



University of Calcutta
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QUOTATION NOTICE

Ref. No.: WISE-PDF/DC/Consumables/25-26/07

Date: 22.01.2026

Quotation for the following item is invited from authorized parties for supplying the under-noted material for the **WISE-PDF project** titled “**Identification of linked markers and their use in developing *Fusarium* wilt-resistant lentils with terminal heat tolerance**” (Ref. No.: DST/WISE-PDF/LS-160/2024 – Consumables Grant), carried out under **Dr. Swagata Ghosh** and mentored by **Dr. Dipankar Chakraborti**, Department of Genetics.

Suppliers are hereby requested to submit their quotations including the current GST registration certificate, PAN no., copy of registration certificate with statutory authorities and other credentials **within 7 days** from the publication of this notice in a sealed envelope addressed to the undersigned. **Please provide a tender complete in all aspects, otherwise, it won't be considered.** The authority reserves the right to accept/reject any quotation without showing any reason thereof.

Sr. No.	Description	Specification	Sample	Quantity
1.	Next-generation sequencing (NGS) services for whole genome sequencing (WGS) of plant samples, including DNA extraction, 80 GB (Q30) data per sample, comparative analysis, polymorphism detection, gene annotation, and sample transport (dry ice).	Service Required: Reference-based Whole Genome Sequencing (WGS) including DNA extraction, high-quality sequencing, variant discovery, gene annotation, and comparative genomic analysis. Sample Type: Young leaf samples (fresh plant tissue) Sample Transport: Transport from field to servicing laboratory in dry ice , until extraction of high-quality DNA suitable for WGS. Cost must be included. Sequencing Platform: Illumina NovaSeq 6000 or latest equivalent high-throughput platform	Fresh Leaf Samples	1 lentil F4 genotype



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		Sample: Minimum ≥90 GB high-quality trimmed data (Q30) per sample Analysis required: 1. DNA Extraction & Sequencing • High-quality DNA extraction from plant leaf tissue • Whole Genome Sequencing generating ≥90 GB Q30 data per sample • Trimmed and quality-filtered paired-end reads 2. Reference-Based Genome Analysis • Alignment of clean reads to <i>Lens culinaris</i> reference genome • Reference-based assembly and mapping statistics • Total reads mapped • Depth and genome coverage • Percentage of genome covered • Mapping quality metrics 3. Variant Discovery (Polymorphism Search) between two genotypes • SNP and InDel calling • Genomic position of all variants • Annotation of variants • Functional impact prediction of variants • Identification of candidate genes linked to phenotypic or agronomic traits		
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		6. Additional Deliverables • Summary reports with all statistical outputs • Raw data and analysis supporting file should be given. • FASTA, GFF3, VCF files for both samples • Detailed compiled report with interpretations		
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Yours faithfully,

Dr. Swagata Ghosh
Principal Investigator
Department of Genetics,
University of Calcutta

Dr. Dipankar Chakraborti
Associate Professor
Department of Genetics,
University of Calcutta