

Supplementary Materials

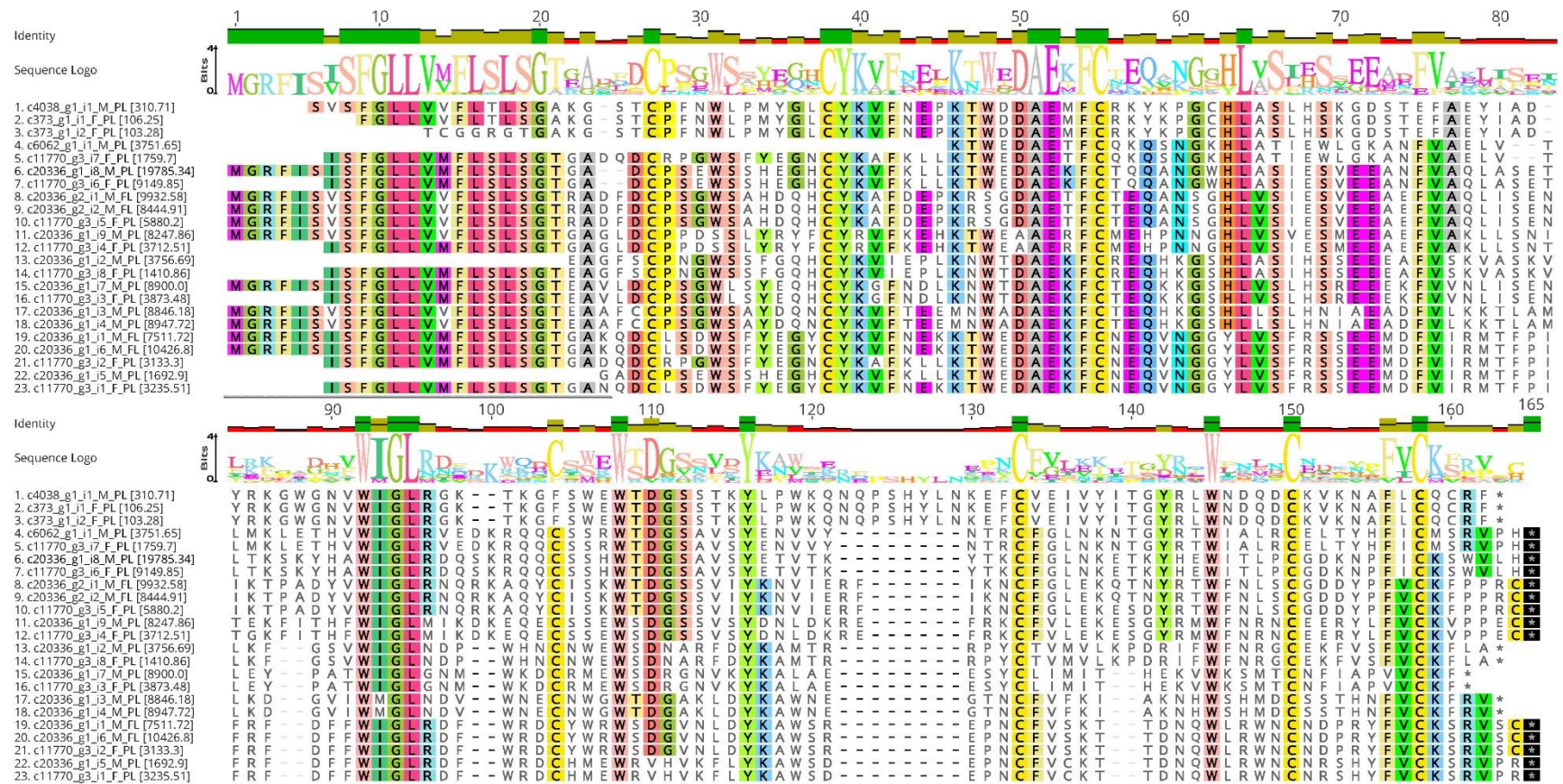


Figure S1. Clustal Omega sequence alignment of the polypeptides encoded by 23 transcripts candidate C-type lectins from Myanmar *D. siamensis*. Signal peptide was underlined, with conserved residues (>50%) highlighted throughout the alignment. Six of the cysteine residues were highly conserved, with each protein having typically 8 cysteine residues. The CTL conserved motif WIGL was highly conserved (position 92-95). The program Geneious Prime 2023.0.2 was used to create this alignment, with SeqLogo [1] to highlight highly conserved amino acid residues. Expression values (TPM) were included in brackets following sequence name.

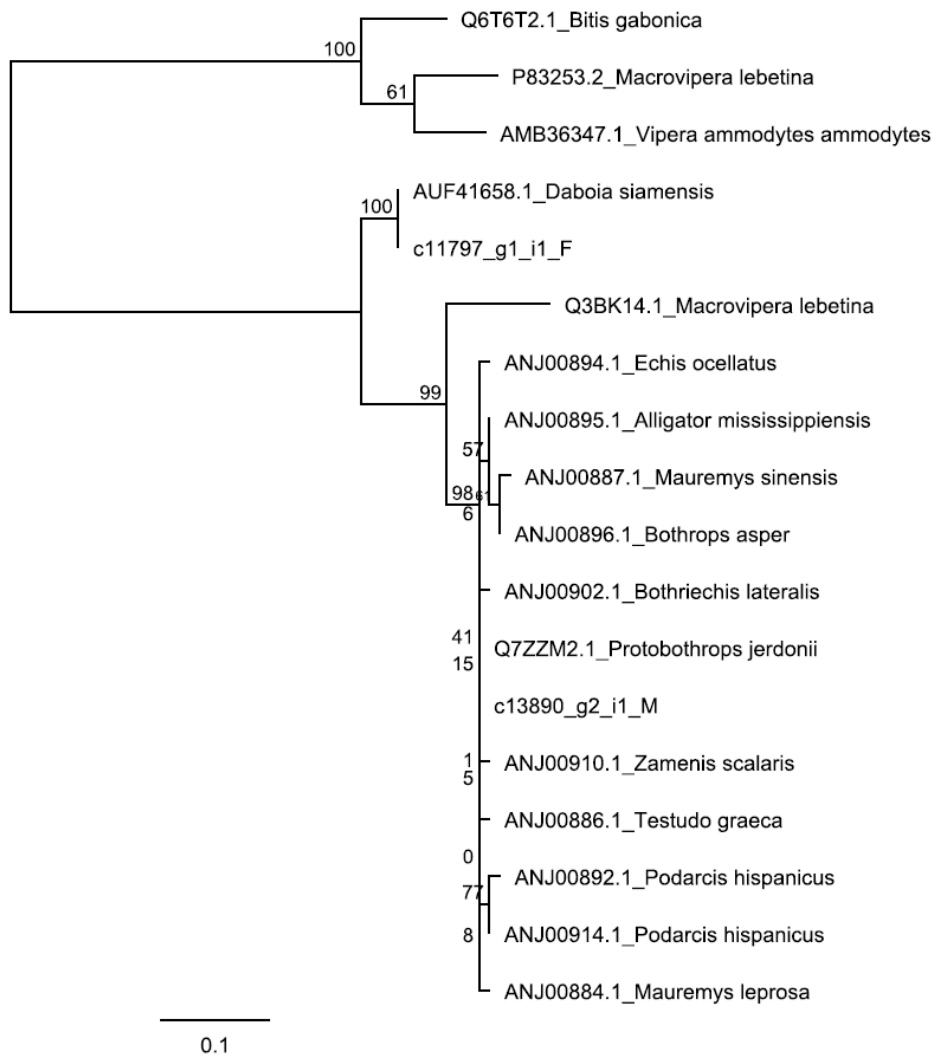


Figure S2. The gene tree analysis of the disintegrins from Myanmar *D. siamensis*, Dis1a (c13890_g2_i1_M) and Dis1b (c11797_g1_i1_F), with disintegrins from other species.

```

RVV_Vγ      -----MVLIKVLANLLVLQLSYAQKSELVVGDEININEHPFLVALYTSASSTI 50
c20548_g3_i4_M_FL -----MVLIRVLANLLVLQLSYAQKSELVVGDEININEHPFLVALYTSASSTI 50
c11820_g1_i1_F_PL -----MVLIRVLANLLVLQLSYAQKSELVVGDEININEHPFLVALYTSASSTI 50
c11820_g1_i3_F_PL MNSLPCRVEAMVLIRVLANLLVLQLSYAQKSELVVGDEININEHPFLVALYTSASSTI 60
c11820_g1_i4_F_PL MNSLPCRVEAMVLIRVLANLLVLQLSYAQKSELVVGDEININEHPFLVALYTSASSTI 60
                ****.******

RVV_Vγ      HCAGALINREWVLTAAHCDRRNIRIKLGMHSKNIRNEDEQIRVPRGKYFGLNTKFPNGLD 110
c20548_g3_i4_M_FL HCAGALINREWVLTAAHCDRRNIRIKLGMHSKNIRNEDEQIRVPRGKYFGLNTKFPNGLD 110
c11820_g1_i1_F_PL HCAGALINREWVLTAAHCDRRNIRIKLGMHSKNIRNEDEQIRVPRGKYFGLNTKFPNGLD 110
c11820_g1_i3_F_PL HCAGALINREWVLTAAHCDRRNIRIKLGMHSKNIRNEDEQIRVPRGKYFGLNTKFPNGLD 120
c11820_g1_i4_F_PL HCAGALINREWVLTAAHCDRRNIRIKLGMHSKNIRNEDEQIRVPRGKYFGLNTKFPNGLD 120
                *****

RVV_Vγ      KDI MLIRLRPVTYSTHIAPVSLPSRSRGVGSRRIMGWGKISTEDTYPDVPHGTNIFI 170
c20548_g3_i4_M_FL KDI MLIRLRPVTYSTHIAPVSLPSRSRGVGSRRIMGWGKIST--DTYPDVPHGTNIFI 168
c11820_g1_i1_F_PL KDI MLIRLRPVTYSTHIAPVSLPSRSRGVGSRRIMGWGKIST--DTYPDVPHGTNIFI 168
c11820_g1_i3_F_PL KDI MLIRLRPVTYSTHIAPVSLPSRSRGVGSRRIMGWGKIST--DTYPDVPHGTNIFI 178
c11820_g1_i4_F_PL KDI MLIRLRPVTYSTHIAPVSLPSRSRGVGSRRIMGWGKIST--DTYPDVPHGTNIFI 178
                *****

RVV_Vγ      VKHKWLEPLYPWVPADSRITLAGILKGGRTCHGDSGGPLICNGEMHGIVAGGSEPCGQH 230
c20548_g3_i4_M_FL VKHKWLEPLYPWVPADSRITLAGILKGGRTCHGDSGGPLICNGEMHGIVAGGSEPCGQH 228
c11820_g1_i1_F_PL VKHKWLEPLYPWVPADSRITLAGILKGGRTCHGDSGGPLICNGEMHGIVAGGSEPCGQH 228
c11820_g1_i3_F_PL VKHKWLEPLYPWVPADSRITLAGILKGGRTCHGDSGGPLICNGEMHGIVAGGSEPCGQH 238
c11820_g1_i4_F_PL VKHKWLEPLYPWVPADSRITLAGILKGGRTCHGDSGGPLICNGEMHGIVAGGSEPCGQH 238
                *****

RVV_Vγ      LKPAVYTKVFDYNWNIQSI IAGNRTVTCP- 260
c20548_g3_i4_M_FL LKPAVYTKVFDYNWNIQSI IAGNRTVTCPP* 258
c11820_g1_i1_F_PL LKPAVYTKVFDYN----- 241
c11820_g1_i3_F_PL LKPAVYTKVFDYN----- 251
c11820_g1_i4_F_PL LKPAVYTKVFDYN----- 251
                *****

```

Figure S3. Sequence alignment of RVV-V_γ from *Daboia siamensis* and deduced amino acid sequences of transcripts from the transcriptomes. Signal peptide is single-underlined. Catalytic triad His57, Asp102 and Ser195 are highlighted in yellow. Cysteine residues for 6 disulfide bridge are highlighted in green. (*) fully conserved residues; (;) strongly similar residues; (.) weakly similar residues.

```

c13118_g1_i1_M_FL MAAYLLAVAILFCIQGWPSGTVQGVQRPFPDVYQRSACQTRETLSVILQEHPDEISDIFR 60
c22505_g1_i1_F_FL MAAYLLAVAILFCIQGWPSGTVQGVQRPFPDVYQRSACQTRETLSVILQEHPDEISDIFR 60
VR_1              MAAYLLAVAILFCIQGWPSGTVQGVQRPFPDVYERSACQTRETLSVILQEHPDEISDIFR 60
                *****

c13118_g1_i1_M_FL PSCVAVLRCSGCCTDESMKCTPVGKHTADIQIMRMNPRTHSSKMEVMKFMEHTACECRPR 120
c22505_g1_i1_F_FL PSCVAVLRCSGCCTDESMKCTPVGKHTADIQIMRMNPRTHSSKMEVMKFMEHTACECRPR 120
VR_1              PSCVAVLRCSGCCTDESMKCTPVGKHTADIQIMRMNPRTHSSKMEVMKFMEHTACECRPR 120
                *****

c13118_g1_i1_M_FL WKQGEPEGPKPEPRRGE*----- 136
c22505_g1_i1_F_FL WKQGEPEGPKPEPRRGE*----- 136
VR_1              WKQGEPEGPKPEPRRGVRAKFPFD 144
                *****

```

Figure S4. Sequence alignment of deduced amino acid sequences of VEGF transcripts with VR-1 from *D. russelii* (P67861). Signal peptide is single-underlined. Cysteine residues are in yellow color. (*) fully conserved residues; (;) strongly similar residues; (.) weakly similar residues.

c11787_g15_i2_F_PL	-----	0
DrLAO	MNVFFMFSLFLATLGSCADDKNPLEECFREDDYEEFLEIAKNGLKKTSPKHIIVVGAG	60
c17343_g1_i1_M_FL	MNVFFMFSLFLATLGSCADDKNPLEECFREDDYEEFLEIAKNGLKKTSPKHIIVVGAG	60
c11787_g15_i1_F_FL	MNVFFMFSLFLATLGSCADDKNPLEECFREDDYEEFLEIAKNGLKKTSPKHIIVVGAG	60
c11787_g15_i2_F_PL	-----MSSVTVLEASERPGGVRVTRHNVKEGWYANLGPMPVPEKHRIIREYI	47
DrLAO	MSGLSAAYVLAGAGHKVTVLEASERPGGVRVTRHNVKEGWYANLGPMPVPEKHRIIREYI	120
c17343_g1_i1_M_FL	MSGLSAAYVLAGAGHKVTVLEASERPGGVRVTRHNVKEGWYANLGPMPVPEKHRIIREYI	120
c11787_g15_i1_F_FL	MSGLSAAYVLAGAGHKVTVLEASERPGGVRVTRHNVKEGWYANLGPMPVPEKHRIIREYI	120
	.*****	
c11787_g15_i2_F_PL	RKFGLKLNFEVQETENGWYFIKNIRKRVGEVKKDPGLLKYPVKPSEAGKSAGQLYQESLG	107
DrLAO	RKFGLKLNFEVQETENGWYFIKNIRKRVGEVKKDPGLLKYPVKPSEAGKSAGQLYQESLG	180
c17343_g1_i1_M_FL	RKFGLKLNFEVQETENGWYFIKNIRKRVGEVKKDPGLLKYPVKPSEAGKSAGQLYQESLG	180
c11787_g15_i1_F_FL	RKFGLKLNFEVQETENGWYFIKNIRKRVGEVKKDPGLLKYPVKPSEAGKSAGQLYQESLG	180

c11787_g15_i2_F_PL	KAHEELKRTNCSYILNKYDTYSTKEYLIKEGNLSPGAVDMIGDLLNEDSGYYVSFIESLK	167
DrLAO	KAHEELKRTNCSYILNKYDTYSTKEYLIKEGNLSPGAVDMIGDLLNEDSGYYVSFIESLK	240
c17343_g1_i1_M_FL	KAHEELKRTNCSYILNKYDTYSTKEYLIKEGNLSPGAVDMIGDLLNEDSGYYVSFIESLK	240
c11787_g15_i1_F_FL	KAHEELKRTNCSYILNKYDTYSTKEYLIKEGNLSPGAVDMIGDLLNEDSGYYVSFIESLK	240

c11787_g15_i2_F_PL	HDDIFAYEKRFEIVGGMDQLPTSMYRAIEESVRFKARVIKIQQNAEKVTVTYQTTQKNL	227
DrLAO	HDDIFAYEKRFEIVGGMDQLPTSMYRAIEESVRFKARVIKIQQNAEKVTVTYQTTQKNL	300
c17343_g1_i1_M_FL	HDDIFAYEKRFEIVGGMDQLPTSMYRAIEESVRFKARVIKIQQNAEKVTVTYQTTQKNL	300
c11787_g15_i1_F_FL	HDDIFAYEKRFEIVGGMDQLPTSMYRAIEESVRFKARVIKIQQNAEKVTVTYQTTQKNL	300

c11787_g15_i2_F_PL	LLETVDYVIVCTTSRAARRITFKPPLPPKKAHALRSVHYRSGTKIFLTCTKKFWEDDGIQ	287
DrLAO	LLETADYVIVCTTSRAARRITFKPPLPPKKAHALRSVHYRSGTKIFLTCTKKFWEDDGIQ	360
c17343_g1_i1_M_FL	LLETVDYVIVCTTSRAARRITFKPPLPPKKAHALRSVHYRSGTKIFLTCTKKFWEDDGIQ	360
c11787_g15_i1_F_FL	LLETVDYVIVCTTSRAARRITFKPPLPPKKAHALRSVHYRSGTKIFLTCTKKFWEDDGIQ	360
	.**	
c11787_g15_i2_F_PL	GGKSTTDLPSRFIYYPNHNFTTGVGVI IAYGIGDDANFFQALNLNECADIVFNDLSSIHQ	347
DrLAO	GGKSTTDLPSRFIYYPNHNFTTGVGVI IAYGIGDDANFFQALNLNECADIVFNDLSSIHQ	420
c17343_g1_i1_M_FL	GGKSTTDLPSRFIYYPNHNFTTGVGVI IAYGIGDDANFFQALNLNECADIVFNDLSSIHQ	420
c11787_g15_i1_F_FL	GGKSTTDLPSRFIYYPNHNFTTGVGVI IAYGIGDDANFFQALNLNECADIVFNDLSSIHQ	420

c11787_g15_i2_F_PL	LPKKDLQTFQYPSIIQKWSLDKYAMGAITTFPTYQFQHFSEALTAPVGRIFFAGEYTANA	407
DrLAO	LPKKDLQTFQYPSIIQKWSLDKYAMGAITTFPTYQFQHFSEALTAPVGRIFFAGEYTANA	480
c17343_g1_i1_M_FL	LPKKDLQTFQYPSIIQKWSLDKYAMGAITTFPTYQFQHFSEALTAPVGRIFFAGEYTANA	480
c11787_g15_i1_F_FL	LPKKDLQTFQYPSIIQKWSLDKYAMGAITTFPTYQFQHFSEALTAPVGRIFFAGEYTANA	480

c11787_g15_i2_F_PL	HGWIDSTIKSGLTAARDVNRASEL*	431
DrLAO	HGWIDSTIKSGLTAARDVNRASEL-	504
c17343_g1_i1_M_FL	HGWIDSTIKSGLTAARDVNRASEL*	504
c11787_g15_i1_F_FL	HGWIDSTIKSGLTAARDVNRASEL*	504

Figure S5. Sequence alignment of DrLAO (*Daboia russelii*, **G8XQX1.1**) with 3 deduced LAAO transcripts obtained from Myanmar Russell's viper transcriptome. Conserved FAD-binding motif and Ile¹-Hse¹¹ fragment is highlighted in green. Three potential N-glycosylation sites are underlined. Cysteine residues making disulfide bridge are highlighted in blue. Key residues in catalytic site are highlighted in yellow. (*) fully conserved residues; (;) strongly similar residues; (.) weakly similar residues.

c55720_g1_i1_M	<u>MIAFIVLPILA</u> AVLQSSGSVDFDSES	PRKPEIQNEIVDLHNSLR	SVTPTASNMLKMEW	60
c17345_g1_i1_F	<u>MIAFIVLPILA</u> AVLQSSGSVDFDSES	PRKPEIQNEIVDLHNSLR	SVTPTASNMLKMEW	60
Dr_CRPK	<u>MIAFIVLPILA</u> AVLQSSGSVDFDSES	PRRPEIQNEIVDLHNSLR	SVTPTASNMLKMEW	60
*****.*****				
c55720_g1_i1_M	YPEAANAERWAFRCILNHSPYNSRVIGGIK	GENIYMSPYPMKWT	AIHEWHDEKKDFV	120
c17345_g1_i1_F	YPEAANAERWAFRCILNHSPYNSRVIGGIK	GENIYMSPYPMKWT	AIHEWHDEKKDFV	120
Dr_CRPK	YPEAANAERWAFRCILNHSPYNSRVIGGIK	GENIYMSPYPMKWT	AIHEWHKEKKDFV	120
*****.				
c55720_g1_i1_M	YGQGASPANAVVGHYTQVVWYKSYRSG	AAAYCP	SSSEYNFYVVCQYCPAGNIIGKIATPY	180
c17345_g1_i1_F	YGQGASPANAVVGHYTQVVWYKSYRSG	AAAYCP	SSSEYNFYVVCQYCPAGNIIGKIATPY	180
Dr_CRPK	YGQGASPANAVVGHYTQIVWYKSYRSG	AAAYCP	SSSEYNFYVVCQYCPAGNIIGKIATPY	180
*****.*****				
c55720_g1_i1_M	TSGPFCGDCPSACDNGLC	TNPSHHDDFTNCKDLVKQGC	HSNYLKTCKPASCFCHNEII	239
c17345_g1_i1_F	TSGPFCGDCPSACDNGLC	TNPSHHDDFTNCKDLVKQGC	HSNYLKTCKPASCFCHNEII	239
Dr_CRPK	TSGPFCGDCPSACDNGLC	TNPSHHDEFNCKDLVKQGC	HSNYLKTCKPASCFCHNEII	239
*****.*****				

Figure S6. Sequence alignment of deduced amino acid sequences of CRISP transcripts from the transcriptomes with cysteine-rich secretory protein Dr-CRPK from Taiwan Russell's viper (ACE73567). Signal peptide is single-underlined. Cysteine residues are in pink color. The two Zn²⁺ binding motifs are highlighted in yellow and blue. (*) fully conserved residues; (:) strongly similar residues; (.) weakly similar residues.

References

1. Bembom, O.; Ivanek, R. seqLogo: Sequence logos for DNA sequence alignments. R package version 1.64.0. Available online: <https://bioconductor.org/packages/release/bioc/html/seqLogo.html> (accessed on 26 March 2022).