Molecular Cloning and Characterization of a Cyclotide Gene Family in Viola modesta Fenzl

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ABSTRACT

Cyclotides are small disulfide-rich proteins that have the unusual feature of a cyclic backbone. Cyclotides have a range of interesting biological activities and are found in a variety of tropical plants from the Rubiaceae, Violaceae, Cucurbitaceae and Fabaceae families. We have cloned and characterized cyclotides in Viola modesta, a Viola species native to western Asia, which was collected from the Kurdistan Province of Iran. Fifteen cyclotide sequences were obtained using homology based PCR strategy. Sequence analysis showed that 14 of them had continued open reading frames and showed high level of similarity to cyclotide genes from other species of the Violaceae. After analyzing the full endoplasmic reticulum signals of V. modesta cyclotides, two conserved sequences, AAFALPA and ATAFALP, were detected. Analysis of isolated cyclotide sequences showed that they all belonged to bracelet family and were separated into two subclasses. Phylogenetic analysis of cyclotide genes from V. modesta and other Viola species revealed that most V. modesta genes showed close relationship with their homologs from the Violaceae, while the V. modesta genes formed two separate clades. Transcription analysis by semi-quantitative RT-PCR revealed that Vmcyc1 and Vmcyc7 were differentially expressed in all tested tissues including roots, stems, leaves, flowers, seeds, peduncles, and capsules with the highest transcript level in the capsules.

Keywords: Bracelet cyclotides, Phylogeny, RT-PCR, Sequences, 3’RACE.

INTRODUCTION

Cyclotides are a family of circular plant proteins containing approximately 30 amino acids (Craik et al., 1999). Their N-terminal and C-terminal are connected via an amide bond that results in a circular peptide backbone. Cyclotides have six cysteine residues that each two cysteines linked by a disulphide bond. Combining three disulphide bonds and cyclic structure define the Cyclic Cysteine Knot (CCK) motif (Herrmann et al., 2006). The CCK motif is responsible for the cyclotides extraordinary stability against chemical and thermal degradation (Herrmann et al., 2008). Cyclotides are responsible for a range of biological activities including anti-HIV, uterotonic, antimicrobial, hemolytic, cytotoxic, neurotensin antagonistic, antifouling, and pesticide (Craik, 2012).

The cyclotide proteins fall into two major families including Mobius and bracelet. The Mobius cyclotides contain a cis-pro peptide bond in loop 5, which creates a twist in the peptide backbone (Herrmann et al., 2006). Most Mobius cyclotides are slightly negatively charged or have an overall net-charge of zero, while bracelet cyclotides are usually positively charged. Bracelet cyclotides are more
abundant, since, until now, the majority (~70%) of more than 200 published cyclotide sequences accessible on CyBase (Wang et al., 2008) belong to this subfamily.

Analysis of cyclotide precursor sequences show that genes encoding them consist of an Endoplasmic Reticulum (ER) signal domain, a pro-region and one to three mature cyclotide domains, each preceded by a N-Terminal Repeat (NTR) sequence (Zhang et al., 2009). The NTR and cyclotide regions can be repeated up to three times in different precursors, encoding different or identical cyclotides (Burman et al., 2010). It has been suggested that an asparaginyl-endoproteinase is involved in cleavage of the C-terminal tail and simultaneous cyclization of the cyclotide. Details of the processing of the precursors, including the order of the events, are not fully understood, but they mostly mediate through the oxidative folding, excision of the mature cyclotide sequence, and head-to-tail cyclization.

More than 198 cyclotides have been discovered from 36 species in the Violaceae, Rubiaceae, Cucurbitaceae, and Fabaceae and cyclotide-like genes in Poaceae plant families (Gerlach and Mondal, 2012). Most of sequenced cyclotides have been isolated from species of the Violaceae. The Violaceae family contains around 23 genera and 800 species of cosmopolitan shrubs, herbs, and rare trees (Gerlach and Mondal, 2012). Within the Violaceae, cyclotides seem to be widely distributed, but the cyclotide complements of the vast majority of Violaceae species have not yet been fully explored. Cyclotide genes have been isolated from V. arvensis (Mulvenna et al., 2005), V. odorata (Dutton et al., 2004), V. biflora (Herrmann et al., 2008), Hybantus floribundus (Simonsen et al., 2005) and V. baoshanensis (Zhang et al., 2009).

Viola modesta Fenzl, also known as V. ebracteolata Fenzl or V. modestula Klokov, is an annual viola species native to Iran, Iraq, Israel, Jordan, Lebanon, Syria, Turkey and Turkmenistan. V. modesta is a diploid plant with chromosome number (2n=2x=4) in an annual species with the lowest chromosome number so far known for a vascular plant (Erben, 1996). V. modesta is mainly distributed in the west of Iran, Kurdistan Province. It is naturally rare and has a patchy distribution.

In the present study, we aimed to describe the cyclotide genes isolated via homology based PCR strategy from V. modesta, and their expression patterns in various tissues.

MATERIALS AND METHODS

Plant Materials

Viola modesta Fenzl was collected from Greize Research Station, Sanandaj, Iran, in May 2010. Plant organs including roots, stems, leaves, flowers, seeds, peduncles, and capsules were harvested and immediately immersed in liquid nitrogen for RNA extraction.

Extraction of RNA and cDNA Synthesis

RNA was extracted from different tissues via Mazzara Protocol (Mazzara and James, 2000). The concentration and integrity of isolated RNA were determined by spectrophotometer and 1.5% agarose gel electrophoresis and stored at −70°C. The first-strand cDNA was synthesized with 4 µg total RNA in 20 µL reaction volume using first strand cDNA synthesis Kit according to the manufacturer’s instruction (Fermentas). Total RNA (1 µg) was treated by DNase1, RNase-free kit (Fermentas). After DNA digestion, the RNA samples were first heated (65°C, 5 minutes) to inactivate the DNase I and avoid RNA secondary structures, and then immediately cooled in ice water.

Isolation of 3' end by RACE

An alignment using CLUSTALW was made of cyclotide genes from Viola biflora; EU046618.1, EU046619.1, EU046621.1, EU046622.1, EU046623.1, that were obtained
from NCBI. A forward primer was designed from conserved regions AAFALPA, SF1, 5' GATTCCAAGATTGTGTGTTTAGCC. Another primer, ATGAAGATGTTTGTTGCCCTT, was designed based on Mobius genes, Vbc7c, Vbc6c, Vbc6d, Vbc6, Vbc7, Vbc7b and Vbc5 From V. baoshanensis to amplify a second class of cyclotides in V. modesta. First strand cDNA for 3'RACE was synthesized through reverse transcription with 3' CDS (5' GACCACGCGTATCGATGTCGACTTTTTTT3') as anchor primer using first strand cDNA synthesis Kit. The first round PCR reaction was carried out in a total volume of 25 µL including 8 µL H2O, 12 Master Mix, 2 µL First strand cDNA template, 1.5 µL SF1, 1.5 µL PCR anchor primer (GACCACGCGTATCGATGTCGAC). PCR temperature program was 1 cycle of 5 minutes at 94°C, 35 cycles of 30 seconds at 94°C, 30 seconds at 53°C, 40 seconds at 72°C, 1 cycle of 20 minutes at 72°C. The resulting PCR product was separated on 1% agarose gels.

**Molecular Cloning and DNA Sequencing**

PCR products were separated on 1.0% agarose gels and the expected fragments were purified from the gels using Nucleic Acid Extraction Kit (Vivantis). The concentration of purified DNA was determined by spectrophotometer, then, DNA fragments were ligated into the TA vector using TA cloning kit (Fermentas) and transformed into competent cells of Escherichia coli DH5a strain. Positive clones were identified by colony PCR, and independent sequences per clone were obtained from a commercial sequencing service (Bioneer Inc. Bioneer Corporation).

**Bioinformatics Analysis**

BLAST program in National Center for Biotechnology Information Server (http://www.ncbi.nlm.nih.gov) was used to verify the cyclotide gene homology. Multiple protein sequence alignment was performed using Clustal W program of Jalview 2.3 version. For phylogenetic and sequence alignment analysis, other cyclotide gene sequences were obtained from the GenBank database (Table 1). The phylogenetic tree of cyclotides was constructed using MEGA4.0.2 software based on the Neighbor-Joining (NJ) Method. Theoretical isoelectric point and mass values for the protein was predicted using ExPASy ProtParam tool (http://us.expasy.org/tools/protparam.html). The 3D structures of two cyclotide Vmcyc1 and Vbc1 (Viola biflora cyclotide 1) were obtained using internet http://swissmodel.expasy.org. The ER signals were predicted using signalP3.0 (Bendtsen et al., 2004).

**Gene Expression Analysis**

For gene expression analysis, roots, stems, leaves, flowers, seeds, peduncles, and capsules of V. modesta were harvested and immediately immersed in liquid nitrogen for RNA extraction. Total RNA was extracted and treated with DNase 1 (DNaseI, RNase-free Fermentas) to exclude the DNA contamination. The first-strand cDNA used as template was synthesized with 4 µg total RNA in 20 µL reaction volume using first strand cDNA synthesis Kit (Fermentas). Cyclotide genes obtained from V. modesta were divided into cluster. For expression analysis, Vmcyc1 and Vmcyc2 were selected and specific primer pairs were designed using primer blast. Vmcyc1 gene fragments was amplified using specific forward primer VmcycF1 (5'GCAGTACTCCTTGTTGGAGAGA3'), and antisense primer Vmcyc R1 (5'AGACAAAGACAACTTCTTCCACA3'). Vmcyc7 fragments was also amplified using specific sense forward primer VmcycF7 (5'ATCTGCACCACACTCAAACATC3')
Table 1. Cyclotide amino acid sequences used in this study.

<table>
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<th>Cyclotide name</th>
<th>Source</th>
<th>Accession Number*</th>
<th>Total Nucleotide bp</th>
<th>Molecular weight (Kd)</th>
<th>Isoelecteric point</th>
<th>Total Amino acid</th>
<th>Cyclotide group</th>
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and antisense primer VmcycF7 (5’GATAAGAAAGAGATGCGAATAGA3’). Tubulin gene fragment from Viola cornuta (GenBank accession number AY294027.1) was amplified as housekeeping gene for normalization using the sense primer TubF, (5’GAGGTTTTGTGGAGCTCTTAATG3’) and antisense primer TubR (5’GGTGGAAATTGGAGATCATGCA3’). The PCR reaction system including 11.5 µL.
H₂O, 12.5 µL 2×Master mix (Fermentas, USA), 1 µL sense primer, 1 µL antisense primer, 1 µL template cDNA. The PCR condition was as follows: 5 min pre-amplification at 94°C, 26 cycles of 30 seconds at 94°C, 40 seconds at 52°C, 1 minute and 30 seconds at 72°C, a final extension of 10 minutes at 72°C. The resulting PCR products were separated on 1% agarose gels. Independent experiment was repeated at least three times with the similar results.

RESULTS

Isolation and Sequence Analysis of Vmcyc Genes

Based on the combination of five Viola biflora Expressed Sequence Tags (ESTs), EU046618.1, EU046619.1, EU046621.1, EU046622.1, EU046623.1, and designing forward primers a band of the predicted size (~500 bp) was observed after PCR amplification with the cDNA synthesized from total RNA extracted from whole plant tissues as a template.

These expected fragments were excised from agarose gel and cloned into the plasmid vector (TA cloning, Fermentas). Positive clones were picked and used for screening. Twenty unique clones were chosen for DNA sequencing, of which 14 clones contained the primer sites. BLAST analysis against GenBank database revealed that the 14 genes were highly homologous to cyclotide genes (Table 1). Conceptual translations of the above 14 sequences revealed the presence of premature stop codons in six clones.

The sequences named as Vmcyc were regarded as cyclotide genes by the presence of continued Open Reading Frame (ORF) and by the characteristics of the motifs such as six cysteines and AAFALPA motif (Figure 1). For these 14 sequences, nucleotide identity among each clone pair was determined. The identity ranged from 54-99%, with the highest identity between Vmcyc7, Vmcyc5, and Vmcyc10, Vmcyc70. BLAST analysis of the V. modesta cyclotide genes against GenBank database revealed that they were homologous to cyclotides gene in Violaceae with E-values 5e⁻⁹⁹< e×10.

Two types of conserved sequences were observed from the ER signals of cyclotide genes of V. modesta. Including ATFLPS (F) and AAFALPA (Figure 1). After sequence alignment and cluster analysis, 14 unique cyclotide sequences were identified and denoted Vmcyc1, 3, 4, 5, 7, 8, 9, 10, 11, 12, 16, 17, 40, and 70 (Table 1). Vmcyc5, 7, 40, 10, 11, and 70 starts with ATFLPS (F) and mature cyclotide in these cyclotides start with GIP (Vmcyc5, 7, 40) and VNG (Vmcyc10, 11, 70), while Vmcyc17, 12, 9, 8, 16, 1, 4, 3 start with AAFALPA and mature cyclotide in these cyclotides start with GGT and GGS (just in Vmcyc1).

Most of V. modesta cyclotides were similar to V. odorata cyclotides (Voc1 and Voc3), except for Vmcyc11 and Vmcyc3 that were more similar to V. biflora cyclotide (vbc.3). The highest identity percentage was observed between V. modesta cyclotide Vmcyc7 and Vmcyc70 with Vmcyc5 and Vmcyc10 (99%), respectively. The smallest identity was observed between Vmcyc40 with Vmcyc4 and Vmcyc1 (54%).

When nucleotide sequences were translated to amino acid sequences, different parts of cyclotide protein were defined (6 cysteines and AAFALPA sequence). Alignment of predicted cyclotide precursors from V. modesta showed that the cyclotide precursors had the overall arrangement in common with previously known cyclotide proteins from other Violaceae family (Figure 1). The cyclotide precursors consisted of an Endoplasmic Reticulum (ER) signal peptide which was 10 bp, similar to previously known cyclotides. N-Terminal ProPeptide (NTPP) was made of N-Terminal ProDomain (NTPD) and N-Terminal Repeat (NTR) and had 19-23 bp length. The mature cyclotide domain was 28-30 bp and a tail region in its C terminus 3-4 bp. The cystine knot motif present in the cyclotides coupled to the head to tail cyclic backbone is a
Figure 1. Violaceae cyclotides amino acid alignment, alignment of predicted cyclotide precursors from *V. modesta* and other viola species. These precursors have the overall arrangement in common with previously known CPs. ER signals were predicted using signalP3.0 (Bendtsen et al., 2004). The Genbank accession numbers of *Viola* species are in Table 1.
unique motif called Cyclic Cystine Knot (CCK), which gives thermal, enzymatic, and chemical stability (Craik et al., 2001). The conserved residues across all bracelets are six Cys residues making up cystine knot and some residues. An efficient way to describe and compare the features of cyclotides is by referring to the intercysteine loops, illustrated in Figure 2 as an amino acid incidence plot for the 15 new V. modesta sequences in sequence logo format. Conserved residues among sequences include Pro3, Cys4, Glu6, Cys8, Val9, Pro1, Cys13, Gly19, Cys20, Ser21, Cys22, Lys25, Val26, Cys27, Tyr28, and Lys29. According to the sequence logo plot, the greatest variations in loop size and/or composition are in loops 3 and 6.

A ribbon representation of the structure of Vmcyc11 (Viola modesta cyclotide 11) and Vbc1 (Viola baoshanensis cyclotide 1) are shown in Figure 3. Both proteins had similar structures and were in good agreement with the previous Viola cyclotides in terms of number and position of beta sheets.

**Phylogenetic Profile of V. modesta Cyclotide Genes**

Phylogenetic profile of V. modesta cyclotide genes was carried out using MEGA software. The phylogenetic tree showed that V. modesta cyclotide genes were separated into two distinct clades, consistent with the similarity based amino-acid sequence analysis as described previously (data not shown). Two

**Figure 2.** The pattern of conserved and variable parts as visualized by a sequence logo (V. modesta cyclotides and other database cyclotides). The cyclotide loops are shown (L1 to L6). The overall height of each stack of letters indicates the sequence conservation. While the height of each letter in a stack reflects the relative frequency of the corresponding amino acid.

**Figure 3.** Vmcyc11 (Viola modesta cyclotide 11) and Vbc1 (Viola baoshanensis cyclotide 1) structures. (http://swissmodel.expasy.org)
types of conserved sequences were observed from the ER signals of CPs, including ALVLIATFA and AAFALPA-LA. An evolutionary relationship among V. modesta cyclotide genes and other known cyclotide genes from Violaceae was further evaluated by phylogenetic analysis. Nucleotide sequences of V. modesta cyclotide genes were used as a query in BLASTn searches against GenBank database for possible homologues in other Viola species. A total of 30 Viola cyclotide genes from three Viola species in NCBI database in addition to 14 genes from the current study were used for phylogenetic analysis.

The phylogenetic tree indicated that Violaceae cyclotide genes were divided into two main subfamilies: the Mobius and bracelet (Figure 4). Most of cyclotides belong to bracelet subfamily. In this work, we designed two primers based on sequences from both subfamilies. However, all cyclotide genes obtained in this work belonged to bracelet subfamily. Cyclotide genes in bracelet subfamily distributed in six clades. V. modesta cyclotide genes were classified in two clades. Vmcyc5, Vmcyc10, Vmcyc70, Vmcyc7, Vmcyc40 and Vmcyc11 in one clade separate from other cyclotides. Vmcyc9, Vmcyc3, Vmcyc16, Vmcyc17, Vmcyc4, Vmcyc12, and Vmcyc8 were in another clade with Voc.1 (V. odorata cyclotide 1), Voc.2 (V. odorata cyclotide 2), Voc.3 (V. odorata cyclotide3), Vbc.3d (V. baoshanensis cyclotide 3d). The first group consisted of 98-100 residues and the ER-region contained a conserved sequence consisting of ATAFALP, while sequences in the other clade consisted of 104 residues and a conserved sequence consisting of AAFALP.

Cyclotide genes from different Viola species separated in one or two clades. These data suggested that the Vmcyc genes in Viola were ancient with multi-origins.

Expression Pattern of Vmcyc1 and Vmcyc7 in Different Tissues

Since V. modesta cyclotides were classified in two clades and cyclotides within each clade were very similar, we chose one cyclotide in each clade: Vmcyc1 and Vmcyc7. Specific primers were designed for each cyclotide. Since we did not have the sequence of any control gene from V. modesta, tubulin sequence from Ricinus communis Populus trichocarpa, V. cornuta, Lotus japonicas from the family Fabaceae were isolated and specific primers were designed. The isolated tubulin fragment showed the highest similarity with its ortholog gene in V. cornuta. Expression levels of the Vmcyc1 and vmcyc7 genes were examined in different tissues including roots, stems, leaves, flowers, seeds, peduncles, and capsules using quantitative reverse transcription-PCR. Normalization was carried out based on tubulin expression as housekeeping gene. Vmcyc1 expression in tissues was different (Figure 5). The highest transcript level was observed in peduncles and capsules, while the lowest transcript level was detected in leaves and flowers. The transcript level of Vmcyc7 was also differing in various tissues: the highest level was observed in flowers and capsules and the lowest in stems (Figure 6).

DISCUSSION

Cyclotides sequences have been isolated based on different methods including extraction of cyclotides protein using MS/MS, 2D NMR and screening a cDNA library or RT-PCR. Cyclotide precursor includes parts that is conserved and can be used for primer design. A degenerative forward primer encoding a conserved region (AAFALPA) of ER-signals in the Violaceae cyclotide proteins have been used as a powerful strategy for cloning of nearly full length precursors of cyclotide genes (Mulvenna et al., 2005; Simonsen et al., 2005). By screening a cDNA library of V. baoshanensis roots and using RACE and RT-PCR methods, 23 cDNA clones were identified (Zhang et al., 2009). Twelve cyclotides from two Panamanian species,
Figure 4. Phylogenetic tree of cyclotide precursors found in the Violaceae plant family. The bootstrap consensus tree was made by Mega4.0. Numbers next to the nodes give bootstrap values. The tree comprises all already reported cyclotide precursor sequences, and *V. modesta* cyclotides (Table 1).
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Gloeospermum pauciflorum Hekking and Gloeospermum blakeanum (Standl.) were characterized through cDNA screening (Burman et al., 2010). The sequences of 11 cyclotides, were determined by isolation and MS/MS sequencing of proteins and screening of a cDNA library of V. biflora in parallel (Herrmann et al., 2007). They used a degenerate primer against a conserved (AAFALPA) motif in the cyclotide precursor ER signal sequence, which yielded a series of predicted cyclotide sequences that were correlated to those of the isolated proteins. In this study, 14 cyclotide genes were identified by screening a V. modesta cDNA using 3’RACE. After analyzing the ER signal regions of these cyclotide genes, two conserved sequences were found, including ATFALPS (F) and AAFALPA with the last one incorporating a known conserved-region (AAFALPA). Conserved region ATFALPS (F) is most likely new and has not been reported yet in other Viola species.

Our first primer was based on conserved region (AAFALPA) which was found in both bracelet and Mobius precursors. All of cyclotide precursors of V. modesta belonged to bracelet subfamily. We used another primers based on AAFALPA-AFA conserved motif, which can amplify Mobius subfamily (Zhang et al., 2009), but still got the bracelet sequences. Other works also have shown that utilizing the AAFALPA primer (Simonsen et al., 2005; Herrmann et al., 2008) yields bracelet precursors. Of the 150 sequences found in the Cybase server (http://www.cybase.org.au), the majority of cyclotides (> 67%) belong to the bracelet subfamily (Simonsen et al., 2005). Most of cloned cyclotide using RACE and RT-PCR belonged to bracelet subfamily (Trabi and Criak 2004; Tang et al., 2010). No detection of Mobius cyclotide in V. modesta may be related to low expression of Mobius genes in tissues.

In this study, 14 bracelet cyclotides sequences were predicted from V. modesta. By constructing a phylogenetic tree combining cyclotides from Violaceae in NCBI database and the above predicted cyclotides, it is clear that these Violaceae cyclotides are classified in two clear classes, namely, bracelet and Mobius, consistent with previous observations that in general bracelet cyclotides are more common than Mobius cyclotides. Bracelets were further separated to six subclasses and V. modesta cyclotide genes were classified in two clades. The bracelets are the more structurally diverse compared to Mobius. In addition, the bracelet cyclotides are generally more cytotoxic than Möbius cyclotides (Lindholm et al., 2002; Svangard et al., 2004; Herrmann et al., 2008). Within the bracelet subfamily, it can be noted that

Figure 5. Relative RT-PCR of Vmcy7(a) Relative RT-PCR of Vmcy7(b) in V. modesta organs. mRNA were determined relative to that of Tubulin gene. Mean values are shown with standard error bars which were calculated based on three replications.

(a)  
(b)  

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cyclotides with several positive residues in loops 5 and 6 have higher activity than those lacking such residues (Burman et al., 2010).

Recent studies have shown that cyclotide expression varies in different tissues. The expression patterns analysis of cyclotides in various Viola species (Violaceae) showed tissue specificity (Trabi et al., 2004). For example, they have isolated a cyclotide which is only expressed in underground parts of V. hederaceae. Tissue dependent expression of cyclotide genes has been observed in VbCP1S-7S of V. baoshanensis, which indicates that cyclotide expression could be regulated at transcript level (Zhang et al., 2009). A leaf-specific cyclotide (vh1-1) isolated from V. hederaceae expressed 31-residue cyclotide (Chen et al., 2005). The high expression levels of cyclotide precursor transcripts were detected in Oldenlandia affinis leaf transcriptome (Qin et al., 2010). In total, 31 ESTs encoded cyclotide precursors, representing a distinct commitment of 2.8% of the transcriptome to cyclotide biosynthesis with the abundance of mature cyclic peptides in O. affinis. V. modesta cyclotides also showed tissue specific pattern. In addition, Vmcy1 and Vmcy2, which belong to two separate subclasses, were differentially expressed in different tissues.

Most of cyclotides discovered to date have shown wide bioactivities including insecticidal (Jennings et al., 2001), antimicrobial activities (Tam et al., 1999), anti-HIV (Chen et al., 2005), cytotoxic (Lindholm et al., 2002), hemolytic (Chen et al., 2006), neuropeptide antagonism (Witherup et al., 1994), uterotonic (Gran, 1973) and trypsin inhibitor (Hernandez et al., 2000). Also, the cyclotides are thought to be a valuable peptide-based template for drug design and agrochemical applications (Craik et al., 1999). V. modesta cyclotides showed significant homology to other known Violaceae cyclotides. More detailed analysis of these genes and finding promising candidates for genetic engineering purpose is needed. In addition, we have enriched the knowledge of the cyclotide family by characterizing novel cyclotides from this family.

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چکیده

سایکلتونایدها دسته ای از پیتیدهای حلقوی هستند که غنی از یاندهای دی سلفیدی می باشند. این پروتئین ها فعالیت‌های زیستی متنوعی دارند و در گیاهان مناطق گرم در خانواده های Violaceae، Cucurbitaceae و Fabaceae گزارش شده است. در این پژوهش ژن‌های کد کننده پروتئین‌های سایکلتوناید در گونه یومی آسیای غربی در استان کردستان ایران (Viola modesta) گونه توانایی داشته و در نهایت پس از تعبیه ۱۴ توالی‌های نوکلئوتیدی به دست آمده که با توالی موجود در پایگاه داده NCBI همتراز و مشخص شد توالی‌های به دست آمده سایکلتوناید Viola tumble به دست آمده در گروه بریست قرار گرفتند، سایکلتونایدهای گیاه بودند. سایکلتونایدهای به دست آمده در گروه بریست قرار گرفتند، سایکلتونایدهای گیاه

بر اساس رسم دندروگرام و مقایسه با سایر سایکلتونایدها، در گروه بریست به دو دسته Vmcyc1 و Vmcyc7 تشکیل شدند. بین دو سایکلتوناید Vmcyc1 و Vmcyc7 به عنوان نماینده از ۱۴ سایکلتوناید به دست آمده از Viola Viola modesta Viola modesta مشخص شد که Vmcyc7 در همه اندازه‌ها بیان شد و بین Vmcyc7 و Vmcyc1 مشخص بود که Vmcyc7 در کسپول و محور گل بیشترین میزان بیان و در گل کمترین میزان بیان را داشت.