GABA receptor protein sequences no common patterns are found more than length of 1 AA, hence here the common patterns length of 1 AA are considered. Table 9 states the conserved regions considering the amino acids individually.

Table 7: Various conserved regions based on chemical groups of amino acids. The patterns are common in all ionotropic glutamate receptor protein sequences taken of both the species

POSITION	PATTERN	AA
753	41	ID/ VD/ VE/ LD
846	413	IDF/ VDF/ ADF/ IEF
1333	43	LF/ VF/ IF

Table 8: Various conserved regions based on chemical groups of amino acids. The patterns are common in all GABA receptor protein sequences taken of both the species

POSITION	PATTERN	AA
129, 156	4	L/I/V
140	2	R
205	3	W
227	8	N
236	4	G
238	4	I/V/L
264	3	Y/F
283, 294	3	W/Y/F
285	3	Y
344	4	L/V
371	3	Y/W
458	4	A/G

Table 9: Various conserved regions based on amino acids individually. The patterns are common in both the species for the GABA and ionotropic glutamate receptor protein sequences taken respectively.

POSITION	AA
GABA Receptors	
193	W
214	N
223	G
272	Y
ionotropic glutamate receptors	
907	G
999	I
1003	R
1009	F
1038	P
1044	W
1331	G
1366	W

3.4. Investigating evolutionary relationships between two species with respect to the chemical properties of the protein sequence

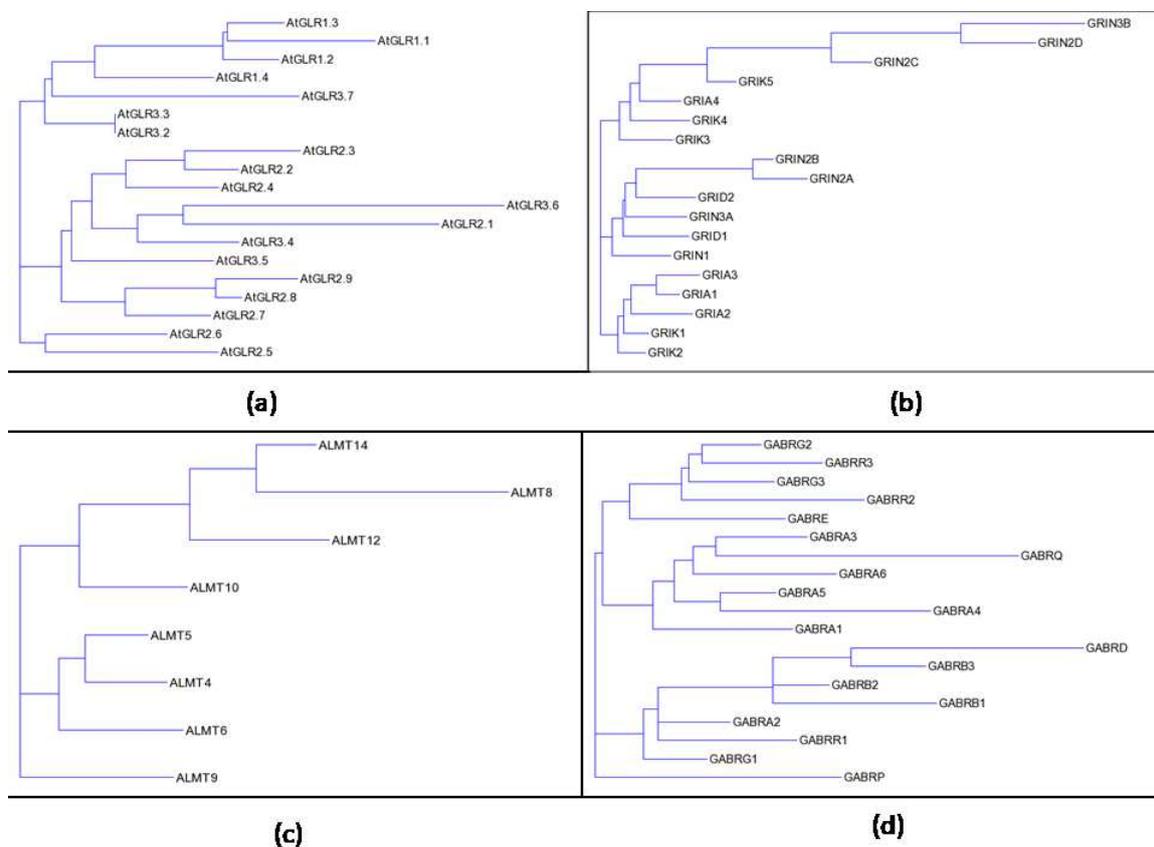


Figure 2: Construction of phylogenetic trees based on the chemical properties of the protein sequence. (a) AtGLRs of Arabidopsis thaliana (b) iGluR of human (c) ALMT of Arabidopsis thaliana (d) human GABA A

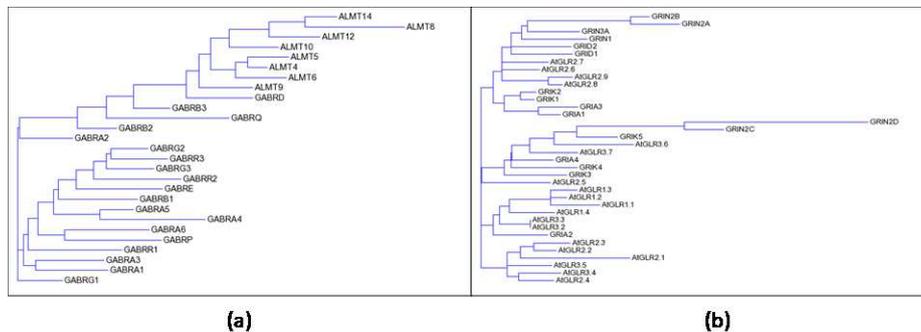


Figure 3: Construction of phylogenetic trees based on the chemical properties of the protein sequence. (a) Phylogenetic tree constructed of all GABA A receptor protein sequences of human and ALMT receptors of Arabidopsis thaliana. (b) Phylogenetic tree constructed of all glutamate receptor protein sequences of both the species.

In this section the pictorial representation of the similarity matrices are stated in the form of phylogenetic tree. The similarity matrices are shown in the supplementary tables S1, S2, S3, S4, S5, and S6. As the phylogenetic trees are constructed to get the ideas of the evolutionary relationships among the species, here figure 2 is showing the species wise evolutionary relationships of ionotropic glutamate receptor protein sequences and GABA receptor genes. Figure 2(a) gives a view of AtGLRs, whereas, Figure 2(b) shows the same between iGluR protein sequences of human. Figure 2(c) and 2(d) are providing us an idea about the species wise status of GABA receptor genes. Figure 3(a) shows evolutionary relationships of glutamate receptor protein sequences of both the species and figure 3(b) draws the evolutionary relationships among the GABA A receptor protein sequences of both the species. According to Figure 3(a) human GABA A receptor protein sequences GABRQ, GABRD, GABRA2, GABRB2, GABRB3 are quite similar with the ALMT receptor protein sequences of Arabidopsis thaliana. In other hand, according to Figure 3(b) AtGRL2.6, AtGRL2.7, AtGRL2.8, AtGRL2.9 of Arabidopsis thaliana are evolutionary more similar to the ionotropic glutamate receptor protein sequences of human. GRIN2C, GRIN2D, GRIA3, GRIK3, GRIK4, GRIK5 of human ionotropic glutamate receptor protein sequences have evolutionary relationships with those of Arabidopsis thaliana.

4. Discussion

Animals and plants both react to wounding. Both of them have specific protein sequences which make control over such functionalities in neuro-transmission. Animals have well defined central nervous system, whereas, plants have alternative sort of sensitive nervous system, able to respond to various external stimuli. As mentioned, animals and plants both have glutamate and GABA signaling and receptors respectively. Animal versions of these receptors are targets of anesthetics in the animal nervous systems, but the plant versions are questionable. Here in this present work the objective is to make quantitative understanding of plant and animal receptor protein sequences which acts as neurotransmitters. It is also aimed at investigating the evolutionary relationships among them (if any). We have selected human from vertebrates and Arabidopsis thaliana from species plants. Our attempt is based on the distribution of eight types of chemical properties which an amino acid sequence may have. The reason behind is, they play active role in molecular evolution, where chemical properties of the side chain of amino acids can determine the essential amino acids in the core catalytic region. 'YTANLAA', a sequence of 7 amino acids length is the conserved region at 872th position in all the human ionotropic glutamat receptor genes. The region resides at M3 domain of glutamate receptors [37]. According to reported research evidences, cysteine substitutions in this region indicates state-dependent accessibility and the region moves in response to receptor activation [38, 39]. Thus, M3 domain acts as transduction element [40]. The numerical representation of the amino acid sequences based on the chemical properties have made the job of pattern matching easier as the time complexity is directly proportional to the sequence length N, that is $O(N)$.

5. Conclusion

We detected the commonalities (conserved elements) during the long evolution of *Arabidopsis thaliana* and human from a common ancestor. Four and eight different conserved regions have been found (based on individual amino acids) in both the species for the GABA and ionotropic glutamate receptor protein sequences taken respectively. Three different conserved regions (length of two to three amino acids) are also found (based on chemical groups of amino acids) in all ionotropic glutamate receptor protein sequences taken of both the species. Fourteen conserved regions are found (based on chemical groups of amino acids) in all GABA receptor protein sequences taken of both the species. The constructed phylogenetic trees depicts higher proximity between certain protein sequences belong to both the species. Plant's behaviour is largely biochemical. The canonical amino acids play significant roles in modulating neurotransmission in animals. Investigations show a close relationship of the neurotransmission mechanism of animal with those of plant. It is the researchers' firm conviction that there exists a close relationship in amino acid transport mechanisms among both the organisms. Thus, there exists a need for a thorough study of plant neurochemicals as some of the compounds that affect human brain function also affect the growth and development of plants [41]. Therefore, the in-silico analysis performed in this study not only claims some common functionalities between human, a vertebrate and *Arabidopsis thaliana*, a plant in neurotransmission, but also initiates a new horizon to the biologists for better understanding of both human and plant physiology.

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Competing interests

The authors declare no competing interests.

Supporting information

Table S1. Similarity matrix of Ionotropic Glutamate receptor protein sequences of *Arabidopsis thaliana*.

Table S2. Similarity matrix of human Ionotropic Glutamate receptor protein sequences.

Table S3. Similarity matrix of human Ionotropic Glutamate receptor protein sequences.

Table S4. Similarity matrix of human GABA A receptor protein sequences.

Table S5. Similarity matrix of all GABA A receptor protein sequences of human and ALMT receptors of *Arabidopsis thaliana*

Table S6. Similarity matrix of all Ionotropic Glutamate receptor protein sequences of both the species.

Table S7. Percentage-wise measurement of amino acid compositions in all the protein sequences