Tel. +91 364 272 1241, 272 2312; Fax. 2550300; E-mail: bicnehu@gmail.com

Next Generation Sequencing (NGS)- based *de novo* assembly of expressed transcripts and genome information of Orchids in North-East India

[DBT, Govt. of India; Sanction no.: BT/325/NE/TBP/2013 dated August 07, 2014]

Dr. Devendra Kumar Biswal, Principal Investigator, NEHU
Dr. Sundar D. Sundar, Principal Investigator, IIT, New Delhi

Bioinformatics Centre
North-Eastern Hill University
Shillong 793 022

F-1/NEHU/BIC/DBT-NER TWINNING/NGS ORCHIDS/240 May 15, 2017

NOTICE INVITING QUOTATIONS dt: 15/05/2017

I. Denovo Whole Genome Sequencing of 2 plant specimens

- **Library Preparation:**
  - TruSeq Nano DNA Library Prep Kit
  - Efficient library preparation from samples with limited available DNA, delivering high coverage quality and reduced bias.
  - Shot Gun Library: Two libraries will be prepared with two different inserts (Short and long inserts, 250-300 bp and 500-600 bp).
  - Mate Pair Library: 2 different mate libraries with two different insert length (3kb and 5kb).
- **Sequencing, Coverage (X) and Read (millions):**
  - Approx 150-200 X coverage of the plant specimens A and B genome (appx 1.5 GB each). Should Include Shot gun libraries and 30x coverage of mate pair libraries.
  - Platform HISEQ ILLUMINA series

- **Bioinformatics-**

  Quality filteration of reads, kmer depth distribution analysis, In silico genome size estimation, denovo assembly generating scaffolds/contigs, assembly statistics, In silico validation of assembly using RNA-Seq data, GC percentage, repeat identification, generation of gene model using transcriptome data (RNAseq data required), gene prediction, gene annotation, GO analysis, SSR discovery, SNP/Indel discovery(if more than one sample), phylogenetic analysis, KEGG pathway analysis, comparative genomics with closely related genomes, circos plot, COG, orthologous groups analysis using Orthomcl, core gene analysis, comprehensive report with **publication standard methodology, graphs and tables.**

- **Whole chloroplast genome sequencing.**

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II. Transcriptome Sequencing from Root, Shoot, Leaf and Flower Tissue

- Total RNA Quality check
- Ribominus depletion of Total RNA and QC of samples.
- Library Preparation: Individual Library preparation will be done for each sample for Illumina NextSeq 500 / Hiseq platform
- Coverage (X) and Read (millions): >100M
- Bioinformatics analysis: QC of Raw data and Trimming of barcoded, Denovo Assembly of RNAseq data and annotation to the closest species, Gene Ontology, Pathway annotation, Differential Gene Expression, Pathway analysis

Comparitive analysis of RNAseq to identify the important biosynthetic pathways of medicinal value through transcriptome based on the literature, inputs provided by researcher and also transcriptome data generated by service provider.

III. Small RNA sequencing of

- **T**otal RNA extraction from 4 different tissues (Root, flower, stem and leaf) samples and quality control using tapestation. denaturing agarose gel electrophoresis, Nanodrop, Qubit flurometer and RIN.
- Preparation of small RNA library.
- Sequencing using Illumina Nextseq500 platform using 75bp SE module to generate 12-15 million reads data per sample.
- Bioinformatics-Quality filteration of reads, homology based identification of known miRNA, expression profiling of miRNA, differential miRNA analysis(if more than one sample), Novel precursor miRNAs and mature miRNA, secondary structures of candidate(novel) precursor miRNAs, target identification of known and novel miRNA, functional annotation of targeted genes, comprehensive report with publication standard methodology, graphs and tables.
- Emphasis should be given to identify the non-coding genes namely the genes of microRNA, TAS, antisense-RNA, long non-coding RNA etc by in silico approaches.
- RNAs of four tissues (with maximum and minimum amount of the compound) to be sequenced and compared for identification of pathways. The predicted pathways are to be validated by expression analysis in various tissues. If possible, the similar orchid species which do not produce the

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compound should be identified and its RNA from the reciprocating tissue should be analysed in the similar ways.

2 -3 Manpower from the Centre to be trained during the ongoing project.

General Terms & Conditions:

1) All interested suppliers/vendors shall send their bids addressed to The Principal Investigator, NGS Orchid Project, Bioinformatics Centre, North-Eastern Hill University, Shillong-793 022, Meghalaya, India.
2) Quotation should be submitted within 15 days. Quotation received after due date will not be considered. (The university will not be responsible for any postal delay).
3) The Department purchase Committee (DPC) can accept or reject any quotation without assigning any reason thereof and does not bind him to accept the lowest rate whatsoever.
4) No separate tender paper will be issued from the office; one should only download the specifications/list from the University website.
5) The price should be quoted on FOR destination.
6) The rates should be inclusive of all taxes, freight charges and applicable tax as per norms should be clearly indicated.
7) Quoted rates should be at least valid for a period of two months.
8) The rates should be quoted along with supporting documents of specifications and technical features for NGS services.
9) Payment will be made only after completion of the deliverables to our full satisfaction and bills may be submitted in triplicate. Under quality/poor quality of NGS (whole genome/transcriptome) data of supply shall not be accepted and payment cannot be released.
10) NGS Data should be supplied in HARD DRIVE to the PI of the Project.

Sd.
Devendra Kumar Biswal
Co-Investigator
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Shillong- 793022.