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

e.mail: somnathbhat@yahoo.com,
bhattacharya.somnath@bckv.edu.in
Mohanpur, Nadia, WB 741252, India

e-Tender Notification

Ref. No. BCKV/CRU/2425/P I (ICAR)/Ten22 **Date. 06.03.25**

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 quoted price will not be considered valid without a separate technical bid and earlier experience on the NGS through Oxford nanopore and 150 bp pair-end (PE) for Illumina Novaseq platform. 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 as described in the tender document and purchase order.

Table 1: Ref. No. BCKV/CRU/2425/P I (ICAR)/Ten22 **Date.**

S.No	Name of the Item	Approx. Qty.	Detailed Specification	Cost (Rs.) +GST
1	NGS based whole genome sequencing of 15 samples (Varieties and NILs) with 30 Gegabases data for each sample and identifying polymorphism thereof for QTL analysis	15	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 library preparation. 3. Library preparation should include barcoded library preparation for (a) the PACBIO/Oxford Nanopore platform and (b) the 150 bp pair-end (PE) library for the Illumina Novaseq platform. 4.Sequencing—The whole genome sequencing work must deliver both long reads (using the PACBIO/Nanopore sequencing platform) and short read data (using the Illumina Novaseq platform), each with 15 Gegabases of 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, pathway analysis, polymorphic SNPs, In/Dels.and their use in bulk segregant analysis. 6. Raw sequencing data files along with analysis report, and supporting files (BAMfiles) and figures should be shared using SSD storage device.	
			Total amount	

Bhattacharyya 06/3/25

(S Bhattacharyya)

As per decision of the 69th meeting of LTC held on 06/03/2025 tender notice is allowed to publish as per rule. Subhra Mukherjee. 06/3/25

Librarian

6/3/25