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List of Publications

1. **Susmita Thakur**, Avni Blothra, Karthikayen Vasudevan, Anita Malhotra, Vishal Santra, Robin Doley. *Proteome decomplexation of Trimeresurus erythrurus from Mizoram, India.* Journal of Proteome Research. 2023, **22**, 215−225 doi.org/10.1021/acs.jproteome.2c00642.
2. **Susmita Thakur**, Anita Malhotra, Surajit Giri, H.T. Lalremsenga, Omesh K. Bharti, Vishal Santra, Gerard Martin, Robin Doley. *Venom of several Indian green pit vipers: Comparison of biochemical activities and cross-reactivity with antivenoms*. Toxicon. 2022, **210**: 66–77 doi.org/10.1016/j.toxicon.2022.02.014
3. **Susmita Thakur,** Avni Blothra, Karthikayen Vasudevan, Anita Malhotra, Vishal Santra, Robin Doley. *Erythrofibrase: An alpha-fibrinogenase enzyme purified from Trimeresurus erythrurus* (under communication).
4. Namita Ojah, **Susmita Thakur**, Dolly Gogoi, Gazi Ameen Ahmed, Manabendra Mandal, Robin Doley, Arup Jyoti Choudhury. 2021. *Effects of Dielectric Barrier Discharge Plasma on Physicochemical Characteristics, Mechanical Properties and Biocompatibility of Silk/PVA Nanofibers.* Plasma Chemistry and Plasma Processing. 2021. **42(1)**: 147-162. doi.org/10.1007/s11090-021-10215-1

Conferences/seminars:

1. **Susmita Thakur**, Robin Doley. *Exploring the Thrombin-like enzymes (TLEs) from Indian green pit viper (Trimeresurus erythrurus).* Advances in Basic and Translational Research in Biology (ABTRiB) held at Dept of MBBT, Tezpur University, Assam on 11-12th March, 2022 *(2nd best poster presentation).*
2. **Susmita Thakur**, Robin Doley. *Cataloguing of Indian green pit viper (Trimeresurus erythrurus) proteome.* Biology is fascinating, inSCIgnis'22, held at Department of MBBT, Tezpur University, Assam on 1st March, 2022 *(3rd best oral presentation).*
3. **Susmita Thakur**, Anita Malhotra, Robin Doley, Vishal Santra, Omesh K Bharti and Surajit Giri. *Green pit vipers of the Himalayas and north-eastern India: a review of their taxonomy, venom, and clinical effects of snakebite.* 8th International Toxinology meeting, Venoms and Toxins 2021, held at University of Oxford, England from 25th-27th August, 2021.
4. **Susmita Thakur**, Robin Doley; *Characterization and variational analysis of Trimeresurus venom: An unstudied venom from North-East India.* Nextgen Genomics, Biology, Bioinformatics and Technologies Conference, held at Taj Lands End, Mumbai from September 30th – October 2nd, 2019.

APPENDIX I

Alignment of peptide fragments obtained from LC-MS/MS of *Trimeresurus erythrurus* venom

Appendix 1

Pairwise sequence alignment of peptide fragments identified in the proteome of *Trimeresurus erythrurus* by LC-MS/MS with their homologous protein in NCBI database. Different colours highlight different peptide fragments identified. Modified Amino acid residues has been underlined.

Phospholipase A_2 (PLA_2):

1. A Chain A, Acidic phospholipase A_2 5 (Peak 3)

```
4RFP:       NLMQFELLIMKVAGRSGIVWYSDYGCFCGKGGHGRPQDATDRCCFVHDCCYGKVNGCDPKEDFYRYSSNNGDIVCEANNPCTKEICECDKAAAICFRDNKDTYDNKYWNIPMESCQESEPC
This study: ----------------------------------------CCFVHDCCYGKVNGCDPK-----YSSNNGDIVCEANNPCTKEICECDKAAAICFR---------YWNIPMESCQESEPC
```

2. Phospholipase A_2 isozyme Ts-K49a (Peak 3)

```
AAP48893.1: SVIELGKMIFQETGKNPATSYGLYGCNCGPGGRRKPKDATDRCCYVHKCCYKKLTDCDPIKDRYSYSWVNKAIVCGEDNPCLKFREMCECDKAVAICENLDTYDKKKKINLKLFCKKTSEQC
This study: -------MIFQETGK-------------------------------------KLTDCDPIKDR----------------------EMCECDKAVAICENLDTYDK----------------
```

3. Phospholipase A_2 isozyme Ts-K49b' (Peak 3)

```
AAP48895.1: GVIELTKMFVQEMGKNALTSYSLYGCNCGPGGRRKPMDATDSCCHVHKCCYKKLTDCDPIKDRYSYSWVNKAIVCGEDNPCLKEMCECDKAVAIRFRENLDTYDKKKKINLKLFCKKTSEQC
This study: -------MFVQEMGKNALTSYSLYGCNCGPGGR-------------------KLTDCDPIKDR------------------------------FRENLDTYDK----------------
```

4. K49a phospholipase A_2-like (Peak 3)

```
AAR14165.1: SVIQLGKMILQETGKNPVKYYGAYGCNCGPLGRRKPLDATDRCCYMHKCCYKKLTDSNPIKDRYSYSWENKAIVCKEKNPRLKEMCECDKAVAICFRENMRTYNKKERINTKIFCKKTPEPC
This study: ------------------------------------------------------------DRYSYSWENKAVAICFR-----EMCECDKAVAICFR-------------------------
```

5. Phospholipase A_2 (Peak 3)

```
AHJ09513.1: SVVQLTKMIVQEMGKNALTSYSLYGCNCGPGGRRKPMDATDRCCFVHDCCYGKVNGCNPKKAVYIYSLENGDIVCGGDDPCRKEVCECDKAAAICFRDNMDTYDNKHWNVPSENCQEESERC
This study: -------MIVQEMGKNALTSYSLYGCNCGPGGRR--------CCFVHDCCYGKVNGCNPK----------------------EVCECDKAAAICFR-------------------------
```

6. Phospholipase A_2 (Peak 3)

```
AHJ09541.1: SLIELTKMIVQEMGKNALTSYSLYGCNCGVGGRRKPVDATDRCCLVHKCCYKKLTDCDPKKDRYSYSWVNKAIVCGEKNPHLKELCECDKAVAICFRENMDTYDKKKKINLKLFCKKTSEQC
This study: -------MIVQEMGKNALTSYSLYGCNCGVGGR-----------------------------------------------NPHLKELCECDKAVAICFR-------------------------
```

7. Phospholipase A_2 (Peak 3)

```
AHJ09518.1: SVIELTKMIVQEMGKNALTSYSLYGCNCGPGRRRQPMDATDRCCFLHKCCYKKLTDCDPKKDRYSYSWVNKAILCGEKDPCLKEMCECDKAMAICFRENLDTYDKKKRIKPKFFCKKTSEPC
This study: -------MIVQEMGKNALTSYSLYGCNCGPGR-------------------------------------------------EMCECDKAMAICFRENLDTYDKK---------------
```

8. Phospholipase A_2 (Peak 4)

AHJ09519.1: NLLQFALLIMKVAGRSGIVWYSDYGCFCGKGGHGRPQDATDRCCFVHDCCYGRVNGCSPKMDFYRYSEENGGIVCEANNPCTKEICECDKAAAICFRGNLNTYDKKYRNVPTESCQESEPC
This study: ----------CCFVHDCCYGR-------MDFYRYSEENGGIVCEANNPCTKEICECDKAAAICFR----------

9. Phospholipase A_2 (Peak 4)

AHJ09543.1: NLMQFELLIMKVAGRSGIMWYSDYGCFCGKGGQGQPQDATDRCCFVHDCCYGKVNGCDPKMDFYKYSSENEDIVCEANNPCTKEICECDKAAAICFRDNKKTYDNKYWNIPKESCQESEPC
This study: ----------CCFVHDCCYGKVNGCDPKMDFYKYSSENEDIVCEANNPCTKEICECDKAAAICFR----------

10. Phospholipase A_2 (Peak 4)

AHJ09586.1: NLLQFELLIMKVAGRSGIVWYSDYGCFCGKGGHGRPQDATDRCCFVHDCCYGRVNGCGPKMDFYRYSEENGDIVCEANNPCTKEICECDKAAAICFRDNINTYDNKYWNVPTESCQESEPC
This study: ----------CCFVHDCCYGRVNGCGPKMDFYRYSEENGDIVCEANNPCTKEICECDKAAAICFRDNINTYDNK----------

11. Phospholipase A_2 (Peak 4)

AHJ09590.1: GHLMQFETMIKKVAGRSGIWWYGSYGCYCGKGGQDRPQDASDRCCFVHDCCYGRVNGCDPKDDFYTYREENGNIVCEEDNPCTKEICECDKDAAICFRDNINTYDNKYWFYPAKYCKEESEPC
This study: ----------SGIWWYGSYGCYCGKGGQDRPQDASDRCCFVHDCCYGRVNGCDPKDDFYTYREENGNIVCEEDNPCTKEICECDKDAAICFRDNINTYDNKYWFYPAKYCKEESEPC

12. Acidic phospholipase A_2 Tpu-E6c (Peak 4)

P0DJP4.1: NLLQFEMMILKMAGRSGIRWYSDYGCYCGKGGHGQPQDATDRCCFVHDCCYGKVSGCDPKDEFYKYSSDNNDIVCGGNNPCLKEICECDRDAAICFRDNLSTYNNKYWNVPSETCQVESEPC
This study: ----------CCFVHDCCYGK----------YSSDNNDIVCGGNNPCLKEICECDRDAAICFR----------

13. Phospholipase A_2 (Peak 5)

AHJ09535.1: HLIQFETLIMKVAGRSGMFSYSAYGCYCGWGGSGQPQDDTDRCCFVHDCCYGKVTGCDPKTDVYTYSEENGDIICGGDDPCKKEVCECDKAAAICFRDNVGTYDRKKYWRFPTKNCQESVPC
This study: ----------CCFVHDCCYGK----------EVCECDKAAAICFR----------

14. Phospholipase A_2 (Peak 5)

AHJ09546.1: HLMQFENMIMKVAGRSGIWWYGPYGCYCGAGGRGRPQDASDRCCFVHDCCYGRVNGCDPKDDFYKYSEENGDIVCEEDNPCTKEICECDKAAAICFRDNIETYQNKYWSYPAKYCKEESEPC
This study: ----------GRPQDASDRCCFVHDCCYGRVNGCDPKDDFYKYSEENGDIVCEEDNPCTKEICECDKAAAICFRDNIETYQNKYWSYPAKYCKEESEPC

15. Phospholipase A_2 (Peak 5)

AHJ09577.1: HLMQFENMIMKVAGRSGIWWYGSYGCYCGKGGQGRPQDASDRCCFVHDCCYGRVNGCDPKDDFYKYSEENGDIVCEEDNPCTKEICECDKAAAICFRDNIETYQNKYWFYPAKYCKEESEPC
This study: ----------SGIWWYGSYGCYCGKGGQGRPQDASDRCCFVHDCCYGRVNGCDPKDDFYKYSEENGDIVCEEDNPCTKEICECDKAAAICFRDNIETYQNKYWFYPAKYCKEESEPC

16. G6D49 phospholipase A2 (Peak 9)

AAR14167.1: SLLEFGRMIKEETGKNPLFSYISYGCYCGWGGQGQPKDATDRCCFVHDCCYGKLWSCSPKTDIYFYYRKNGAIVCARGTWCEKQICECDKAAAICFRENLGTYKAEYESYGKSRCTEKSLKC
This study: ----------CCFVHDCCYGK----------QICECDKAAAICFR----------

17. Phospholipase A_2 (Peak 10)

AHJ09512.1: HLMQFETMIMKVAGRSGIWWYGSYGCYCGKGGQGRPQDASDRCCFAHDCCYGKVNGCDPKDDFYTYSEENGDIVCEEDNPCTKEICECDKAAAICFRDNIETYQNKYWFYPAKYCKEESEPC
This study: ----------SGIWWYGSYGCYCGK----------EICECDKAAAICFRDNIETYQNKYWFYPAKYCKEESEPC

Snake venom serine proteases (SVSPs):

1. Venom plasminogen activator (Peak 6)

```
P0DJF5.1:   VFGGRPCNINEHRSLVVLFNSSGFLCGGTLINQDWVVTAAHCDSNNFQLLFGVHSKKTLNEDEQTRDPKEKFFCPNRKKDDEVDKDIMLIKPSVGSVCRLDSSVNNSEHIAPLSLPSSP
This study: ------------------------------------------------------TLNEDEQTRDPKEKFFCPNRKKDDEVDKDIMLIK----------------------------
P0DJF5.1:   IMGWGKTIPTKDIYPDVPHCANINILDHAVCRTAYSWRQVANTTLCAGILQGGKDTCHFDSGGPLICNEQFHGIVSWGGHPCGQPREPGVYTNVFDYTDWIQSIIAGNKDATCPP
This study: IMGWGKTIPTKDIYPDVPHCANINILDHAVCRTAYSWR-------------------------------------------------------------------------DATCPP
```

2. Thrombin-like enzyme 1, GPVTL1 (Peak 7)

```
A7LAC6.1:   VIGGDECNINEHRFLVALYDVWSGDFLCGGTLINKEYVLTAAHCETRNMYIYLGMHNKNVQFDDEQRRYPKKKYFFRCSNNFTRWDKDIMLIRLNRPVRNSEHIAPLSLPSSPPSVGSVCR
This study: ----------------------------------EYVLTAAHCETRNMYIYLGMHNKNVQFDDEQRRYPKKKYFFRCSNNFTRWDKDIMLIRLNRPVRNSEHIAPLSLPSSPPSVGSVCR
A7LAC6.1:   VMGWGTITSPNETLPDVPRCANINLLNYTVCRGVFPRLPARSRTLCAGVLQGGIDTCKRDSGGPLICNGQLQGVVFWGPKPCAQPRKPALYTKVFNHLDWIQSIIAGNTTVTCPP
This study: -------------------CANINLLNYTVCR---------SRTLCAGVLQGGIDTCKRDSGGPLICNGQLQGVVFWGPKPCAQPR-------VFNHLDWIQSIIAGNTTVTCPP
```

3. Thrombin-like enzyme 2, GPVTL2 (Peak 7)

```
A7LAC7.1:   VIGGDECNINEHRFLVALYDVWSGDFLCGGTLINKEYVLTAAHCETRNMYIYLGMHNKMYQFDDEQRRYPKKKYFFRCSNNFTRWDKDIMLIRLNRPVRNSEHIAPLSLPSSPPSVGSVCRV
This study: ----------------------------------EYVLTAAHCETRNMYIYLGMHNK------------KKYFFRCSNNFTRWDKDIMLIRLNRPVRNSEHIAPLSLPSSPPSVGSVCRV
A7LAC7.1:   MGWGTITSPNETLPDVPRCANINLLNYTVCRGVFPRLPARSRTLCAGVLQGGIDTCKRDSGGPLICNGKLQGVVFWGPKPCAQPRKPALYTKVFDHLDWIQSIIAGNTTVTCPP
This study: ------------------CANINLLNYTVCR---------SRTLCAGVLQGGIDTCKRDSGGPLICNGKLQGVVFWGPKPCAQPR-------VFDHLDWIQSIIAGNTTVTCPP
```

4. Alpha-fibrinogenase albofibrase (Peak 7)

```
P0CJ41.1:   VVGGDECNINEHHSLVAIFNSTGFFCSGTLINQEWVVTAAHCDSKNFKMKFGAHSKKLLNEDEQIRNPKEKFICPNKKSNEILDKDIMLIKLDSPVSNSAHIAPLSLPSSPPSVGSVCR
This study: ------------------------------------------------------KLLNEDEQIRNPKEKFICPNKKSNEILDKDIMLIKLDSPVSNSAHIAPLSLPSSPPSVGSVCR
P0CJ41.1:   IMGWGSTTPIEVTYPDVPYCANINLLDDAECKPGYPELLPEYRTLCAGIVQGGKDTCGGDSGGPLICNEKLHGIVSYGGHPCGQSHKPGIYTNVFDYNDWIQSIIAGNTDATCLS
This study: IMGWGSTTPIEVTYPDVPYCANINLLDDAECKPGYPELLPEYRTLCAGIVQGGKDTCGGDSGGPLICNEKLHGIVSYGGHPCGQSHKPGIYTNVFDYNDWIQSIIAGNTDATCLS
```

5. Thrombin-like enzyme chitibrisin (Peak 7)

```
P0CJF6.1:   VIGGDECNINEHRSLVVLFNSSGALCGGTLINQEYVLTAAHCDMPNMQILLGVHSASVLNDDEQARDPEEKYFCLSSNNDTKWDKDIMLIRLNRPVNNSVHIAPLTLPSSPPRLGAICR
This study: ------------------------------------------------------------------YFCLSSNNDTKWDKDIMLIR----------------------------
P0CJF6.1:   IMGWGAITSPNETYPDASQCANINILRYSLCQAVYRGMPAQSRIVCAGILRGGKGSCKGDSGGPLICNAQLQGIVSAGGDPCAQPRVPVLYIRVFDYTDWIQSIIEGNRTVTCPP
This study: ----------------------------------------IVCAGILRGGKGSCKGDSGGPLICNAQLQGIVSAGGDPCAQPR----------------------TVTCPP
```

6. Serine protease KN1 precursor (Peak 7)

```
AAQ02894.1: VVGGHPCNINEHRFLVLVYSDGIQCGGTLINKEWMLTAAHCDGKKMKLQFGLHSKNVPNKDKQTRVPKKKYFFPCSKNFTKWDKDIMLIRLNHPVNNSTHIAPLSLPSKPPSQDTVCN
This study: ------------------------GSGTLINPEWVLTAAHCETEEMKLQFGLHSK----------------FFCESNK---WNKDIMLIK------NSAHIEPLSLPSSPPSVGSVCR
AAQ02894.1: IMGWGTISPTKEIYPDVPHCANINIVDHAVCRAFYPGLLEKSKTLCAGILEGGKDTCQGDSGGPLICNGQIQGIVSVGGDPCAEPRVPALYTKVFDHLDWIKSIIAGNTAATCPL
This study: ----------------------------------------SRTLCAGILEGGK-----------------------------------------------------------
```

7. Serine protease KN6 precursor (Peak 7)

```
AAQ02895.1: VIGGDECNINEHRFLVALYDVSSGDFRGSGTLINPEWVLTAAHCETEEMKLQFGLHSKRVPNKDKQTRVSKEKFFCESNKNYTKWNKDIMLIKLNRPVKNSAHIEPLSLPSSPPSVGSVCR
This study: ---------------------------GSGTLINPEWVLTAAHCETEEMKLQFGLHSK---------------FFCESNK----WNKDIMLIK------NSAHIEPLSLPSSPPSVGSVCR
AAQ02895.1: IMGWGTLSDTEMILPDVPHCANINLLNYSDCQAAYPELPAKSRTLCAGILEGGKDTCSGDSGGPLICNGTFQGIASWGSTLCGYVREPGSYTKVFDHLDWIQSIIAGNTNVTCPL
This study: ----------------------------------------SRTLCAGILEGGK-------------------------------------------------------------
```

8. Serine protease (Peak 7)

```
BAA19979.1: VVGGDECNINEHRSLVAIFNSTGFFCSGTLINQEWVVTAAHCDSNNFKMKFGAHSQKVLNEDEQIRNPKEKFICPNKKNNEVLDKDIMLIKLDSSVSNSEHIAPLSLPSSPPSVGSVCR
This study: ------------------------------------------------------------------------EKFICPNKKNNEVLDKDIMLIK----------------------------
BAA19979.1: IMGWGSITPTKVTYPDVPYCANINLLDDAECKPGYPELLPEYRTLCAGIVQGGKDTCGGDSGGPLICNGQFHGIVSYGAHPCGQSLKPGIYTTVFDYNDWIKSIIAGNTAATCPP
This study: IMGWGSITPTKVTYPDVPYCANINLLDDAECKPGYPELLPEYRTLCAGIVQGGK-------------------------------------------------------------
```

9. Snake venom serine protease homolog 2A (Peak 7)

```
O13060.1:   IIGGDECNINEHRFLVALYTFRSRRFHCGGTLINQEWVLSAARCDRKNIRIKLGMHSTNVTNEDVQTRVPKEKFFCLSSKTYTKWNKDIMLIRLKRPVNNSTHIAPVSLPSNPPSLGSVCR
This study: -------------------------FHCGGTLINQEWVLSAAR-------------------------------FFCLSSK----WNKDIMLIR----------------------------
O13060.1:   VMGWGTISATKETHPDVPHCANINILDYSVCRAAYARLPATSRTLCAGILEGGKDTCHGDSGGPLICNGQVQGIVSWGGHPCGQPRKPGLYTKVFDHLDWIKSIIAGNKDATCPP
This study: ----------------------------------------TLCAGILEGGK-------------------------------------------------SIIAGNKDATCPP
```

10. Snake venom serine protease KN2 (Peak 7)

```
Q71QJ0.1:   VIGGHPCNINEHPFLVLVYHDGYQCGGTLINEEWVLTAAHCDGKKMKLQFGLHSKNVPNKDKQTRVPKEKFFCLSSKNFIKWGKDIMLIRLNRPVNNSTHIAPLSLPSSPPSQNTVCN
This study: ------------------------------------------------LQFGLHSK---------------FFCLSSK-------DIMLIR----------------------------
Q71QJ0.1:   IMGWGTISPTKEIYPDVPHCANINILDHAVCRAFYPGLLEKSKTLCAGILQGGKDICQGDSGGPLICNGQIQGIVSVGGDPCAEPRVPAIYTKVFDHLDWIKSIIAGNTAATCPL
This study: -----------EIYPDVPHCANINILDHAVCRAFYPGLLEK--TLCAGILQGGKDICQGDSGGPLICNGQIQGIVSVGGDPCAEPRVPAIYTK----------------------
```

11. Snake venom serine protease 2C (Peak 8)

```
O13062.1:   VIGGHPCNINEHPFLVLVYHDGYQCGGTLINEEWVLTAAHCDGKKMKLQFGLHSKNVPNKDKQTRVPKEKFFCLSSKNFIKWGKDIMLIRLNRSVNNSTHIAPLSLPSSPPSQNTVCN
This study: ------------------------------------------------------------------------------------------------------------------------
O13062.1:   IMGWGTISPTKEIYPDVPHCANINILDHAVCRAFYPGLLEKSKTLCAGILQGGKDICQGDSGGPLICNGQIQGIVSVGGNPCAEPRVPAIYTKVFDHLDWIKSIIAGNTAATCPL
This study: --------------------------------AFYPGLLEK--TLCAGILQGGK-------------------------------------------------------------
```

12. Serine protease (Peak 8)

```
BAA19981.1: VVGGDECNINEHRFLVALYEYTSMTFICGGTLINQEWVLTAAHCDRDTIYIYIGMHDKYVKFDDEQGRHPKEKYIFNCSNNFTKWDKDIMLIKLDYPVNYSEHIAPLSLPSSPPSMGSVCR
This study: ------------------------------------------------------------------------WDKDIMLIK----------------------------
BAA19981.1: VMGWGAITPTNETLPDVPHCANINILDHALCRAVFPGLPATSRTLCAGVLQGGTDTCNRDSGGPLICNGQFQGIVFWGWYPCAQPRVPALYTKVFDHLDWIQSIIAGNTDAACPP
This study: ----------------------------------------TLCAGVLQGGTDTCNR---------------------------------VFDHLDWIQSIIAGNTDAACPP
```

Snake c-type lectin-like proteins (Snaclecs):

1. Stejaggregin-A alpha chain (Peak 7)

```
AAQ15166.1: DCPSGWSAYDWYCYKPFNEPQTWDDAERFCTEQAKGGHLVSIESSGEADFVGQLVSENIQRPEIYVWIGLRDRRKEQQCSSEWSDGTSIIYVNWNKGESQMCQGLSKWTNFLKWDNTDCQAK
This study: ------------------------------------------------------------------------------------------------------------WTNFLKWDNTDCQAK
AAQ15166.1: NPFVCKFPPQC
This study: NPFVCKFPPQC
```

2. Snaclec purpureotin subunit alpha (Peak 8)

```
P0DJL2.1:   DCPSDWSSFKQYCYQIIKQLKTWEDAERFCLDQMKGAHLVSIESYREAVFVAELLSENVKTTKYHVWIGLSVQNKGQQCSSEWSDGSTVSYENLVKPNPKKCFVLKKESERTWSNVYCEQK
This study: DCPSDWSSFKQYCYQIIKQLKTWEDAERFCLDQMKGAHLVSIESYREAVFVAELLSENVK----------------GQQCSSEWSDGSTVSYENLVKPNPKK------ESERTWSNVYCEQK
P0DJL2.1:   HIFMCKFLGSR
This study: HIFMCK-----
```

3. Snaclec alboaggregin-A subunit alpha; AL-A subunit 2 (Peak 8)

```
P81112.1:   DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAKQADSGHLVSIETMGEADFVAQLISENIQSEKHYVWIGLKVQNKEQQCSSEWSDGSSVTYENLIKLYMRKCGALEQESGFRK
This study: DFHCLPGWSAYDQYCYRVFNEPKNWEDAERFCAK-------------------------------------VQNKEQQCSSEWSDGSSVTYENLIK----KCGALEQESGFRK
P81112.1:   WINLGCIQLNPFVCKFPPQ
This study: WINLGCIQLNPFVCK----
```

4. Snaclec alboaggregin-A subunit beta; AL-A subunit 3 (Peak 8)

```
P81113.1:   GFDCPFGWSSYEGYCYKVYNKKMNWEDAESFCREQHKRSHLVSFHSSGEVDFVVSKTFPILRYDFVWMGLSDIWKECTKEWSDGARLDYKAWSGKSYCLVSKTTNNEWLSMDCSR
This study: ------------------------------------------------------------------------ECTKEWSDGAR---------SYCLVSKTTNNEWLSMDCSR
P81113.1:   TRYPVCKFXG
This study: TRYPVCK---
```

5. Snaclec alboaggregin B, N-terminal partial peptide (Peak 9)

```
AAB26045.1: DCPSDWSSYDLYCYRVFQEKKNXEDAEKFCTQQHTDSHIV
This study: --YKAWAEES-YCVYFK----------------------
```

6. Snaclec purpureotin subunit beta (Peak 9)

```
P0DJL3.1:   DCPSDWSSYDLYCYKVFQQRMNWEDAEKFCRQQHTGSHLLSFHSSEEVDFVVSKTLPILKADFVWIGLTDVWSACRLQWSDGTELKYNAWTAESECIASKTTDNQWWTRSCSR
This study: DCPSDWSSYDLYCYK-----MNWEDAEKFCRQQHTGSHLLSFHSSEEVDFVVSKTLPILKADFVWIGLTDVWSACRLQWSDGTELKYNAWTAESECIASKTTDNQWWTR----
P0DJL3.1:   TYPFVCKLEV
This study: TYPFVCKLEV
```

7. Snaclec alboaggregin-A subunit alpha; AL-A subunit 1 (Peak 9)

```
P81111.1:   DCPSDWSSYDQYCYRVFKRIQTWEDAERFCSEQANDGHLVSIESAGEADFVTQLVSENIRSEKHYVWIGLRVQGKGQQCSSEWSDGSSVHYDNLQENKTRKCYGLEKRAEFRTWSNV
This study: DCPSDWSSYDQYCYR-------------------------------------------------------------------------------------CYGLEK----------
P81111.1:   YCGHEYPFVCKFXR
This study: --------------
```

8. Snaclec alboaggregin- B subunit alpha (Peak 9)

```
P81115.2:   DCPSDWSSFKQYCYQIVKELKTWEDAEKFCSEQANDGHLVSIESYREAVFVAELLSENVKTTKYNVWIGLSVQNKGQQCSSEWSDGSSVSYENLVKPNPKKCFVLKKESEFR
This study: ----------QYCYQIVK---TWEDAEK-----------------EAVFVAELLSENVK---------------GQQCSSEWSDGSSVSYENLVKPNPKK-----------
P81115.2:   TWSNVYCEQKHIFMCKFLGSR
P81115.2:   TWSNVYCEQKHIFMCK-----
```

9. Snaclec coagulation factor IX/factor X binding protein subunit B2 (Peak 9)

```
Q71RR1.1:   DCLSGWSSYEGHCYKPFNELKNWADAENFCTQQHAGGHLVSFQSSEEADFVVKLAFETFGHSIFWMGLSNVWNQCNWQWSNAAMLRYKAWAEESYCVYFKSTNNKWRSRSCR
This study: ------------------------------------------------------------------------------------YKAWAEESYCVYFK------------
Q71RR1.1:   MMANFVCEFQV
This study: -----------
```

10. Snaclec alboaggregin-A subunit beta (Peak 10)

```
P81114.1:   DCPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHKGSHLVSFQSSEEADFVVQMTRPILNANLVWIGLSNLWNQCNSQWSDGTXLDYKXWREQFECLVSRTTNNEWLSMDCSSTHS
This study: DCPSDWSSYEGHCYRVFNEPQNWADAEKFCTQQHK-------------------------------------------------EQFECLVSR----------------
P81114.1:   SFVCEFQA
This study: --------
```

Disintegrins:

1. Purpureomaculin (Peak 2)

```
QJA41976.1: EAGEDCDCGSPANPCCNAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCNGISAGCPRNPLHA
This study: EAGEDCDCGSPANPCCNAATCKLLPGAQCGEGLCCDQCSFMKK-----RARGDDLDDYCNGISAGCPRNPLHA
```

2. Trigramin precursor protein (Peak 10)

```
CAA35910.1: RYIKLGIFVDHGMYTKYSGNSERITKRVHQMINNINMMCRALNIVTTLSVLEIWSEKDLITVQASAPTTLTLFGAWRETVLLNRTSHDHAQLLTATIFNGNVIGRAPVGGMCDPKRAVAI
This study: ------------------------------------------------------------------------------------TSHDHAQLLTATIFNGNVIGR----------------
CAA35910.1: VRDHNAIVFVVAVTMTHEMGHNLGMHHDEDKCNCNTCIMSKVLSRQPSKYFSECSKDYYQTFLTNHNPQCILNAPLRTDTVSTPVSGNELLEAGEDCDCGSPANPCCDAATCKLIPGA
This study: --------------------------------CNCNTCIMSK-----------------------------------------------------------------------
CAA35910.1: QCGEGLCCDQCSFIEEGTVCRIARGDDLDDYCNGRSAGCPRNPFHA
This study: ---------------------------------------------
```

Snake venom metalloproteinases (SVMPs):

1. Zinc metalloproteinase-disintegrin albolatin (Peak 8)

```
P0C6B6.1:   LEKRCIELVMVADHRMYTKYDGDKTEISSKIYEIANNLNVDYRPMKIRVALIGTEIWSTGNLSKVTLSADETLDSFGEWRERDLLKRKSHDNVQLLTGMIFNEKIEGRAYNKSMCDPKR
This study: ---RCIELVMVADHR-----------------------------------------------------------------------------------------------
P0C6B6.1:   SVGIVRDHRTRPHLVANRMAHGLGHNLGIHHDGDSCSCGANSCIMSATVSNEPSSRFSDCSLNQYSNDIIYNPWTSYCLYNEPSKTDIVSPPVCGNYYLEVGEDCDCGPPANCQNPC
This study: SVGIVR------------MAHGLGHNLGIHHDGDSCSCGANSCIMSATVSNEPSSR---------- ----------------------------------------------
P0C6B6.1:   CDATTCKLTPGSQCAEGLCCAQCKFIEEGTVCRVAKGDWNDDHCTGQSGDCPWIGYYG
This study: -------LTPGSQCAEGLCCAQCK---------------------------------
```

2. Zinc metalloproteinase-disintegrin stejnitin (Peak 10)

```
P0DM87.1:   QRFIELVIVADHRMYTKYDGDETEISSKIYEIANDLNVIFRALYIHVALIGLEIWPSGELCNVTLSADDTLDSFAEWTKRDLQKRKRHDNAQLLTGMIFNEKIEGRAYKKTMCHWKRSVGIVR
This study: ----------------------------------------------------------------------------------------RHDNAQLLTGMIFNEKIEGR----------------
P0DM87.1:   DHRTRPHFVANRMAHGLGHNLGINHDGDSCTCGANSCIMSATVSNDPSSRFSDCSLNQYSSDIIHNPYTSRCLYNGPWKTDIVSPPVCGNYYVEVGEDCDCGPPANCQNRCCDAATCR
This study: ----------------------------------------------------------------------------------------------------------------------------
P0DM87.1:   LTPGSQCAEGLCCEQCRFSTEGKLCREAKGDWNNDYCSGQSGDCPRNPFRA
This study: LTPGSQCAEGLCCEQCR--------------------------------
```

3. Zinc metalloproteinase-disintegrin-like, TSV-DM (Peak 1)

```
Q2LD49.1:   QQSYLNAPKYVKFFLVADHIMYLKYGRNLTTLRTRIFDTVNVVYLILLRINIHVLLVGMEIWSHKDKIIVQSVPAVTLKLFATWREADLLKHKSHGCAHLLTGINFNGPTAGLAYLGAICNPMY
This study: ----------------------------------------------------------IIVQSVPAVTLK----------------------------------------------------
Q2LD49.1:   SAGIVQDHNKIHHLVAIAMAHELGHNLGINHDKDTCTCRAKACVMAGTISCDASYLFSDCSRQEHREFLIKNMPQCILKKPLKTDVVSPPVCGNYFVEVGEDCDCGSPTCRDSCCNPTNCK
This study: ------------------------------------------------------------------NMPQCILK----------------------------------------------
Q2LD49.1:   LRQGAQCAEGLCCDQCRFKGAGTECRPASSECDMADLCTGRSAECTDRFQRNGQPCQNNNGYCYNGTCPSMTDQCIALFGPNAAVSQDACFQFNREGNHYGYCRKEQNTKIACEPEN
This study: LRQGAQCAEGLCCDQCR----------------------SAECTDRFQR----------------------------------------------------------------
Q2LD49.1:   VKCGRLYCIDSSPANKNPCNIVYLPNDEEKGMVLAGTKCADGRACNSNGQCVGVNGAYKSTTGFSQI
This study: -----LYCIDSSPANKNPCNIVYLPNDEEK-----------------------------------
```

4. Stejnihagin-A (Peak 10)

```
ABA40760.1: RYVKLAIVADRRMYMKHQKNLKPWVFQMVNSVHQIYRSMNVLIALVYLNIWKKNDKITVQSASDVTLDLFAEWRETVLLRRKKHDCAHLLTAIDFDGPTIGRAHIASMCNSKLSV
This study: ----------------------------------------------------------------------------------------AHIASMCNSK---
ABA40760.1: GIVQNYTEINLVNAIVMAHELGHNLGISHDGNQCNCHTCIMSAVISNPPSERFSNCSEDYHQSFLTAYNPQCILNAPSKTDIITPPVCGNELLEEGEECDCGSPENCQYQCCDAASCK
This study: ----------------------------------------------------------------------TDIITPPVCGNELLEEGEECDCGSPENCQYQCCDAASCK
ABA40760.1: LHSWVKCESGECCDQCRFTSAGTECRAARSECDIAESCTGQSADCPTDDFHRNGQPCLSNHGYCYNGNCPVMHYQCIALFGSNAIVGQDECFDFNMKGEQYFYCRKEYEKYIPCA
This study: ---------CESGECCDQCR----------------------------------------------------------------------------------------
ABA40760.1: QEDVKCGRLFCFYTNNMDICRYNYSDIGIVDHGTKCADGKVCNSNRHCVDVTTVY
This study: ----------------------YNYSDIGIVDHGTK-----------HCVDVTTVY
```

5. Stejnihagin-B (Peak 9)

```
ABA40759.1: RYVKLAIVADHRMYTKHKKNLKPWVFQMVNSVHQIYRSMNVLIALVYLNIWKKNDKITAQSASNVTLDLFGNWRETVLLKRKRHDCAQLLTAIDFDGPTIGRAHVSSVCDPKRSTGI
This study: ----------------------------------------------------------------------------HDCAQLLTAIDFDGPTIGR----------------
ABA40759.1: VQNYTEINLVNAVIMAHELGHNLGMDHDGNQCNCHACIMSAVINNPPSERFSGCSMGYYQTFLTAYNPQCILNALSKRDIITPPVCGNELLEEGEECDCGSPENCQYQCCNATTCK
This study: ----------------------------------------------------------------------------------------------------------------------
ABA40759.1: LHSWVECESGECCEQCRFKKAGAVCRAARTECDIPENCTDQSADCPTDSFHRNGQPCLYNHGYCYNGNCPVMHYQCYGLFGPNATVGQDGCFDANDRGDEYFYCRKENEK
This study: LHSWVECESGECCEQCR----------------------------------------------------------------------------------------------
ABA40759.1: YIPCAQEDVKCGRLFCTYIYDINLCRYDYSANGMVAQGTKCADGKVCNSNRQCADVNTAY
This study: ------------------------------------------------------------
```

L-Amino acid oxidases (LAAO):

1. L-amino acid oxidase (Peak 1)

```
AAQ16182.1: MSGLSAAYVLAGTGHEVTVLEASERAGGRVRTYRNDEEGWYANLGPMRLPEKHRIVREYIRKFNLQLNEFSQENDNAWHFVKNIRKVGEVKKDPGVLKYPVKPSEEGKSAEQLYEESR
This study: -------------------------------------------------------------------------------------------KDPGVLKYPVKPSEEGK----------
AAQ16182.1: EVEKELKRTNCSYILNKYDTYSTKEYLIKEGNLSPGAVDMIGDLMNEDAGYYVSFIESMKHDDIFAYEKRFDEIVDGMDKLPTSMYRAIEEKVHFNAQVIKIQKNAEEVTVTYQTPEKDTSF
This study: --------------------------------------------------------------------------------------------------------------------------
AAQ16182.1: VTADYVIVCTTSGAARRIKFEPPLPLKKAHALRSVHYRSGTKIFLTCTKKFWEDEGIHGGKSTTDLPSRFIYYPNHNFTSGVGVIIAYGIGDDANFFQALDLKDCGDIVINDLSLIHQLPREEIQ
This study: ------------------------------------------IFLTCTK----------------------------------------------------------------------------
AAQ16182.1: TFCYPSMIQKWSLDKYAMGGITTFTPYQFQHFSEALTSHVDRIYFAGEYTAHAHGWIDSSIKSGLTAARDVNRASENPSGIHLSNDNEL
This study: -----------------------------------------------------------------------------------------
```

2. L-amino oxidase (Peak 8)

```
P0DPS2.1:   MNVFFMFSLLFLAALGSCADDRNPLEECFRETDYEEFLEIARXXXXTSNPKHVVRVGAGMSGLSAAYVLAGAGHQVTVLEASERPGGRXXXXXXXXEGWYANLGPMRXXXXXXXXXXXXX
This study: ----------------------NPLEECFRETDYEEFLEIAR------------------------------------------------------------------------------
P0DPS2.1:   KFGLNLNEFSQENDNAWYFIKXXXXXXXXXXXDPGLLKYPVKPSEAGKSAGQLYEESLGKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
This study: ----------------------------------------------------------------------------------------------------------------------------
P0DPS2.1:   XXXXFDEIVDGMDKLPTSMYQAIXXXXXXXXXXXXXXXXXXKVTVTYQTPAKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIFLTCTKKFWEDDGIHGGKSTTDLPSR
This study: ------------------------------------------VTVTYQTPA-------------- --------------------------------------KFWEDDGIHGGKSTTDLPSR
P0DPS2.1:   XXXXXXXXXXXXXXVIIAYGIGDDANFFQALDFKDCADIVFNDLSLIHQLPKEEIPSFCYPSMIQKXXXXXXXXXXITTFFTPYQFQHFSEAXXXXXXXIYFAGEYTAQAHGWIDSTIK
This study: -----------------------------------------------------------------------------------------------------------------------
```

Cysteine rich secretory proteins (CRiSPs):

1. Cysteine-rich seceretory protein Ts-CRPYa (Peak 8)

```
ACE73572.1: MIAFIVLPILAAVLQQSSGNVDFDSESPRKPEIQNEIVDLHNSLRRSVNPTASNMLRMEWYPEAADNAERWAYRCIESHSSYESRVIEGIKCGENIYMSPYPMKWTDIIHAWHDEYKDFK
This study: ---------------------------------------------RSVNPTASNMLRMEWYPEAADNAERWAYR----------------------------------------------
ACE73572.1: VGADPPNVTGHYTQIVWYKSYRIGCAAAYCPSSPYSYFFVCQYCPAGNFIGKTATPYTSGTPCGDCPSDCDNGLCTNPCTQENKFTNCNTMVQQSSCQDNYMKTNCPASCFCQNKII
This study: ---------------------------------------------------------------------------------------------------------------------
```

2. Cysteine-rich secretory protein, Stecrisp, Chain A (Peak 9)

```
1RC9:       NVDFDSESPRKPEIQNEIVDLHNSLRRSVNPTASNMLRMEWYPEAADNAERWAYRCIESHSSYESRVIEGIKCGENIYMSPYPMKWTDIIHAWHDEYKDFKYGVGADPPNAVTGHYTQV
This study: NVDFDSESPR---------------------------RSVNPTASNMLRMEWYPEAADNAER---------------------------------------------------------
1RC9:       WYKSYRIGCAAAYCPSSPYSYFFVCQYCPAGNFIGKTATPYTSGTPCGDCPSDCDNGLCTNPCTRENKFTNCNTMVQQSSCQDNYMKTNCPASCFCQNKII
This study: -----------------------------------------------------------------------------------------------------
```

C-type lectins:

1. C-type lectin TsL (Peak 7)

```
Q9YGP1.1:   SCCTNDSLPMNGMCYKIFDEPKTWEDAEMFCRKYKPGCHLASFHRLAESLDIAEYISDYHKRQAEVWIGLLDRKKDFSWEWTDRSCTDYLNWDKNQPDHYKDKEFCVELVSLTGYHR
This study: ----------------IFDEPKTWEDAEMFCRKYKPGCHLASFHR----------------------------KKDFSWEWTDRSCTDYLNWDKNQPDHYKDKEFCVELVSLTGYHR
Q9YGP1.1:   WNDQVCESKNSFLCQCKF
This study: WNDQVCESK---------
```

C-type natriuretic peptide:

1. Bradykinin-potentiating C-type natriuretic peptide (Peak 2)

```
P0C7P6.1:   QEKPGRSPPISPLLVPPPPPPPHWPPPHHIPPLSVQKFPPGWKPTHPHHIPPLEVQQWSQGGPRSELVQPHESPAGGTTAFREELSLGPEAASGPAAPQRLPKRKGASATSAASRSMRDLR
This study: ------------------------------------------------------------------------------------EELSLGPEAASGPAAPQR--------------------
P0C7P6.1:   ADGKQARQKWGRMVQPDHHAAPGGGGGGGGGARRLKGLAKKAVGKGCFGLPLDRIGSMSGMGC
This study: ---------------------------------------------GCFGLPLDR---------
```

Glutaminyl-peptide cyclotransferases:

1. Glutaminyl-peptide cyclotransferases (Peak 10)

```
AFE84763.1: MARERRDSKAATFFCLAWALCLALPGFPQHVSGREDRADWTQEKYSHRPTILNATCILQVTSQTNVNRMWQNDLHPILIERYPGSPGSYAVRQHIKHRLQGLQAGWLVEEDTFQSHTPYGYR
This study: ------------------------------------------------------------MWQNDLHPILIERYPGSPGSYAVR------LQGLQAGWLVEEDTFQSHTPYGYR
AFE84763.1: TFSNIISTLNPLAKRHLVIACHYDSKYFPPQLDGKVFVGATDSAVPCAMMLELARSLDRQLSFLKQSSLPPKADLSLKLIFFDGEEAFVRWSPSDSLYGSRSLAQKMASTPHPPGAR
This study: TFSNIISTLNPLAKRHLVIACHYDSKYFPPQLDGKVFVGATDSAVPCAMMLELAR----------------------LIFFDGEEAFVRWSPSDSLYGSR----------------
AFE84763.1: NTYQIQGIDLFVLLDLIGARNPVFPVYFLNTARWFGRLEVIERNLYDLGLLNNYSSERQYFRSNLRRHPVEDDHIPFLRRGVPILHLIPSPFPRVWHTMEDNEENLDKPTIDNLSK
This study: --------------------NPVFPVYFLNTAR---------------------------------RHPVEDDHIPFLRRGVPILHLIPSPFPRVWHTMEDNEENLDKPTIDNLSK
AFE84763.1: ILQVFVLEYLNLG
This study: -------------
```

APPENDIX II

Permissions and Approvals from Ethical committee

No. FFE-B-F(10)-3/2017
Government of Himachal Pradesh,
Department of Forests.
***

From

Additional Chief Secretary (Forests) to the
Government of Himachal Pradesh, Shimla-2.

To

The Principal Chief Conservator of Forests (Wildlife)-cum-
Chief Wildlife Warden, Himachal Pradesh, Shimla-171001.

Dated Shimla-171002, the 1st August, 2017.

Subject:- **Application for access to Biological Resources in Himachal Pradesh.**

Sir,

I am directed to refer to your letter No. WL/Research Study/WLM/1607, dated 01-07-2017 on the subject cited above and to convey the approval of the Government under Section 12(b) of the Wildlife (Protection) Act, 1972 to collect venom, blood samples and tissue (scales clips) from snakes of Elapidae, Viperidae and Colubridae families from Solan, Bilaspur, Palampur, Una, Chamba & Paonta Sahib forest areas in favour of Dr. Omesh Kumar Bharti, Set-9, Block-1, US Club Shimla and team members Dr. Anita Malhotra, Mr. Vishal Santra, West Bengal, Prof. Kartik Shankar, Bangalore, Dr. Robin Doley, Associate Professor, Tezpur and Dr. BL Dhanajaya, Bangalore subject to completion of all codal formalities.

You are, therefore, requested to take further necessary action accordingly.

Yours faithfully,

(Sat Pal Dhiman) 01-08-2017
Joint Secretary (Forests) to the
Government of Himachal Pradesh.
Phone No. 0177-2621874.

*****

GOVERNMENT OF MIZORAM
OFFICE OF THE CHIEF WILDLIFE WARDEN
ENVIRONMENT, FOREST & CLIMATE CHANGE DEPERTMENT
MIZORAM :: AIZAWL
****

No.A.33011/5/2011-CWLW/305 : Dated Aizawl the 18th July/ 2016

To,

Dr. H.T. Lalremsanga
Assistant Professor
Mizoram University
Aizawl, Mizoram.

Subj : ***Permission to collect biological samples from Medically Significant Venomous snakes of Mizoram for the project titled 'Biodiversity Informatics and Technology Exchange for Snakebite Management'.***

Ref : Your application No: nil dt. 29th June 2016.

Permission is hereby granted to you for non-invasive collection of biological samples from medically significant venomous snakes of Mizoram for the Project titled 'Biodiversity Informatics and Technology Exchange for snakebite Management within Mizoram.

However, you are requested to deposit Rs. 100.00 (one hundred) only as per the provision of Mizoram State Biodiversity Rule, 2010 Claused (1) of Rule 17 to Chief Wildlife Warden by Bank Draft or IPO

Further it will be obligatory on your part to share all the information and research findings with this department, whatever collected through this permit.

18/7/16
(LIANDAWLA)
Chief Wildlife Warden
Mizoram :: Aizawl

Memo No.A.33011/5/2011-CWLW/305 : Dated Aizawl the 18th July/ 2016
Copy to:-

1) All CFs viz, SC Lunglei, CC Aizawl, NC Aizawl, Wildlife for information.

Chief Wildlife Warden
Mizoram :: Aizawl

DATE: 8.06.2012

CERTIFICATE

THIS IS TO CERTIFY THAT THIS SNAKE VENOM RELEASED ONLY FOR RESEARCH PURPOSE AND THIS PARCEL CONTAINS THE FOLLOWING SNAKE VENOMS.

1. COBRA SNAKE VENOM	1.000 gm
2. KRAIT SNAKE VENOM	1.000 gm
3. RUSSELL'S VIPER SNAKE VENOM	1.000 gm
4. SAW SCALED VIPER SNAKE VENOM	1.000 gm

SNAKE VENOMS WEIGHED BY

C.V. 8.6.12

Special Officer
IRULA SNAKE CATCHERS ICS LTD.,

SNAKE VENOM WEIGHMENT INSPECTED

8.6.12

FOREST RANGE OFFICER,
WILDLIFE ENFORCEMENT RANGE.
CHENNAI – 32.

FOREST RANGE OFFICER HEAD QUARTERS RANGE (WILD) Date: 8.6.12

SNAKE VENOM PARCEL DESPATCH

TO
Dr. Dr. D.Velmurugn,
Professor,
University of Madras,
Dept. of Crystallography and Biophysics,
Guindy Campus,
Chennai - 25.

Tezpur University Ethics Committee
Tezpur: 784028 : Assam

Communication of Decision of Tezpur University Ethics Committee (TUEC)

IEC No: DoRD/TUEC/PROP/2022/01

Protocol title: Identification and characterisation of anti-platelet proteins/peptides from Indian *Daboia russelli* venom and understanding its molecular mechanism
Principal Investigator: Prof. R. Doley
Name & Address of Institution: Tezpur University, Tezpur, Assam 784028
[√] New review [ ] Revised review [ ] Expedited review
Date of review (D/M/Y): 29-09-2022 Date of previous review, if revised application:
Decision of the IEC/IRB: [ ] Recommended [√] Recommended with suggestions [ ] Revision [ ] Rejected
Suggestions/Reasons/Remarks: a) Blood will be collected under the supervision of concerned doctors. b) Initial approval is recommended for one year, with subsequent approval being subjected to satisfactory reports.
Recommended for a period of: 1 year

Please note

-Inform TUEC immediately in case of any adverse events and serious adverse events
-Inform TUEC in case of any change of study procedure, site and investigator
-This permission is only for period mentioned above. Annual report to be submitted to TUEC
-Members of TUEC have right to monitor the trial with prior intimation

Date: 21/03/2023

Signature of Chairperson (with seal)

TUEC

Chairperson
Tezpur University Ethics Committee

No. 834

Date. 02.02.2022

TO WHOM IT MAY CONCERN

This is to certify that Dr. Surajit Giri is an Anesthesiologist under National Health Mission in Demow Community Health Centre, Sivasagar Assam. District Health has no objection to publish the data on Green Pit Viper in Toxicon Journal.

2/02/22
(Dr. H. K Baruah)
Joint Director of Health Services,
Sivasagar.

Jt. Director of Health Services
Sivasagar

APPENDIX III

Reprint of publication

Toxicon 210 (2022) 66–77

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Venom of several Indian green pit vipers: Comparison of biochemical activities and cross-reactivity with antivenoms

Susmita Thakur [a], Anita Malhotra [b], Surajit Giri [c], H.T. Lalremsenga [d], Omesh K. Bharti [e], Vishal Santra [f,g], Gerard Martin [h], Robin Doley [a,*]

[a] Molecular Toxinology Laboratory, Department of Molecular Biology and Biotechnology, Tezpur University, Assam, 784028, India
[b] Molecular Ecology and Evolution at Bangor, School of Natural Sciences, Bangor University, Bangor, LL57 2UW, Gwynedd, UK
[c] Demow Government Community Health Centre, Raichai, KonwarDihingia Gaon, Sivasagar, Assam, India
[d] Department of Zoology, Mizoram University, Aizawl, 796004, Mizoram, India
[e] State Institute of Health & Family Welfare Parimahal, Shimla, HP, India
[f] Society for Nature Conservation, Research and Community Engagement (CONCERN), Nalikul, Hooghly, West Bengal, 712407, India
[g] Captive and Field Herpetology, 13 Hirfron, Anglesey, LL65 1YU, Wales, UK
[h] The Liana Trust, Survey #1418/1419, Rathnapuri, Hunsur, Karnataka, India

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ABSTRACT

Green pit vipers, a name that can refer to several unrelated species, comprise a large group of venomous snakes found across the humid areas of tropical and sub-tropical Asia, and are responsible for most of the bite cases across this region. In India, green pit vipers belonging to several genera are prevalent in the northern and north-eastern hilly region, unrelated to species present in the peninsular region. In the present study, crude venom of representative species of green pit vipers present in the north and north-eastern hilly region of India (*Trimeresurus erythrurus*, *T. septentrionalis, Viridovipera medoensis*, and *Popiea popieorum*) were characterized to elucidate venom composition and venom variation. Profiling of crude venoms using SDS-PAGE and RP-HPLC methods revealed quantitative differences among the species. Further, *in vitro* biochemical assays reveal variable levels of phospholipase activity, coagulation activity, thrombin-like activity, fibrinogenolytic and haemolytic activity. This correlates with the pseudo-procoagulant effects on the haemostatic system of victims, which causes consumptive coagulopathy, frequently observed in patients bitten by green pit vipers. The immunoreactivity of Indian polyvalent antivenom and Thai green pit viper antivenom towards crude venoms were also evaluated by western blotting and inhibition of biochemical activities. The results exhibited poor efficacy of Indian polyvalent antivenom in neutralizing the venom toxins of crude venoms; however, Thai green pit viper antivenin (raised against the venom of *Trimeresurus allbolabris*, not present in India) showed higher immunoreactivity towards congeneric venoms tested. Analysis of green pit viper bite patients records from a community health centre in Assam, India, further revealed the inability of Indian polyvalent antivenom to reverse the extended coagulopathy featured.

1. Introduction

The *Trimeresurus* radiation, belonging to the Crotalinae subfamily of the family Viperidae, comprises the largest group of venomous snakes in tropical and sub-tropical Asia. This group consists of around 55 species (listed under *Trimeresurus* and *Craspedocephalus* in www.reptile-database) that were reclassified into different genera (Malhotra and Thorpe, 2004), which some authors prefer to treat as subgenera (David et al., 2011). Their distribution ranges from the Indian subcontinent throughout Southeast Asia, southern China and the Indo-Malayan and Philippine archipelagos. A large number of species have a characteristic bamboo green to yellow body colour and are generally described as "Green Pit Vipers". The literature on green pit viper bites in Southeast Asian countries (including Thailand, China, Sri Lanka, Singapore, Vietnam, Nepal) suggests their medical importance and considerable role in global snakebite epidemiology (Blessmann et al., 2018; Fuchs et al., 2019; Mong and Tan, 2016; Pandey et al., 2019; Rathnayaka et al., 2017; Zeng et al., 2019). Clinical manifestations observed in victims of green pit viper envenomation include local symptoms such as extensive swelling of bite site, mild dyspnoea, nausea and significant pain,

* Corresponding author.
E-mail address: doley@tezu.ernet.in (R. Doley).

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Journal of proteome research

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Article

Proteome Decomplexation of *Trimeresurus erythrurus* Venom from Mizoram, India

Susmita Thakur, Avni Blotra, Karthikeyan Vasudevan, Anita Malhotra, Hmar Tlawmte Lalremsanga, Vishal Santra, and Robin Doley*

Cite This: *J. Proteome Res.* 2023, 22, 215−225

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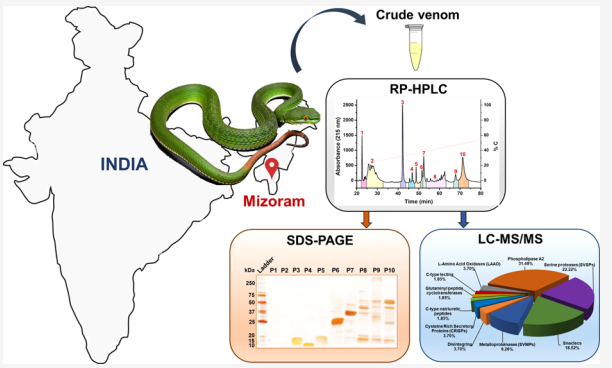
ABSTRACT: Green pit vipers are the largest group of venomous vipers in tropical and subtropical Asia, which are responsible for most of the bite cases across this region. Among the green pit vipers of the Indian subcontinent, *Trimeresurus erythrurus* is the most prevalent; however, limited knowledge is available about its venomics. Proteome decomplexation of *T. erythrurus* venom using mass spectrometry revealed a blend of 53 different proteins/peptides belonging to 10 snake venom protein families. Phospholipase A_2 and snake venom serine proteases were found to be the major enzymatic families, and Snaclec was the major nonenzymatic family in this venom. These protein families might be responsible for consumptive coagulopathy in victims. Along with these, snake venom metalloproteases, L-amino acid oxidases, disintegrins, and cysteine-rich secretory proteins were also found, which might be responsible for inducing painful edema, tissue necrosis, blistering, and defibrination in patients. Protein belonging to C-type lectins, C-type natriuretic peptides, and glutaminyl-peptide cyclotransfreases were also observed as trace proteins. The crude venom shows platelet aggregation in the absence of any agonist, suggesting their role in alterations in platelet functions. This study is the first proteomic analysis of *T. erythrurus* venom, contributing an overview of different snake venom proteins/peptides responsible for various pathophysiological disorders obtained in patients. Data are available via ProteomeXchange with the identifier PXD038311.



KEYWORDS: *snake venom, green pit viper, Trimeresurus, proteomics, coagulopathy, platelet aggregation*

1. INTRODUCTION

Studies elucidating the venom composition of various snakes and understanding their mechanism of action causing various pathophysiological alterations have remained a fruitful subject of investigation for toxinologists all around the world. The advancement in "omics" technology has made the understanding of venom dynamics more feasible. Consequently, venom composition of various Asian pit vipers has been studied with the help of proteomic approach, e.g., *Viridovipera stejnegeri*, *Trimeresurus albolabris*, *Popeia nebularis*, *T. insularis*, *T. purpureomaculatus*, *Craspidocephalus malabaricus*, and *C. puniceus*.[1−6] Various studies have established a correlation between venom composition and the clinical toxicity presented by snakebite victims, thereby adding to the knowledge of venom-induced pathophysiology. For instance, the predominance of snake venom metalloproteases (SVMPs) in the venom of *Popeia nebularis* has been found to be responsible for acute edema and hemorrhage in envenomated victims.[3] Similarly, the abundance of cytotoxin 3FTx and PLA_2 in the venom of Indian *Naja kaouthia* causes severe tissue necrosis.[7]

Trimeresurus erythrurus (Reptilia: Serpentes: Viperidae: Crotalinae), commonly known as the red-tailed or spot-tailed pit viper, is a member of the widespread *Trimeresurus* complex of Asiatic pit vipers. They are nocturnal and arboreal pit vipers that are green in overall coloration, possessing a prehensile tail adorned with reddish- or brownish-colored spots. They are distributed from India and Bangladesh into western Myanmar. In India, *T. erythrurus* is present in coastal mangrove forests in the Sundarbans of West Bengal, Odisha, and as far south as Kakinada in Andhra Pradesh[8] but is also prevalent in the hills of the north-eastern region (including in Assam, Mizoram, Manipur Meghalaya, Nagaland, and Tripura). However, envenomation reports of *T. erythrurus* are scarce in the literature, at least partly because of the morphological similarity among several species of green pit viper that are prevalent in the same area (e.g., *Trimeresurus salazar*). In most cases, the snake is identified as a "green snake" by snakebite victims, a description

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ORIGINAL PAPER

Effects of Dielectric Barrier Discharge Plasma on Physicochemical Characteristics, Mechanical Properties and Biocompatibility of Silk/PVA Nanofibers

Namita Ojah[1] · Susmita Thakur[2] · Dolly Gogoi[3] · Gazi Ameen Ahmed[1] · Manabendra Mandal[2] · Robin Doley[2] · Arup Jyoti Choudhury[1,4]

Received: 13 January 2021 / Accepted: 21 October 2021

Abstract
This work reports an investigation of the discharge characteristics of atmospheric dielectric barrier discharge (DBD) plasma in terms of I-V curves and Lissajous figures and their effect on the surface functionalities of electrospun silk/PVA nanofibers. The results show that the filamentary discharge is predominant at lower electrode gap (3 mm) and then significantly reduces at higher electrode gaps of 6 mm and 10 mm, respectively and in the applied voltage range of 11–17 kV. The silk/PVA nanofibers which are treated with 6 mm electrode gap shows good wettability, higher surface energy, higher tensile strength, young's modulus values and improved anti-thrombogenic property. All these findings suggest that, although the silk/PVA nanofiber itself can be used in biomedical applications however, nanofibers plasma treated at 6 mm electrode gap shows better results in terms of physical and biological performances.

Keywords Dielectric barrier discharges (DBD) · Plasma treatment · Surface modification · Mechanical properties, cell viability

Introduction

Silk fibroin based nanofibers have rapidly emerged as potential biomaterials for various biomedical applications [1–3]. The advantages of silk fibroin based nanofibers include but not limited to their outstanding properties such as biocompatilibity, flexibility, controlled microporous structure, large surface to volume ratio and morphology similar to that of native

✉ Arup Jyoti Choudhury
arupjchoudhury@gmail.com

[1] Laboratory for Plasma Processing of Materials, Department of Physics, Tezpur University, Napaam, Tezpur, Assam 784028, India

[2] Department of Molecular Biology and Biotechnology, Tezpur University, Napaam, Tezpur, Assam 784028, India

[3] Central Instruments Facility, Indian Institute of Technology, Guwahati, Assam 781039, India

[4] Department of Physics, Guwahati College, Bamunimaidam, Guwahati, Assam 781021, India