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In silico Characterization of Rhizome coding genes in Ginger and Bamboo

Research Article

Dhanalakshmi T[1], Geethalakshmi S[2]* and Barathkumar S[3]

[1]*Department of Microbiology, Nehru Arts and Science College, India*

[2]*Department of Biotechnology, Nehru Arts and Science College, India*

[3]*Department of Biotechnology, Karpagam Academy of Higher Education, India*

***Corresponding author:** Geethalakshmi S, Department of Biotechnology, Nehru Arts and Science College, Coimbatore, Tamilnadu, India, Tel no: +91-9952411764, E-mail: s.geethalakshmi@gmail.com

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Abstract

Rhizome is an underground, horizontal plant stem which helps in propagation of the plants. Growth of rhizome may be facilitated by the genes that are involved in axillary bud initiation. The present study aims at characterizing the genes that are involved in development of rhizome in ginger (*Zingiber officinale*) and bamboo (*Bambusoideae*) using *in silico* tools. The initial dataset was collected from the plant databases and BLASTed against the standard data set. The resulting sequences were subjected to physical parameters, secondary and tertiary structure prediction. The results will form a foundation for analyzing the genetic characters of rhizome which can be extended further for transgenic plant development which has a rich vegetative propagation.

Introduction

The primary storage organ of many perennial grass species is the rhizome which is an underground, horizontal plant stem. It also serves as a primary character for persistence of the plant species [1]. The advantage of rhizome in a plant is it helps in propagation of the plant; whereas the disadvantage is the rhizome in the weeds does not permit the plant to be eradicated completely [2]. Rhizomes were originally identified in plants like ginger (*Zingiber officinale*) and turmeric (*Curcuma longa*) based on their ability to develop into a new plant from the buds. The study then extended to grass family where bamboo (Bambusoideae), *Sorghum bicolor* and *Oryza* were taken as model plants for the EST analysis [3]. Though several studies has been carried out to characterize the genes involved in propagation of rhizome, due to the polyploidy nature of these perennial plants, identification of full length EST using *in vitro* techniques is still under progress.

Plant rhizomes originate from axillary buds on the most basal portion of the seedling shoot and hence genes involved in plant axillary bud initiation and outgrowth may contribute to rhizome development and growth [4]. Identification of those genes and its expression can pave way for isolating and using them for transgenic plant development so that plants having a rich vegetative propagation can be developed. This property can be used to protect RET (Rare, Endangered, Threatened) plant varieties.

The present study aims at characterizing the rhizome coding genes from ginger (*Zingiber officinale*) and bamboo (Bambusoideae) *in silico* which will provide a base for gaining knowledge about the role and expression of the genes involved in plant propagation via rhizome. The plants considered for the study are not only considered as traditional medicine but also have great economic importance [5].

Materials and Methods

Data set collection and characterization

Rhizome coding nucleotide sequences of Ginger and Bamboo

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were downloaded from National Centre for Biotechnology (NCBI; www.ncbi.nlm.nih.gov/) for computational analysis [6]. Using the BioEdit tool version 7.0.9 (http://www.mbio.nscu.edu/Bioedit) [7], the downloaded sequences were subjected to six frame translation and the protein sequences were analyzed using PROSITE program in ExPASy server (http://prosite.expasy.org/scanprosite) to locate the characteristic domains specific to the sequences [8,9]. The nucleotide and its deduced protein sequence of the test rhizome coding genes were subjected to nucleotide and amino acid composition analysis using BioEdit version 7.1.3.0 (http://www.mbio.nscu.edu/Bioedit).

Physical parameters prediction

To get more information about the physical nature of the identified rhizome coding genes, protein sequences of predicted genes were subjected to various physical properties analysis such as pI, molecular weight and GRAVY (Grand Average Hydropathy) using PROTPARAM online software was used through the website http://expasy.org/ tools/protparam.html [10].

Secondary structure prediction

The secondary structure of the predicted protein sequences were determined by SOPMA (self optimized prediction method) which is a versatile tool for secondary structure prediction (http://npsa-prabi.ibcp.fr/) [11].

Three dimensional structure prediction using i-TASSER

For the three dimensional structure prediction of the test rhizome coding genes from bamboo and ginger, the iterative threading assembly tool i-TASSER was used (http://zhanglab.ccmb.med.umich.edu/I-TASSER) [12]. The stereochemical properties of the predicted three dimensional structures were confirmed by Ramachandran plot.

Errat analysis of modelled structure

ERRAT is a program for verifying protein structures determined by crystallography. Error values are plotted as a function of the position of a sliding 9-residue window. The error function is based on the statistics of non-bonded atom-atom interactions in the reported structure (compared to a database of reliable high-resolution structures). According to the analysis by ERRAT, the final model is significantly improved relative to the initial model. The method is sensitive to smaller errors than 3-D Profile analysis [13].

Results and Discussion

Nucleic acid analysis

Using the software BIOEDIT, predicted gene sequences of the rhizome of Ginger and Bamboo were subjected to nucleotide analysis (Figure 1a and 1b). According to this, the lengths of the isolated gene were 2211 bp and 339 bp respectively. The number of amino acids coded by the genes was 736 and 112 respectively. The nucleotide number and molecular percentage of the gene sequences are shown in Table 1.

Nucleotide composition of rhizome coding gene in bamboo (Figure 2a)

DNA molecule: Gene 1

Length = 2211 base pairs

Molecular Weight = 668964.00 Daltons, single stranded

Molecular Weight = 1342173.00 Daltons, double stranded

G+C content = 44.87%

A+T content = 55.13%

Nucleotide composition of rhizome coding gene in ginger (Figure 2b)

DNA molecule: Gene 2

Length = 339 base pairs

Molecular Weight = 102980.00 Daltons, single stranded

Molecular Weight = 206140.00 Daltons, double stranded

G+C content = 50.44%

A+T content = 49.56%

Protein analysis-primary structure

The physical parameters of the identified protein sequences were subjected to PROTPARAM analysis at ExPASy server. Based on the parameters predicted, the identified protein sequences were stable and the GRAVY score indicated that the proteins were hydrophilic in nature. This result indicated that the protein has a good interaction with water in the soil which is essential for the enlargement of rhizome and nitrogen translocation [14]. Accumulation of nitrogen in the nodules and rhizome region of plants is mediated by movement of water using the principle of hydraulic lift, which means in the absence of water, the movement of nitrogen is unidirectional and only in the presence of sufficient water the nitrogen gets accumulated throughout the rhizome.

Amino acid analysis

Amino acids were analyzed by using BIOEDIT software, and the composition of the identified protein sequences was depicted in Table 2a and 2b. The amino acid composition of the protein sequences is indicated diagrammatically in Figure 3a and 3b.

Amino acid composition analysis of Bamboo rhizome protein showed 49.4% of hydrophobic (Gly, 5.84%, Ala, 9.24%; Val, 7.20%; Leu 10.05%; Ile, 4.62%; Pro, 4.62%; Phe, 2.72%; Trp, 0.95%; Met, 2.85%), amino acid residues. Based on the secondary structure predictions, 36.58% of α- helices, 0.00% 3_{10} helix, 18.75% B-turn, and 16.51% contributed the overall helical conformation of Bamboo rhizome coding gene.

Amino acid composition analysis of Ginger rhizome protein showed 49.4% of hydrophobic (Gly, 8.21%, Ala, 8.00%; Val, 6.95%; Leu 6.74%; Ile 4.84%; Pro, 4.00%; Phe, 2.53%; Trp, 2.11%; Met, 1.05%) amino acid residues. Based on the secondary structure predictions, 6.25% of α- helices, 0.00% 3_{10} helix, 18.75% β-turn contributed the overall helical conformation of ginger rhizome coding gene.

From the amino acid composition, it was clear that the identified proteins are capable of forming α helices interconnected by loops. So, the protein can be classified under the helical protein category.

Citation: Dhanalakshmi T, Geethalakshmi S, Barathkumar S. *In silico* Characterization of Rhizome coding genes in Ginger and Bamboo. J Plant Sci Res. 2018;5(1): 177.

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1    ATG ACG CAA TTT GAT TTG GCT CTT ACT TGT TAC GAG AAA GCT GCA   45
1    Met Thr Gln Phe Asp Leu Ala Leu Thr Cys Tyr Glu Lys Ala Ala   15

46   TTG GAG AGA CCA TTG TAT GCC GAA GCT TAT TGC AAC ATG GGA GTT   90
16   Leu Glu Arg Pro Leu Tyr Ala Glu Ala Tyr Cys Asn Met Gly Val   30

91   ATT TAC AAG AGT CGG GGA GAG CTA GAA GCA GCA ATT GCC TGT TAC   135
31   Ile Tyr Lys Ser Arg Gly Glu Leu Glu Ala Ala Ile Ala Cys Tyr   45

136  GAG AGG TGC TTG ACT ATT TCC CCA AAC TTT GAG ATT GCT AAG AAC   180
46   Glu Arg Cys Leu Thr Ile Ser Pro Asn Phe Glu Ile Ala Lys Asn   60

181  AAC ATG GCA ATA GTG CTA ACC GAC TTG GGT ACA AAG GTA AAA ATT   225
61   Asn Met Ala Ile Val Leu Thr Asp Leu Gly Thr Lys Val Lys Ile   75

226  GAA GGT GAC ATC AAT CAA GGA GTG GCG TAT TAC AAG AAA GCT CTG   270
76   Glu Gly Asp Ile Asn Gln Gly Val Ala Tyr Tyr Lys Lys Ala Leu   90

271  TTC TAC AAT TGG CAT TAT GCT GAT GCC ATG TAT AAT CTT GGC GTT   315
91   Phe Tyr Asn Trp His Tyr Ala Asp Ala Met Tyr Asn Leu Gly Val   105

316  GCG TAT GGT GAA ATG CTG AAT TTT GAG ATG GCT ATT GTT TTT TAC   360
106  Ala Tyr Gly Glu Met Leu Asn Phe Glu Met Ala Ile Val Phe Tyr   120

361  GAG CTT GCT CTG CAC TTT AAT CCT CGC TGT GCG GAG GCG TGC AAC   405
121  Glu Leu Ala Leu His Phe Asn Pro Arg Cys Ala Glu Ala Cys Asn   135

406  AGC CTG GGA GTA ATA TAC AAG GAT AGG GAT AAT CTT GAC AAA GCT   450
136  Ser Leu Gly Val Ile Tyr Lys Asp Arg Asp Asn Leu Asp Lys Ala   150

451  GTC GAA TGT TAT CTA TTG GCC TTG TCA ATT AAA CCA AGC TTC TCT   495
151  Val Glu Cys Tyr Leu Leu Ala Leu Ser Ile Lys Pro Ser Phe Ser   165

496  CAG TCA TTG AAT AAC CTT GGA GTT GTC TAT ACT GTT CAG GGT AAG   540
166  Gln Ser Leu Asn Asn Leu Gly Val Val Tyr Thr Val Gln Gly Lys   180

541  ATG GAT GCT GCT GCA AGC ATG ATT GAG AAG GCC ATA ATT GCG AAT   585
181  Met Asp Ala Ala Ala Ser Met Ile Glu Lys Ala Ile Ile Ala Asn   195

586  CCC ACG TAT GCT GAA GCA TAT AAT AAC TTA GGT GTT CTT TAC AGA   630
196  Pro Thr Tyr Ala Glu Ala Tyr Asn Asn Leu Gly Val Leu Tyr Arg   210

631  GAT GCA GGG AGT ATT ACT TTA GCT GTA CAG GCT TAT GAG AGA TGC   675
211  Asp Ala Gly Ser Ile Thr Leu Ala Val Gln Ala Tyr Glu Arg Cys   225

676  CTA CAA ATT GAT CCT GAT TCA CGA AAT GCC GGT CAG AAT CGT TTA   720
226  Leu Gln Ile Asp Pro Asp Ser Arg Asn Ala Gly Gln Asn Arg Leu   240

721  CTT GCA ATG AAC TAT ATT GAT GAG GGC TCA GAT GAC AAA CTT TAT   765
241  Leu Ala Met Asn Tyr Ile Asp Glu Gly Ser Asp Asp Lys Leu Tyr   255

766  GAA GCT CAC AGG GAG TGG GGG GAG CGC TTT ATG AAA TTG TGT CCA   810
256  Glu Ala His Arg Glu Trp Gly Glu Arg Phe Met Lys Leu Cys Pro   270

811  CAG TAT ACT ACT TGG GAT AAC TCA AAA GTC GCT GAT CGT CCG CTG   855
271  Gln Tyr Thr Thr Trp Asp Asn Ser Lys Val Ala Asp Arg Pro Leu   285

856  GTT ATC GGC TAC GTC TCT CCT GAT TAC TTT ACT CAC TCT GTG TCA   900
286  Val Ile Gly Tyr Val Ser Pro Asp Tyr Phe Thr His Ser Val Ser   300

901  TAC TTC ATT GAA GCT CCC CTT ACA CAC CAT GAC TAC ACA AAT TAC   945
301  Tyr Phe Ile Glu Ala Pro Leu Thr His His Asp Tyr Thr Asn Tyr   315

946  AAG GTG GTT GTC TAT TCT GGT GTT GTG AAG GCA GAT GCC AAG ACC   990
316  Lys Val Val Val Tyr Ser Gly Val Val Lys Ala Asp Ala Lys Thr   330

991  CTT CGG TTC AAG GAT AAG GTG TTA AAA AAG GGT GGA TTG TGG AGA   1035
331  Leu Arg Phe Lys Asp Lys Val Leu Lys Lys Gly Gly Leu Trp Arg   345

1036 GAT ATA TAT GGT ATT GAT GAA AAG AAG GTT GCT AGC TTG GTG AGA   1080
346  Asp Ile Tyr Gly Ile Asp Glu Lys Lys Val Ala Ser Leu Val Arg   360

1081 GAG GAT AAA GTG GAC ATA CTT GTG GAA CTT ACT GGC CAT ACG GCA   1125
361  Glu Asp Lys Val Asp Ile Leu Val Glu Leu Thr Gly His Thr Ala   375

1126 AAT AAT AAG TTA GGA ACA ATG GCA CGC CGG CCT GCT CCT ATT CAG   1170
376  Asn Asn Lys Leu Gly Thr Met Ala Arg Arg Pro Ala Pro Ile Gln   390

1171 GTT ACC TGG ATT GGT TAC CCT AAT ACG ACA GGT TTG CCA ACA ATT   1215
391  Val Thr Trp Ile Gly Tyr Pro Asn Thr Thr Gly Leu Pro Thr Ile   405

1216 GAC TAC CGA ATA ACG GAT TCA TTC GCT GAC CCA CCT AAT ACA AAC   1260
406  Asp Tyr Arg Ile Thr Asp Ser Phe Ala Asp Pro Pro Asn Thr Asn   420

1261 CAA AAG CAT GTT GAA GAG TTG GTG CGT CTT CCC GAA AGC TTT CTT   1305
421  Gln Lys His Val Glu Glu Leu Val Arg Leu Pro Glu Ser Phe Leu   435

1306 TGC TAC ACT CCT TCC CCA GAA GCT GGG CCA GTT TGT CCA ACG CCA   1350
436  Cys Tyr Thr Pro Ser Pro Glu Ala Gly Pro Val Cys Pro Thr Pro   450

1351 GCA ATT TCA AAT GGT TTC ATC ACA TTT GGG AGT TTT AAC AAT CTA   1395
451  Ala Ile Ser Asn Gly Phe Ile Thr Phe Gly Ser Phe Asn Asn Leu   465

1396 GCA AAG ATT ACA CCA AAA GTA TTG CAA GTT TGG GCC AGA ATT TTA   1440
466  Ala Lys Ile Thr Pro Lys Val Leu Gln Val Trp Ala Arg Ile Leu   480

1441 TGT GCG GTC CCT AAC TCG CGG CTT GTG GTT AAG TGT AAG CCA TTC   1485
481  Cys Ala Val Pro Asn Ser Arg Leu Val Val Lys Cys Lys Pro Phe   495

1486 TGC TGT GAC AGT ATC AGA CAG AAA TTT TTA TCA ACA TTG GAG GAG   1530
496  Cys Cys Asp Ser Ile Arg Gln Lys Phe Leu Ser Thr Leu Glu Glu   510

1531 TTG GGT TCG GAG TCA TTA CGA GTT GAT TTG CTG CCA CTC ATC CAT   1575
511  Leu Gly Ser Glu Ser Leu Arg Val Asp Leu Leu Pro Leu Ile His   525

1576 CTC AAC CAT GAT CAC ATG CAA GCA TAT TCC TTA ATG GAC ATC AGC   1620
526  Leu Asn His Asp His Met Gln Ala Tyr Ser Leu Met Asp Ile Ser   540

1621 CTG GAT ACG TTT CCG TAT GCT GGA ACT ACC ACG ACA TGT GAA TCT   1665
541  Leu Asp Thr Phe Pro Tyr Ala Gly Thr Thr Thr Thr Cys Glu Ser   555

1666 CTA TAC ATG GGG GTT CCA TGT GTT ACT ATG GCT GGT TCA GTC CAT   1710
556  Leu Tyr Met Gly Val Pro Cys Val Thr Met Ala Gly Ser Val His   570

1711 GGT CAT AAT GTC GGT GTT AGC CTA CTC ACT AAA GTT GGA TTG GGT   1755
571  Gly His Asn Val Gly Val Ser Leu Leu Thr Lys Val Gly Leu Gly   585

1756 AGG CTG GTT GCC AAA CCG GAG GAT GAA TAC ATT AGC TTA GCA TTG   1800
586  Arg Leu Val Ala Lys Pro Glu Asp Glu Tyr Ile Ser Leu Ala Leu   600

1801 GAT TTG GCG TCA GAC GTC ACT GCC TTA CTA GAA CTG AGA ATG AGC   1845
601  Asp Leu Ala Ser Asp Val Thr Ala Leu Leu Glu Leu Arg Met Ser   615

1846 CTC CGA AAG CTG ATG ATC AAA TCA TCA GTC TGT GAC GGA GAG AAT   1890
616  Leu Arg Lys Leu Met Ile Lys Ser Ser Val Cys Asp Gly Glu Asn   630

1891 TTC ACA CGT GGC CTG GAA TCT GCA TAC AGA AAC ATG TGG TGC AGG   1935
631  Phe Thr Arg Gly Leu Glu Ser Ala Tyr Arg Asn Met Trp Cys Arg   645

1936 TAC TGT GAT GGG GAT GCA CCA GCT CTG AGG CGC TTA GAA GTG TTA   1980
646  Tyr Cys Asp Gly Asp Ala Pro Ala Leu Arg Arg Leu Glu Val Leu   660

1981 CAG GAA CAG CCA GGC TCC AAT AAG CAA GAC ACG GAA AAG ATG GCC   2025
661  Gln Glu Gln Pro Gly Ser Asn Lys Gln Asp Thr Glu Lys Met Ala   675

2026 GTG AAG CTT GCT GAT CTG AAA GCA CAG AGA GCG AGT ACC ACG GTG   2070
676  Val Lys Leu Ala Asp Leu Lys Ala Gln Arg Ala Ser Thr Thr Val   690

2071 GAG GAA GAT AAG CAG GCC CCA GTA ATG GCG AAT GCC ACG GTG GAG   2115
691  Glu Glu Asp Lys Gln Ala Pro Val Met Ala Asn Ala Thr Val Glu   705

2116 GAA GAT AAG CAG GGC CCA GTA ATG GCG AAC GGT GTG AGT TCA CCC   2160
706  Glu Asp Lys Gln Gly Pro Val Met Ala Asn Gly Val Ser Ser Pro   720

2161 GAT TCT TCC GCT TCT GGC AGA TGT GAA GCA AAT GGG CAT AGC AGC   2205
721  Asp Ser Ser Ala Ser Gly Arg Cys Glu Ala Asn Gly His Ser Ser   735

2206 CGA TGA   2211
736  Arg End   737
```

Figure 1a: Nucleotide and protein sequence of the rhizome coding gene of Bamboo.

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1     ATG GCC AGG AAC CTA CTG ACG AAC GGT GAA GGA CTC TAC GCA GGC   45
1     Met Ala Arg Asn Leu Leu Thr Asn Gly Glu Gly Leu Tyr Ala Gly   15

46    CAA TCA CTG GAT GTA GAA CAA TAC AAG TTT ATA ATG CAG GAT GAC   90
16    Gln Ser Leu Asp Val Glu Gln Tyr Lys Phe Ile Met Gln Asp Asp   30

91    TGC AAC CTC GTG CTG TAC GAA TAC AGC ACC CCC ATC TGG GCC TCT   135
31    Cys Asn Leu Val Leu Tyr Glu Tyr Ser Thr Pro Ile Trp Ala Ser   45

136   AAC ACC GGT GTC ACC GGC AAA AAC GGG TGC AGG GCT GTC ATG CAG   180
46    Asn Thr Gly Val Thr Gly Lys Asn Gly Cys Arg Ala Val Met Gln   60

181   AGG GAT GGC AAC TTT GTG GTC TAC GAT GTT AAC GGA CGT CCC GTC   225
61    Arg Asp Gly Asn Phe Val Val Tyr Asp Val Asn Gly Arg Pro Val   75

226   TGG GCC AGT AAC AGT GTA AGA GGG AAC GGG AAC TAT ATC CTG GTG   270
76    Trp Ala Ser Asn Ser Val Arg Gly Asn Gly Asn Tyr Ile Leu Val   90

271   CTT CAG AAG GAC AGG AAC GTT GTC ATT TAC GGA TCT GAT ATT TGG   315
91    Leu Gln Lys Asp Arg Asn Val Val Ile Tyr Gly Ser Asp Ile Trp   105

316   TCT ACT GGT ACC TAC AGA AGA TAG   339
106   Ser Thr Gly Thr Tyr Arg Arg End   113
```

Figure 1b: Nucleotide and protein sequence of the rhizome coding gene of Ginger.

Table 1: Nucleotide composition of rhizome coding genes.

Gene	Rhizome coding gene of Bamboo		Rhizome coding gene of Ginger	
Nucleotide	Number	Mol%	Number	Mol%
A	783	28.31	94	27.73
C	544	19.67	77	22.71
G	701	25.34	94	27.73
T	738	26.68	74	21.83

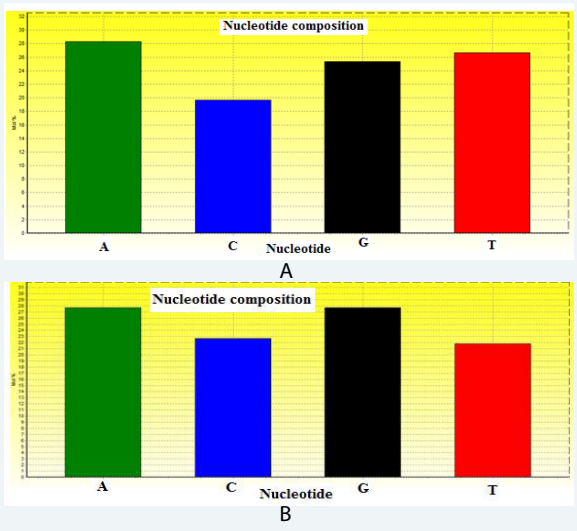

Figure 2: a) Diagrammatic representation of nucleotide composition in rhizome coding gene of Ginger. **b)** Diagrammatic representation of nucleotide composition in rhizome coding gene of Bamboo.

Table 2a: Amino acid composition of rhizome coding gene in Bamboo.

Aminoacid	Number	Molecule
Ala A	68	9.24
Cys C	21	2.85
Asp D	43	9.24
Glu E	45	2.85
Phe F	20	5.84
Gly G	43	6.11
His H	14	2.72
Ile I	34	5.84
Lys K	42	1.90
Leu L	74	4.62
Met M	21	5.71
Asn N	38	10.05
Pro P	34	2.85
Gln Q	19	5.16
Arg R	34	4.62
Ser S	47	6.39
Thr T	41	5.57
Val V	53	7.20
Trp W	7	0.95
Tyr Y	38	5.16

Table 2b: Amino acid composition of rhizome coding gene in Ginger.

Amino Acid	Number	Mol%
Ala A	38	8.00
Cys C	21	4.42
Asp D	21	4.42
Glu E	27	5.68
Phe F	12	2.53
Gly G	39	8.21
His H	9	1.89
Ile I	23	4.84
Lys K	15	3.16
Leu L	32	6.74
Met M	5	1.05
Asn N	35	7.37
Pro P	19	4.00
Gln Q	12	2.53
Arg R	29	6.11
Ser S	50	10.53
Thr T	24	5.05
Val V	33	6.95
Trp W	10	2.11
Tyr Y	21	4.42

Prosite analysis

Prosite analysis of test protein sequence of rhizome coding gene in bamboo and ginger revealed the presence of two domains:

(a) Six TPR domains which is Tetratricopeptide Repeat (TPRs) (Figure 4a), a degenerate 34-amino acid repeated motif that is widespread among all organisms. In the cell, TPR containing proteins are localized in a variety of subcellular compartment, including the nucleus, the cytoplasm and mitochondria. Processes involving TPR proteins include cell-cycle control, transcription repression, stress response, protein kinase inhibition, mitochondrial and peroxisomal protein transport and neurogenesis. TPR repeats mediate protein-protein interactions and the assembly of multiprotein complexes. The smallest functional unit that is widely used appears to be three tandem-TPR motifs

(b) Bulb Lectin super-family domain (Figure 4b) which occurs commonly in *Amaryllidaceae*, *Orchidaceae* and *Aliaceae*. The domain contained a ~115-residue-long domain whose overall three dimensional fold is very similar to that of

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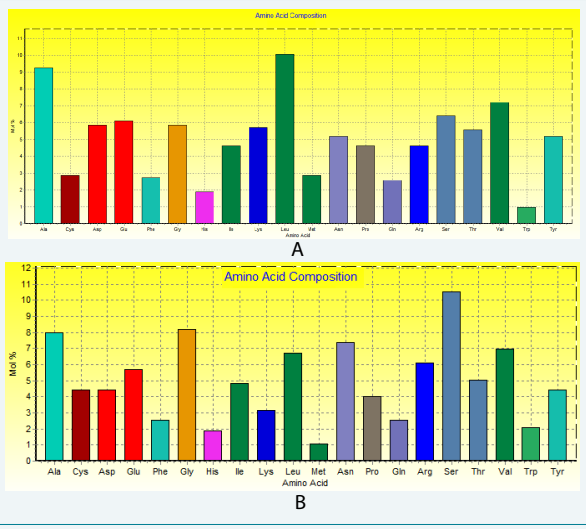

Figure 3: a) Diagrammatic representation of amino acids composition rhizome coding gene in Bamboo. **b)** Diagrammatic representation of amino acids composition present in test rhizome coding gene in Ginger.

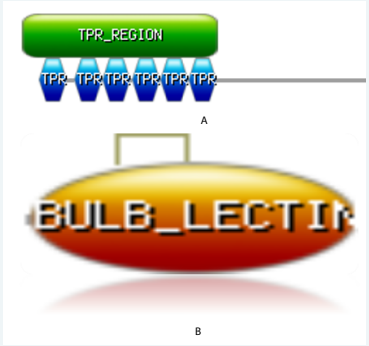

Figure 4: a) Prosite analysis of the rhizome protein indicating the presence of TRP domain. **b)** Prosite analysis of the rhizome protein indicating the presence of Bulb Lectin Domain.

- Dictyostelium discoideum comitin, an actin binding protein,
- Curculigo latifolia curculin, a sweet tasting and taste-modifying protein.

Although this domain is a mannose-binding lectin in the bulb super-family, curculin is considered as a non-functional mannose-binding protein devoid of mannose-binding activity.

Secondary structure prediction

For the secondary structure analysis of bamboo rhizome, SOPMA tool was used. The results revealed that the identified protein was predominantly ɑ-helical protein, which mainly consisted of ɑ -helices (41.17%) and random coils (29.62%), extended stand (20.65%) (Figure 5a).

Similarly, SOPMA analysis of ginger rhizome gene revealed that was predominantly ɑ-helical protein, which mainly consisted of ɑ -helices (26.74%) and random coils (39.62%), extended stand (22.53%) (Figure 5b). The secondary structure prediction is in line with the amino acid composition analyzed.

Three dimensional structure of rhizome coding genes

The quality of the model generated was checked by ProSA, PROCHECK and Verify-3D and Ramachandran plot was constructed (Figure 6a and 6b). The R-plot indicated that 75% of the input residues were present in the most favourable region, 17.8% in additional allowed region and 6.7% in generously allowed region. Only one residue (0.5%) was present in disallowed region indicating the overall stereo chemical stability of the predicted structure. PROCHECK, Verify-3D and ERRAT results also confirmed the stability and reliability of the predicted 3D structure (Figure 7a and 7b). From this result, it is clear that the protein is highly stable with stabilized three dimensional structure which is highly hydrophilic in nature encompassing helical domain, which is the major domain which contributes to the function of the protein.

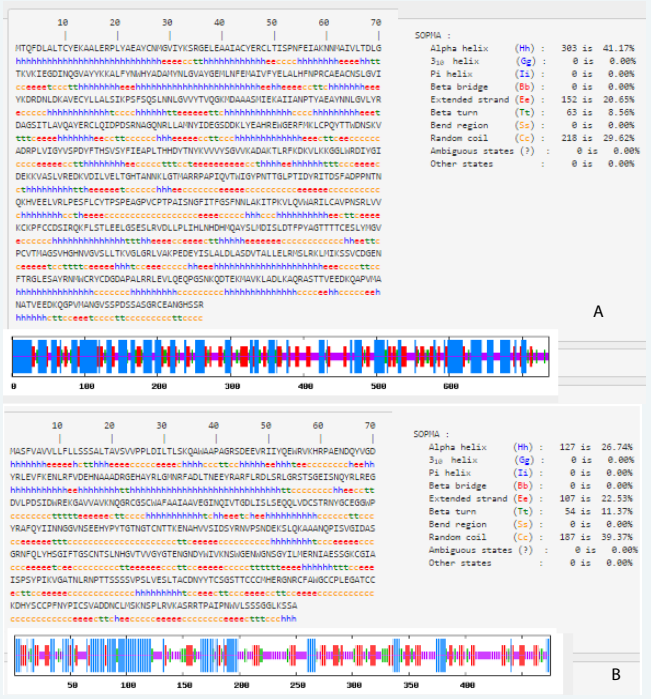

Figure 5: a) Secondary structure of rhizome coding gene of Bamboo. **b)** Secondary structure of rhizome coding gene of Ginger.

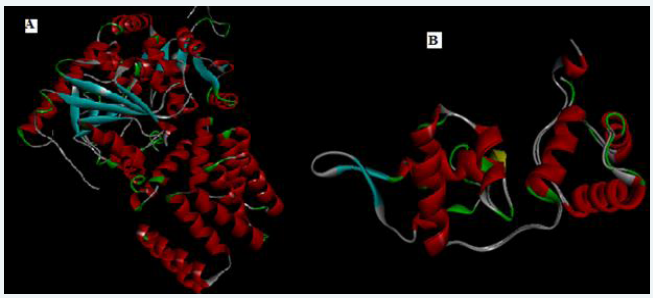

Figure 6: Three dimensional structure of test Rhizome coding gene of (a) Bamboo and (b) Ginger.

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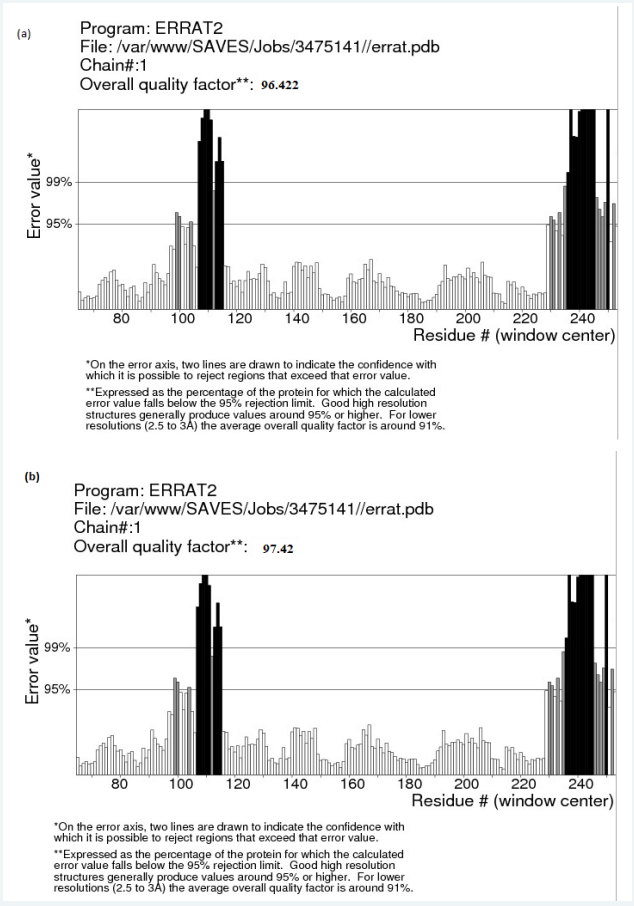

Figure 7: ERRAT analysis of predicted 3D structure of test Rhizome coding gene of (a) Bamboo and (b) Ginger.

Summary

Rhizome families are well-known for its medicinal and economic significances. Many species are used as sources of indigenous medicines, vegetables, food flavours, spices, dyes, condiments as well as ornamentals. This family is widely known for its broad range of pharmacological activities [15]. To study on its compounds offers many opportunities to investigate the various functions and prospects in various pharmaceutical studies. The present study forms the basis for understanding the structure of rhizome coding gene's structure from its sequence level; it will become more evident about its potential from the bioactivities, in reviewing sequence to structure to functions in wide group of rhizome families. Detailed study of the functional role of rhizome coding protein may be utilized for regeneration and protection of RET plants.

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