



राष्ट्रीय पादप जीनोम अनुसंधान संस्थान

(जैव प्रौद्योगिकी विभाग, विज्ञान एवं प्रौद्योगिकी मंत्रालय, भारत सरकार का स्वायत्त अनुसंधान संस्थान)

NATIONAL INSTITUTE OF PLANT GENOME RESEARCH

(An Autonomous Institution of the Department of Biotechnology, Ministry of Science and Technology, Government of India)

अरुणा आसफ अली मार्ग, पो. बाक्स नं. 10531, नई दिल्ली-110067
Aruna Asaf Ali Marg, Post Box Number 10531, New Delhi-110067

संख्या: 9/2015-16/रा.पा.जी.अनु.सं./एस एण्ड पी

दिनांक: 06/7/2015

विषय / Subject: मुहरबंद कोटेशन का निमंत्रण / Invitation of Sealed Quotations

Sealed Tenders are invited on behalf of Director, NIPGR from the service provider or their authorized dealers for **Fungal genome sequencing (3 samples)** as per the specifications attached at Annex – I for our Institute.

You are therefore requested to please send your offer in **two bid system** indicating the maximum discount offered. The quotations must accompany a Demand Draft amounting to ₹ 20,000/- (Rupees Twenty Thousand only), being the EMD in the name of Director, NIPGR, New Delhi and must be sent in a **Sealed Envelope** duly super-scribed on top of envelope as **Outsourcing of Custom high-throughput SNP genotyping services** so as to reach to the undersigned latest by **27/7/2015 (3:00 p.m.)**, the same shall be opened on same day at **3:30 p.m.**

धन्यवाद,

(कय एवं भण्डार अधिकारी)

Encl: Terms & Conditions (Annex – II)

De novo sequencing for creation of reference genome for a fungal species (polyploidy) and another two related fungal genomes sequencing with comparative genomics studies

Part 1. De novo sequencing for creation of reference genome for a fungal species (polyploidy, approximate total size of the genome would be approximately 140-160 Mb): 1 sample

The service provider should perform quality extraction of DNA, followed by long (500- 600 bp) and short insert (300- 400 bp) library preparation for denovo sequencing with minimum 150X coverage on illumina platform with long read sequencing (150bp PE), sequencing of two mate pair library (illumina) of 3 kb and 8Kb insert size with minimum 50X coverage and Pac bio sequencing (20 Kb insert library) for better assembly with minimum 5X-10 X coverage.

Part 2. Multiple fungal genomes (polyploidy, approximately total genome size would be 140-160 Mb) sequencing & denovo/reference assisted assembly depending on the fungal variation and comparative genomics analysis with an aim of synteny development: 2 samples

The service provider should perform quality extractions of DNA, followed by short insert (300-400 bp) library preparation for denovo sequencing with minimum 150X coverage on illumina platform with long read sequencing (150bp PE), sequencing of two mate pair library (illumina) of 3 kb insert size with minimum 20X coverage.

The sequencing service should include,

Appropriate quality and quantity of DNA Extraction supported by appropriate DNA QC parameters.

DNA Library preparation and QC reports.

Appropriate specified sequencing and coverage statistics and QC reports. More than 90% should be Q30 and above. The minimum coverage should be as specified above.

Bioinformatics analysis for Part 1: De novo sequencing and creation of reference genome.

- ✓ Statistics of data production and SeqQC/FastQC reports.
- ✓ De novo assembly, scaffolding and super scaffolding. Super scaffolding and gap closure reports when applicable post mate-pair or hybrid assembly – Scaffolds number should be less than 1000 which is more than 1 kb.
- ✓ Assembly and Alignment report summarizing mapping results. Provide episomal assembly statistics.

- ✓ Statistic report detailing coverage, orientation of mapped reads, and numbers of unmapped reads.
- ✓ Summary of coverage available in both graphical and tabular format.
- ✓ Build consensus sequence of the sequenced genome.
- ✓ Chromosome wise segregation of contigs from the build consensus.
- ✓ Abinitio Gene prediction & ORF prediction
- ✓ Mapping of reads on most closely related reference genome for reference based assembly and provide comparative genomics statistics.
- ✓ GO annotation of identified genes, pathway match and pattern match to specified signatures/motifs.
- ✓ Genome annotation and functional classification using GO, KEGG, KOG, etc
- ✓ SSR prediction.
- ✓ Identification of gene families and functional classification.
- ✓ Prediction of plant-pathogenicity gene candidates by comparative omics.
- ✓ Discovery of transposable elements and retro sequences

Bioinformatic analysis for Part 2: Denovo/Reference assisted assembly depending on the fungal variation and comparative genomics analysis with an aim of synteny development.

- ✓ Statistics of data production and SeqQC/FastQC reports.
- ✓ De novo/reference based assembly and scaffolding. Using sequences from short insert libraries and mate pair library.
- ✓ Assembly and Alignment report summarizing mapping results for individual fungus. Provide episomal assembly statistics.
- ✓ Statistic report detailing coverage, orientation of mapped reads, and numbers of unmapped reads.
- ✓ Summary of coverage available in both graphical and tabular format.
- ✓ Gene prediction & ORF prediction
- ✓ Mapping of reads on reference created through denovo and provide comparative genomics analysis.
- ✓ SSR prediction and comparison.
- ✓ Phylogenetic analysis.
- ✓ Synteny map development based on comparative genomics analysis.
- ✓ Genome annotation and functional classification using GO, KEGG, KOG, etc
- ✓ Identification of gene families and functional classification.
- ✓ Prediction of plant-pathogenicity gene candidates by comparative omics.
- ✓ Discovery of transposable elements and retro sequences

Other Terms and conditions:

1. The bidder should provide proof of in-house NGS facility and Bioinformatics analysis in India and allow scientists to visit for inspection at any stage of project process.
2. Sequencing and Bioinformatics analysis should be carried out by an experienced person (with publication on the same with his or her credit) who should have a PhD degree in the given subject.
3. Bioinformatics analysis and post analysis requirements, may change depending on the initial leads, bioinformatics support should be given until manuscript preparation and even to satisfy the reviewers comment and publication.
4. Service provider should have standardized Lab and bioinformatics pipeline and should provide free training and support on Lab work and data analysis upon project completion at their facility and help in publication of research paper.
5. The turnaround time for the project should be less than 90 days.
6. The service provider should be certified as per ISO standards and any other certification/authorization related to the genomics platforms should be provided and will be considered during bid.
7. Service provider should have demonstrated expertise in 'De novo sequence assembly for **'higher eukaryote'** as publication. Minimum one reference publication (Co-authored) as a proof of technical capability for De novo whole genome sequencing project.
8. If there are discretions between technical bid and **financial bid such bid will be disqualified and service provider would not be entertained in the future.**

Annexure – II

नियम और शर्तें:

- The quotations must accompany a Demand Draft amounting to ₹ 20,000/- (Rupees Twenty Thousand only), being the EMD in the name of Director, NIPGR, New Delhi. In the event of non fulfillment of work awarded / withdrawal of quotations, the EMD will be forfeited by the Institute.
- The rates quoted by you for the said services shall be valid for a period of one year from the date of Work Order and no requests for any increase in the rates will be entertained during the contract period. No advance payment will be made.
- The Director, NIPGR reserves the right to amend any of the terms and conditions contained in the Tender Document or reject any or all applications (offers) or not to award the contract to the lowest bidder without giving any notice or assigning any reason thereof. The decision of the Director, NIPGR in this regard will be final and binding.
- The successful tenderer shall be required to deposit an interest free amount equal to 10% of the tender value of the contract in the form of Demand draft as Performance Security after adjusting the EMD, within 10 days from the date of issue of Letter of Acceptance of Tender, which will be released after expiry of the defect liability period of the contract as per terms and conditions failing which the same will be forfeited.
- The bids will be accepted in respect of those companies having successfully completed one similar work costing not less than ₹ 8,00,000/- or two similar works each costing not less than ₹ 5,00,000/- or three similar works each costing not less than ₹ 4,00,000/- and having annual financial turnover of ₹ 10,00,000/- during the last three financial years. Similar works means, work related to analysis of similar samples in Government National Laboratories / Institutions / Universities and reputed Organizations, engaged in the area of Research & Development. Intending tenderers must enclose documents such as Completion Certificates and Work / Supply orders / certified Balance Sheet / ITR Returns for three last financial years.

(कय एवं भण्डार अधिकारी)