



INCT Fungi of Brazil

SOP 3: Planning, Demand Survey, and Price Quotation

Disclaimer: *This document was translated from brazilian portuguese with the assistance of generative AI (Gemini).*

Recommendation for Genomic Coordination and Steering Committee

Objective:

To guide the Steering Committee in collecting sequencing requests across the network, organizing project demands (scientific prioritization), and estimating costs (price quotation) with the US sequencing facility.

1. Survey of Sequencing Requests

Before requesting DNA extraction, the Committee must map the strains network researchers intend to sequence. This allows for logistical planning, cost optimization, and prioritization of high-impact scientific samples.

Action: Distribute "Spreadsheet 2: Sequencing Requests and Demands" to all associated laboratories.

Researchers must provide essential biological and taxonomic details:

- Genus and Species (if identified).
- Indication if it is a novel species (*sp. nov.*).

- Indication if it is a Type strain.
- Estimated genome size (in Mb) – Essential for coverage calculation.
- Brief justification of scientific interest.

2. Analysis and Selection by the Committee

Once the spreadsheet is consolidated, the Committee will evaluate proposals based on criteria pre-established by the INCT Fungi of Brazil.

Suggested Prioritization Criteria:

- **Taxonomic Relevance:** Type strains and novel species receive top priority for establishing reference genomes.
- **Biotechnological/Clinical/Agricultural/Environmental Impact:** Strains with applied potential or economic/health significance.
- **Genome Size vs. Budget:** Genome size dictates the data volume (Gigabases - Gb) required to achieve optimal coverage (e.g., 50x to 100x). Very large genomes consume more resources.
- **Execution Capacity:** Does the submitting lab possess the capacity to extract DNA at the required quality, or will it require logistical support (Regional Hub)?

3. Quotation and Budgeting with the Facility

Once samples are selected, the Committee will structure the quote request for the facility.

Required Information for the Facility:

- **Total number of samples:** Batches of 50 to 96 samples are ideal. Batches larger than 96 require multiple robotic runs, adding approximately 1 week to Turnaround Time (TAT).
- **Library Type:** PCR-free library prep.
- **Platform and Insert Size:** Specify whether Illumina (e.g., NovaSeq, PE 150bp) or long-read technology (PacBio/Nanopore) is required, depending on project goals (draft vs. finished genome).
- **Data Output:** Specify desired Gb per sample or average genome size and desired coverage depth.

4. Approval and Extraction Workflow Kick-off

Upon budget approval, the Committee will notify selected laboratories, authorizing the start of DNA extractions in accordance with SOP 1 guidelines (User Manual) and activating the National Logistics Plan.

