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QUOTATION NOTICE

Ref. No.: **WISE-PDF/DC/Consumables/26-27/01** Date: **17.08.26.**

Quotations for the following items are invited from authorized parties for supplying the under-noted materials 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.

Sl. 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, Bulked Segregant Analysis (BSA-seq), variant discovery, comparative analysis, polymorphism detection, gene annotation, candidate region /gene identification and linked-marker discovery. and	**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 young leaf samples 15 Resistant+ 15 Susceptible Total-30 plants	2 DNA bulks prepared from 30 individual samples

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	sample transport (dry ice).	**Sample:** Minimum **≥80 GB** high-quality trimmed data **(Q30)** per sample, PE x150bp **Analysis required:** **1. DNA Extraction, QC and Bulk Preparation** · High-quality genomic DNA extraction from each of the 30 individual lentil leaf samples. · DNA quantity and purity assessment · DNA integrity assessment · Separate QC record for each of the 30 DNA samples. · Normalization of DNA concentration followed by equal-quantity/equimolar pooling of 15 resistant DNAs and 15 susceptible DNAs. · Documentation of the exact contribution of each individual plant to the R-bulk and S-bulk. **2. WGS Data Generation and Quality Control (Sequencing from 2 Bulks (R bulk and S bulk)** ·Trimmed and quality-filtered paired-end whole-genome sequencing of R-bulk and S-bulk. ·Minimum ≥80 GB high-quality Q30 trimmed data per bulk, unless the service provider proposes a scientifically justified equivalent coverage. · Adapter removal and quality filtering/trimming. · FastQC/MultiQC or equivalent quality-control assessment. · Raw-read and clean-read statistics, Q30, GC content, read count and duplication statistics. **3. Reference-Based Genome Analysis** · Alignment of clean reads to the latest appropriate *Lens culinaris* reference genome. · Reference genome accession/version must be explicitly reported.		

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		· Reference-based mapping/alignment statistics. · Total reads mapped and percentage mapped. · Mapping quality statistics. · Mean/median sequencing depth. · Genome-wide coverage and percentage of genome covered at relevant depth thresholds. · Coverage/depth plots for both R-bulk and S-bulk. Reference-based assembly and mapping statistics • Total reads mapped • Depth and genome coverage • Percentage of genome covered • Mapping quality metrics **4. Variant Discovery / Polymorphism Detection** · High-confidence SNP calling between R-bulk and S-bulk. · Small InDel calling between R-bulk and S-bulk. · Genomic coordinates of all detected variants. · Reference and alternative alleles. · Read depth, genotype/allele information and quality score for each variant. · Variant quality filtering to remove low-confidence/false-positive variants. · Separate final high-confidence SNP and InDel datasets. **5. Bulked Segregant Analysis (BSA-seq)** · SNP-index calculation for both resistant and susceptible bulks. · Δ SNP-index (SNP-index R − SNP-index S) calculation across the genome. · Allele-frequency difference analysis between R-bulk and S-bulk.		

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		· Sliding-window analysis of SNP-index and Δ SNP-index. · Identification of statistically/significantly differentiated genomic regions/peaks. · Where scientifically appropriate, statistical confidence intervals/thresholds should be estimated by an accepted BSA-seq methodology. · Genome-wide plots of SNP-index, Δ SNP-index and allele-frequency differences. · Identification of candidate genomic intervals associated with *Fusarium* wilt resistance/susceptibility. **6. Variant Annotation and Functional Impact** · Annotation of SNPs and InDels against the Lens culinaris gene annotation. · Classification into intergenic, upstream/downstream, intronic, exonic and other relevant categories. · Synonymous, missense, nonsense/stop-gain, splice-site and other predicted effects where applicable. · Functional impact prediction/prioritization of variants. · Identification of variants located within or near candidate genes. **7. Additional Deliverables** • Summary reports with all statistical outputs • Raw data and analysis supporting file **including BAM** file must be given. • Raw sequencing data, pre-processed and quality-filtered datasets, together with the complete output files, intermediate files, and relevant reports generated by all bioinformatics tools and software used for genome assembly, read alignment, comparative genomic analysis, variant detection and annotation, and functional-effect prediction.		

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		• FASTA, GFF3, VCF files for both samples • Detailed compiled report with interpretations • CIRCOS Plot		

Yours faithfully,

Dr. Swagata Ghosh
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Dr. Dipankar Chakraborti
Professor
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