

Dr. Somnath Bhattacharyya Professor in Genetics and Plant Breeding Officer in Charge, Crop Research Unit Research Directorate Bidhan Chandra Krishi Viswavidyalaya,

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Tender Notification

Ref. No. BCKV/CRU/2425/P I (ICAR)/Ten22(A)

Date. 20.3.25

The officer in Charge of the Crop Research Unit and PI of the Adhoc-funded project is inviting price quotations from the competent and bonafide vendors/ dealers having registration of GST for the supply of the following to the University within seven days from the date of publication of this notice in the newspaper as per the specifications appended below (Table 1). Vendors are requested to quote the cost with GST, valid by 30th June 2025. The number of samples in the purchase order may vary subject to the availability of funds. The payment will be processed only after satisfying the supplied data and analysis per the desired quality and quantity described in the tender document and purchase order.

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Date, 20.3.25

	S.No	Name of the Item	Approx. Qty.	Detailed Specification	Cost (Rs.) +GST
As per decir of the 71st mer of LTC held on 21/3/18 tende notice is onlo to publish as per mer.	1 Ang med	NGS based whole genome sequencing of 04 samples (2 genotypes and 02 Bulks) with 30 Gegabases data for each sample and identifying polymorphism thereof for QTL analysis	04	1.Samples will be picked up from BCKV and shipped to the sequencing firm on dry ice. If required, samples will be picked up repeatedly until the quality passes. 2.QC analysis of genomic DNA using gel electrophoresis and flurometer; confirmation about QC from indenter before proceeding to library preparation. 3.Library preparation should include barcoded library preparation for (a) PACBIO/Oxford Nanopore platform and (b) 150 bp pair-end (PE) library for Illumina Novaseq platform. 4. Sequencing The whole genome sequencing work should deliver both long reads (using PACBIO/Nanopore sequencing platform), and short read data (using Illumina Novaseq platform), each with 15 Gegabases data. 5. Bioinformatic analysis should include Primary read Statistics and mapping report, Sequence QC (FASTQC/MultiQC) results, de novo assembled genome with hybrid reads, chromosomal assembly/anchorage, sequence gap polishing, genome annotations including gene and repeat elements, gene ontology and pathway analysis. 6. Raw sequencing data files along with analysis report, and supporting files and figures should be shared using SSD storage device. Total amount	