Benchling | A Foundational Platform to Accelerate Gene Editing in Agriculture

As companies build genome editing pipelines, they rely on tools for managing samples, data, and results that have barely changed in the past decade. Scientists still use emails, spreadsheets, and standalone molecular biology tools to design and track hundreds of sequences and samples. Alternatively, gene editing data flows and sample tracking are made to fit existing, GMO-based systems despite the unique requirements of gene editing. This means scientists often struggle to find the right samples, have difficulty in managing day-to-day lab operations such as consumable tracking and greenhouse management, and can't easily iterate on development processes. Furthermore, key decisions early in R&D are made with incomplete and inadequate data, with consequences for efficiency and the quality of the desired product.

Benchling is a modern informatics platform that powers agricultural gene editing from early-stage genome editing research through downstream development workflows. By centralizing and standardizing data throughout the gene editing process, Benchling is a one-stop-shop for sample tracking, inventory management, instrument data acquisition, data-driven process optimization, and more. When transitioning from legacy point solutions to Benchling, gene editing companies report productivity increases of 2-4x and unprecedented increases in knowledge retention, improved decision making, and process iteration.

Key Challenges

LARGE MOLECULE REGISTRATION

Tracking gRNA, sequence libraries, plasmids, plant strains, and other samples with spreadsheets and GMO-based legacy systems creates unreliable data and sacrifices experimental context.

PROCESS DEVELOPMENT

Without a system that can associate results data back to samples and process versions, it's difficult to iterate on and optimize development processes.

LAB OPERATIONS

Day-to-day lab operations, such as reagent and consumable tracking, synthetic RNA and DNA design, and greenhouse management are hampered by scattered software.

STRUCTURED DATA CAPTURE

Disparate systems make it impossible to ensure data integrity and accessibility throughout R&D. Reliance on GMO-based data flows causes data to be lost, duplicated, or decontextualized, rendering it useless.

BENCHLING'S SOLUTION

Benchling tracks DNA reagents from gRNAs to constructs, tracks all plant material, captures the diversity of edits in each experiment and associates them with a full lineage, manages physical inventory, and links assay data back to DNA reagents and cell lines.

BENCHLING'S SOLUTION

Structure complex development workflows into assignable, trackable steps. Track your outputs and results against each version of your process. Create new versions in a user interface to iterate quickly.

BENCHLING'S SOLUTION

Track any physical inventory and any physical location, from individual plants and bacterial strains, to plates, freezers, and greenhouses. Trace the full history of any experiment or process.

BENCHLING'S SOLUTION

Benchling is flexible enough to model any biological sample and associate any assay results back to it, through one-to-many and many-to-many correlations. Ensure that all data is being entered in a compliant manner that contextualizes it within specific experiments and processes. Capture the totality of edits' diversity to better-inform decisions and accelerate process iteration.

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Large Molecule Registration System

- **Benchling's registration system** tracks DNA reagents including libraries of sequence parts (e.g. promoters, terminators), synthetic gRNA, primers, genes of interest, constructs and more.
- Track all plant material developed by the research team intelligently compute the material's properties and attributes based on its lineage and related entities.
- **Document transformation SOPs** and capture key process parameters in support of process optimization.
- Manage all physical inventory of strains and DNA reagents.
- **Captures DNA analysis of edited regions**. Correlates individual gRNAs to the totality of edits they produce.
- Store phenotypic and genomic data associated to various DNA probes and plant material.
- **Compatible with third-party** molecular biology tools (ex. Geneious).

Flexible Workflow Engine for Process Development

- **Benchling's Workflows application** is unified with sample registration and tracking functionality.
- Support complex workflows that involve branching and pooling of runs.
- **Capture process and analytical data** in a structured fashion provide infrastructure for automated data acquisition from instrumentation.
- Register and track output seeds and plants.
- Interface with third-party outputs (ex. NGS).
- Version control and change management functionality.
- End-user configurability to support evolving processes.
- Ensure completeness of data sets for better decision making.

Manage Day-to-Day Lab Operations

- **Inventory management system** for tracking labs, freezers, boxes, plates and containers.
- Integrated barcode generation and printing.
- Flexible configuration supports plant and greenhouse management.
- Rich collaboration features (internally and with third-party providers).
- Unification with lab notebook and workflow system improves traceability for all experiments and makes for a seamless user experience.

| € 0 Ⅲ ▲ | WORKFLOWS / PD-3 : Soy Bean - PD Generate Report Configure Report | Initial Culture Setup V Transformation | V Spit Cells V | Pool Cells V | Seed / Plant V Plan | t Phenotying Collapse |
|--|--|--|----------------|--------------|-------------------------|-----------------------|
| Ø | Initial Culture Setup | Input | Output | Process Day | Cell Density (cells/mL) | Volume (mL) |
| • | Init-1 PD-3 Initial Culture Setup Entry | PA Glycine max (soybean) | CULTURE004 | DO | 1e+6 | 25 |
| + | Transformation V | 2 completed | | | | |
| | Split Cells V | Input | Output | Process Day | Cell Density (cells/mL) | Volume (mL) |
| ٩ | Spli-1 | CULTURE005 | CULTURE007 | D3b | 2.9e+6 | 22.5 |
| | Spli-4 PD-3 Split Cells Entry | CULTURE005 | CULTURE008 | D3b | 3.1e+6 | 25 |
| | Spil-5 PD-3 Split Cells Entry | CULTURE005 | CULTURE009 | D3b | 3.3e+6 | 24.6 |
| | SplI-6 ☑ PD-3 Split Cells Entry | CULTURE005 | CULTURE010 | D3b | 4e+6 | 23.3 |
| | Spil-9 PD-3 Split Cells Entry | CULTURE005 | CULTURE011 | D3b | 3.8e+6 | 25.3 |
| | Spli-10 PD-3 Split Cells Entry | CULTURE005 | CULTURE012 | D3b | 2.9e+6 | 24.1 |
| | Spil-11 Z PD-3 Split Cells Entry | CULTURE006 | CULTURE013 | D3b | 3.1e+6 | 25.1 |
| SA | Spli-14 | CULTURE006 | CULTURE014 | D3b | 3.5e+6 | 34.1 ? |



Structured Data Capture

- **Fully configurable data model** for biologics and samples, accessible through point-and-click interface.
- Flexible storage system allows creating locations like labs, freezers, and greenhouses.
- JSON and point-and-click configuration for assay data capture.
- Robust data validation and review functionality.
- Extract structured results from experiments and sync to read only Data Warehouse.
- Mine and visualize data using third-party analytics tools connected to Data Warehouse at the SQL level.

