

Accelerating crop improvement with AI

A platform for accurate & efficient target discovery

March 2024



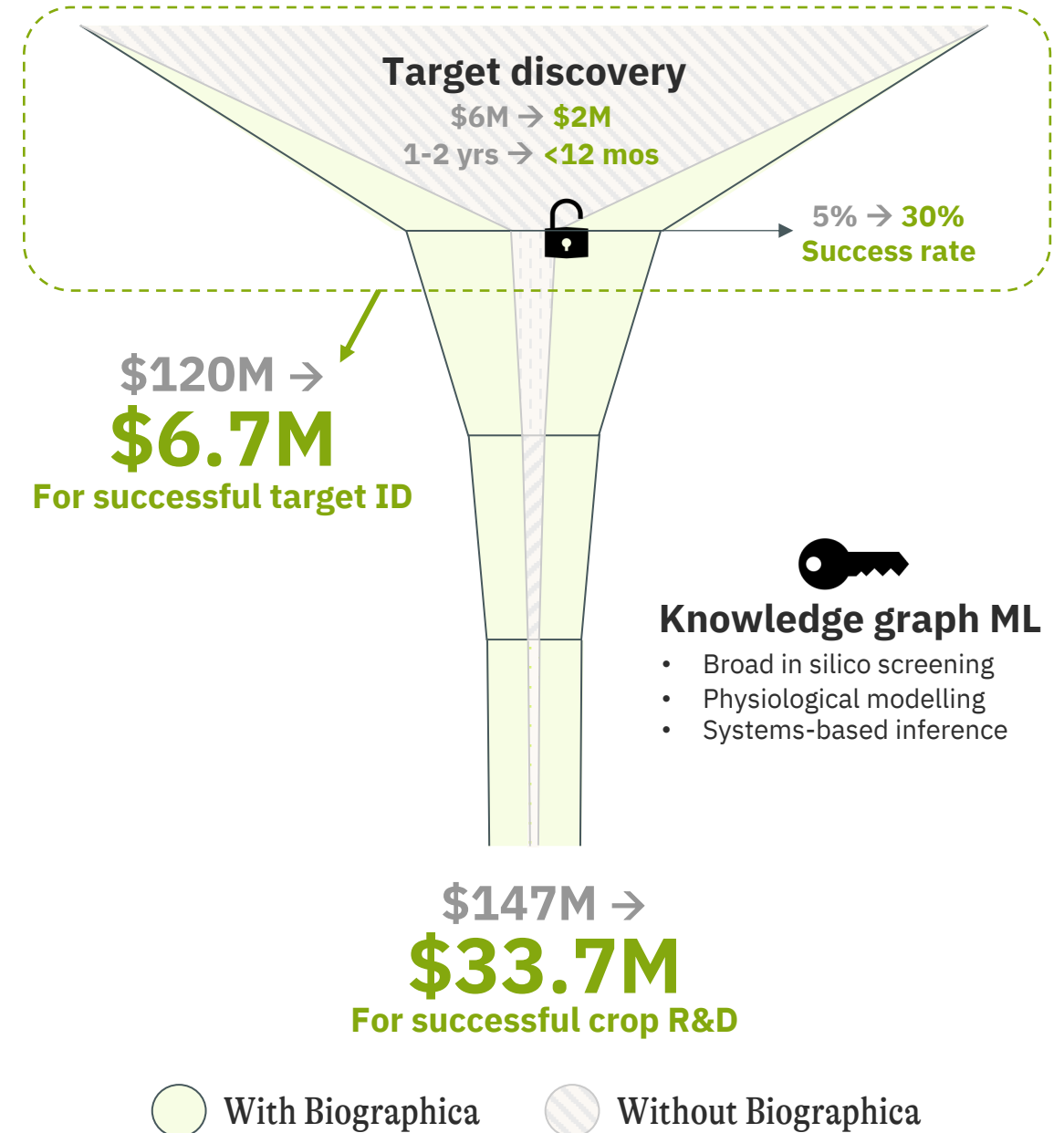
What we do

Reshaping the crop development funnel

Target discovery is a major bottleneck in gene-edited crop R&D. Our mission is to streamline editing pipelines using machine learning (ML)

- ✓ **6x higher target discovery success rates**
- ✓ **2-3x faster target discovery cycles**
- ✓ **18x lower costs for discovery of a successful target**

R&D pipeline for gene-edited crops¹



How we do it

Our discovery platform: decoding crop genetics with AI



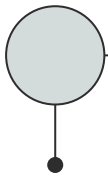
To guide CRISPR use, we need **an efficient discovery platform** that tests things with *in silico* models that recognize genes, metabolic processes, or signalling pathways, and that get strengthened by *in vivo* testing **to predict the 2 or 3 genomic changes for a given trait outcome.**



Head of Crop Trait & Technology Discovery, Syngenta

Current capabilities

Gene ID

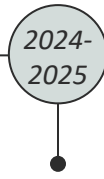


Ranked list of lead genes for given crop trait in weeks

“Gene x then gene y are top-priority targets for trait z”

Next steps

Perturbation ID

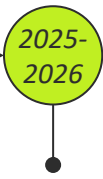


Gene perturbations for quantified trait effects

“Down-regulate gene x for y% increase in trait z”

Mature platform

Holistic editing strategy

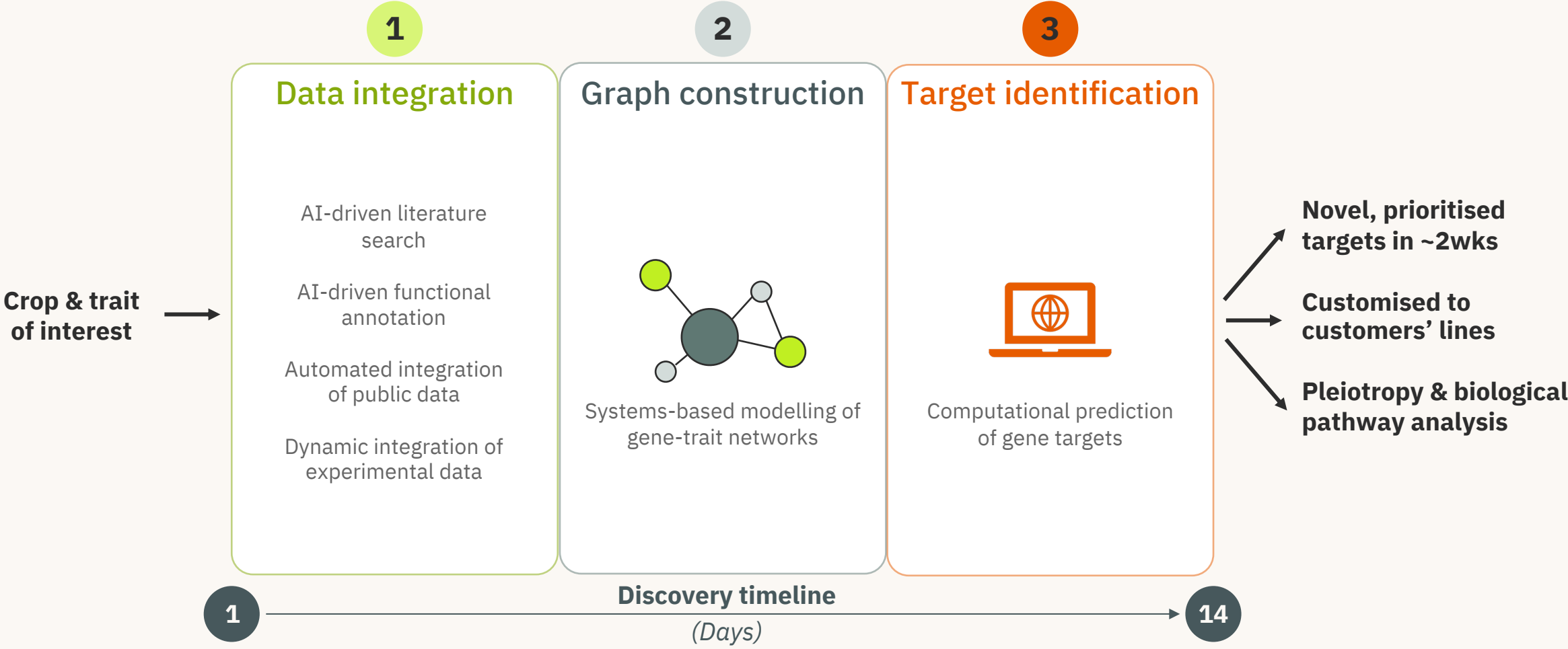


Edit / allele combinations for quantified trait effects

“Combine edits a & b for y% increase in trait z”

Current capabilities

An iterative platform for accurate, rapid & cost-effective gene identification

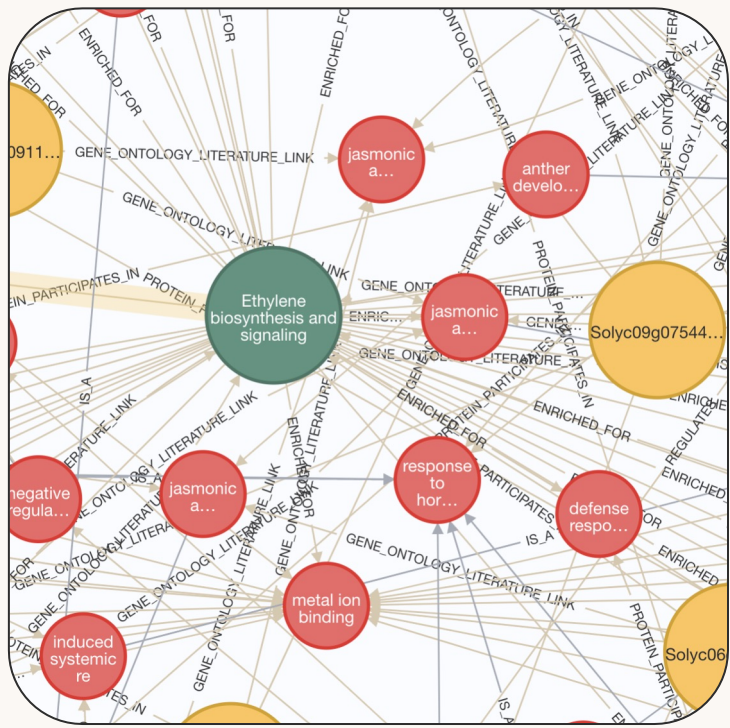


Successful proof-of-concept for gene ID in tomato

“ I’m really impressed with the tomato genes you identified. The results are very exciting. ”

CEO, Partner Company

Custom graph construction *



Project deliverables

- Report:
- Ranked target list
 - Pleiotropic analysis
 - Supporting evidence
- Subgraphs to support hypothesis generation & explainability

Project outcomes

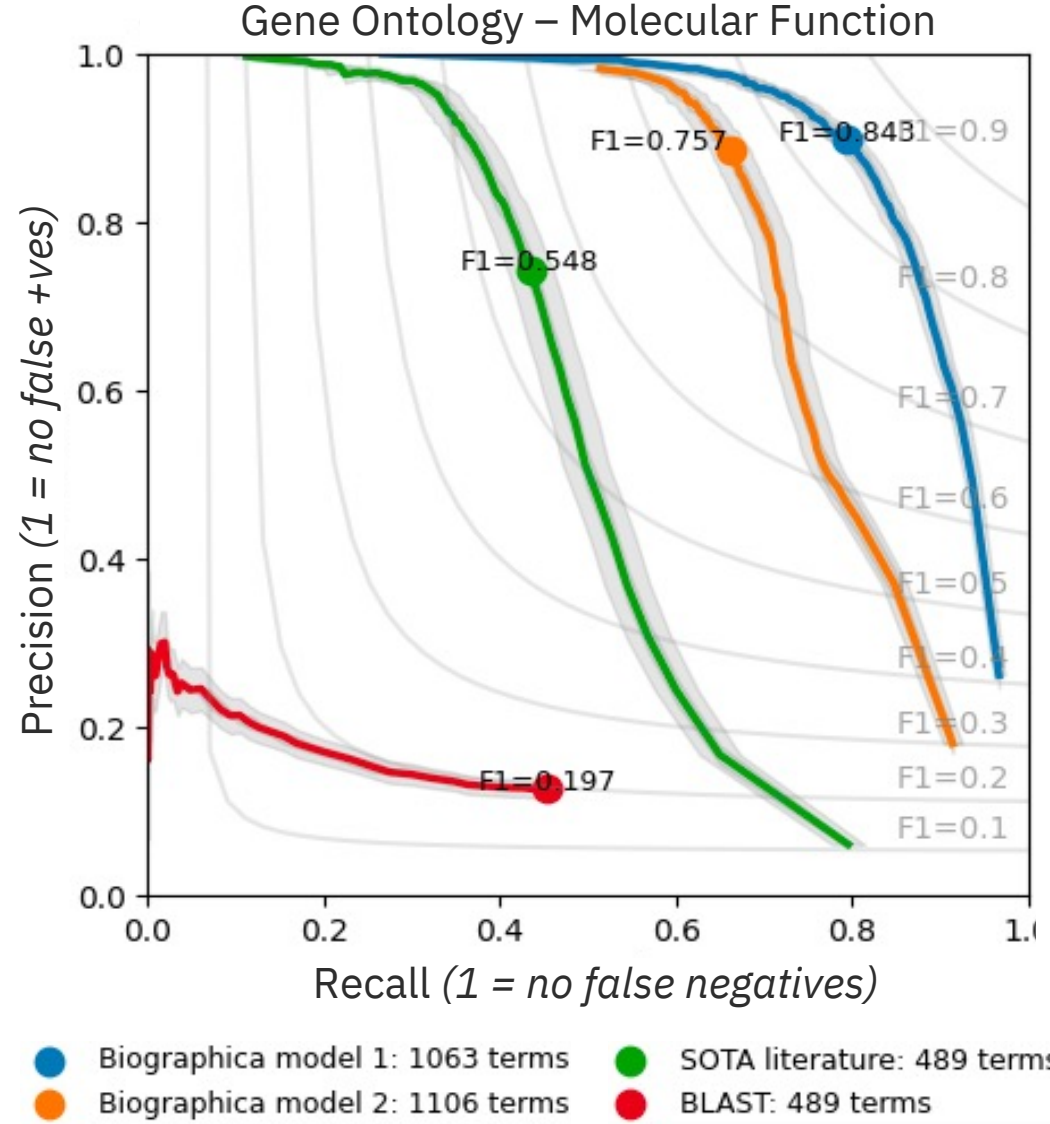
- ✓ Recalled **7/7 'ground truth' targets** for trait
- ✓ Identified 14 further high priority targets
- Targets to be validated experimentally starting Q4 2023

State-of-the-art Protein Function Prediction



- Vs other published methods, we predict:
- **More annotations** per plant protein
 - With **higher accuracy**
 - **From protein sequence** alone
- Highly accurate, proprietary annotations:
- **Boost success rate** of target ID
 - **Reveal biological mechanisms** of targets

We outperform BLAST by 328% at prediction of plant molecular functions



Validated Discovery of Drought Resistance Target

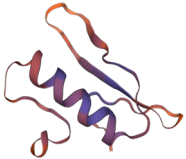





Our protein function prediction models confidently predict novel* gene-trait links (e.g. **ABR1** see right)

Implications:

1. Predictions confidently diverge from public databases → **1000's of novel potential targets**
2. We only use sequence → **can annotate arbitrary protein variants in your germplasm**
3. Annotation is just one tool → **also tell you about efficacy, pleiotropy & evidence for each target**

Case Study:

Biographica Predicts Novel Function for ABR1 in Drought Response

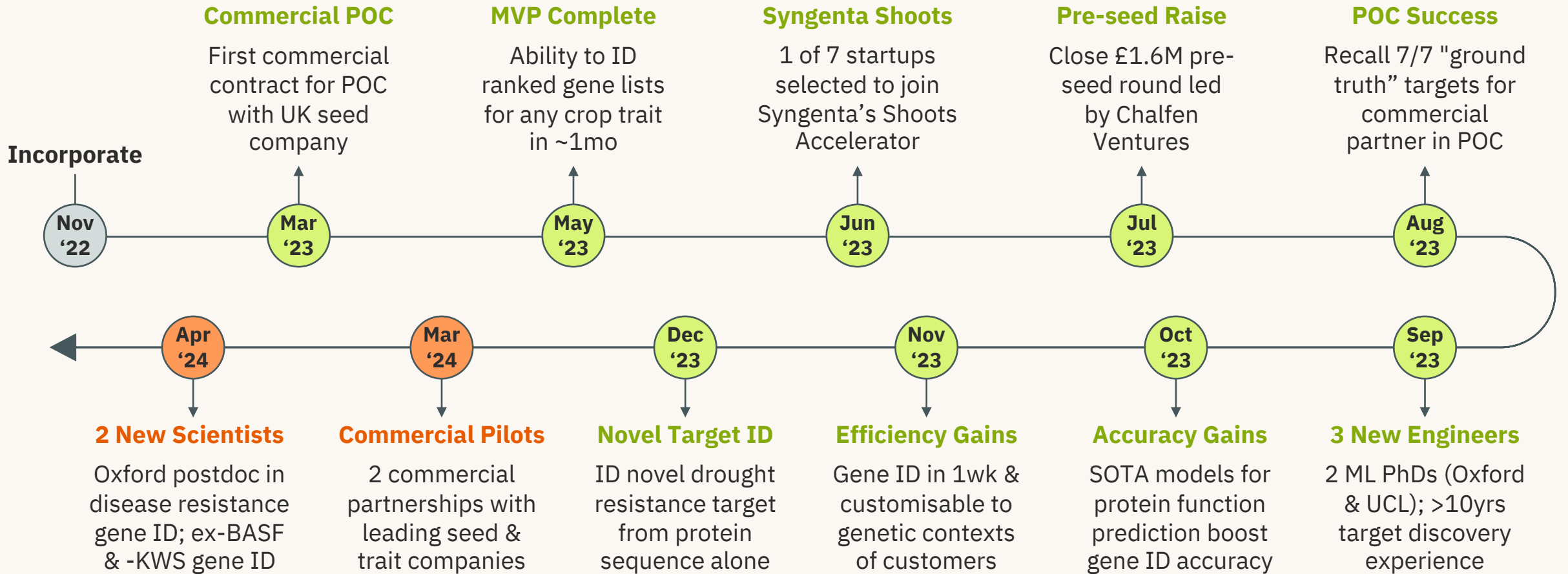
 <i>ABR1</i>	GO:0003700 DNA-binding TF activity	GO:0009414 Response to water deprivation
pBLAST		??
Uniprot (AOA178UFQ7)		??
	 99% confident	 95% confident

2023 Publications Validate Biographica's Discovery

- [PtrABR1 Increases Tolerance to Drought Stress by Enhancing Lateral Root Formation in Populus trichocarpa](#)
- [Transcription factors ABF4 and ABR1 synergistically regulate amylase-mediated starch catabolism in drought tolerance](#)

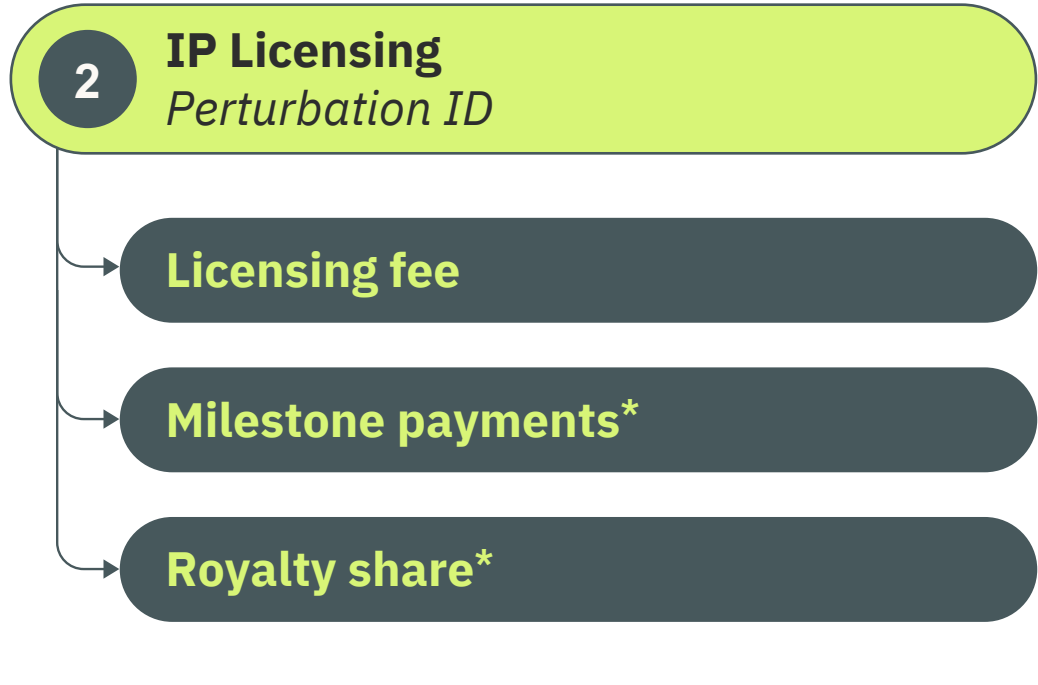
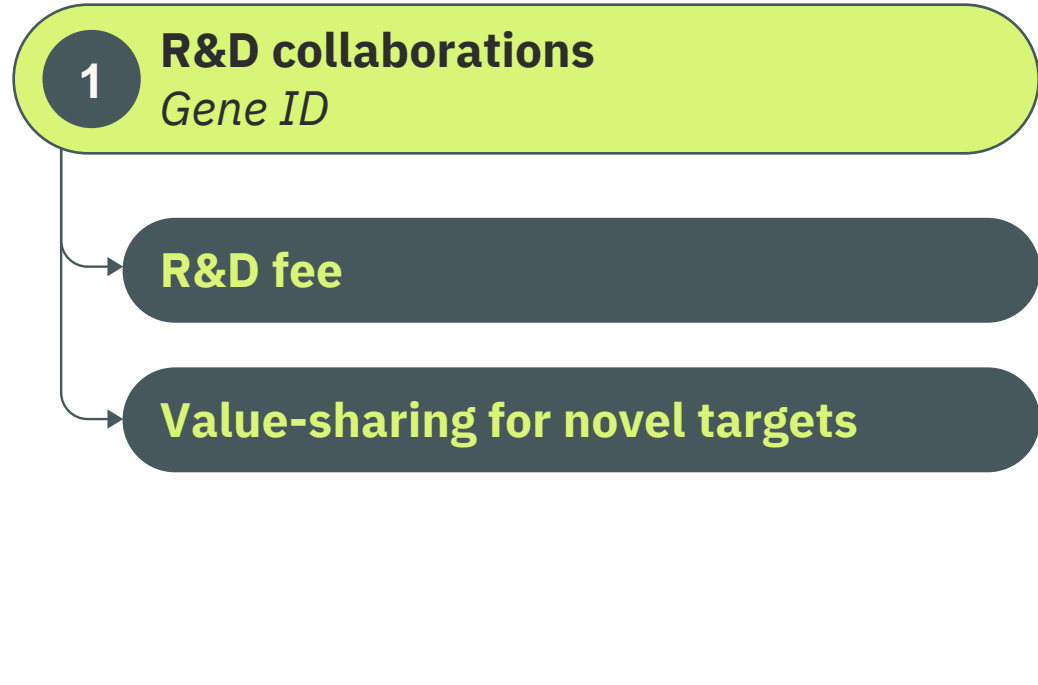
Where we're at

Milestones to date



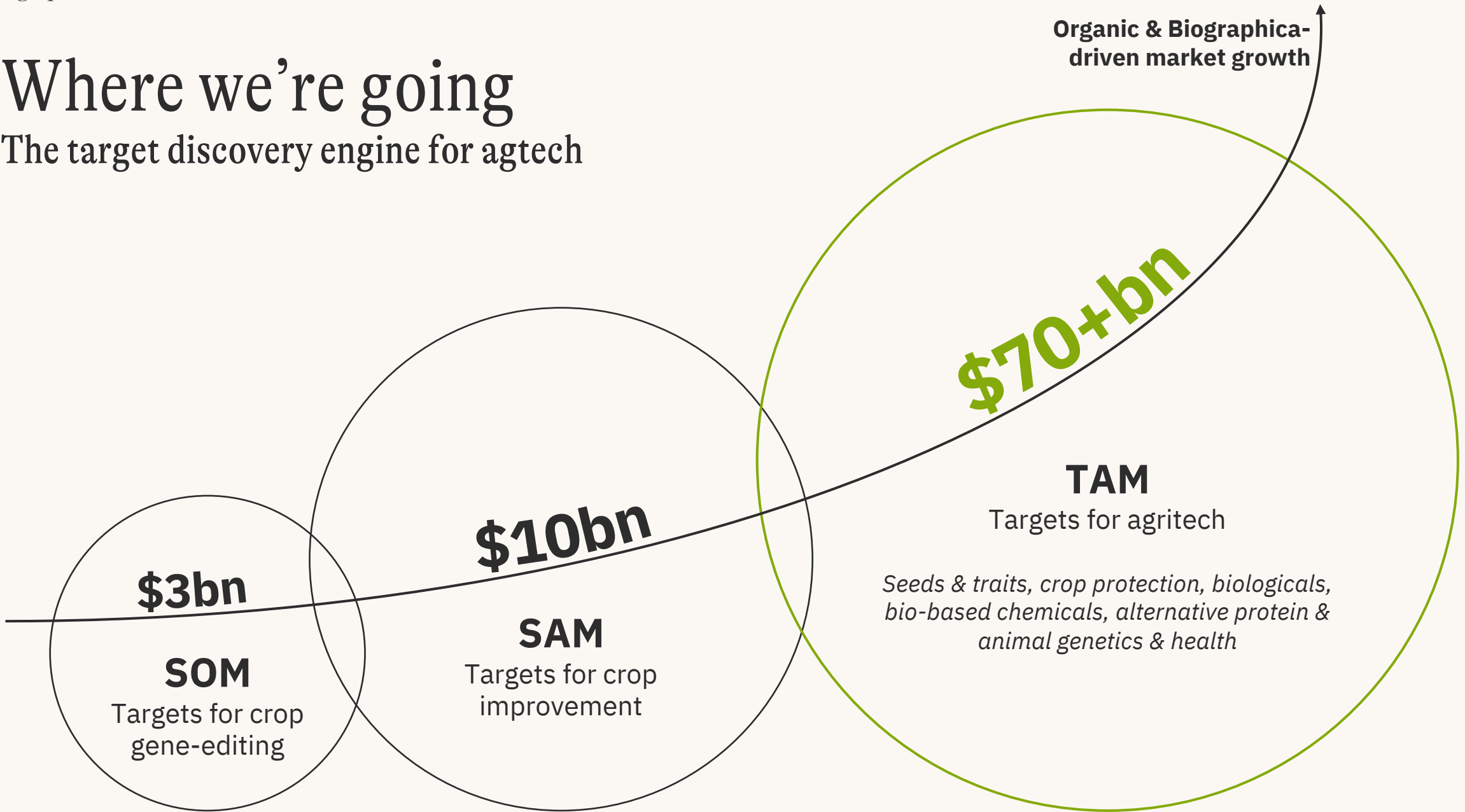
Business model

Development & out-licensing of target IP



Where we're going

The target discovery engine for agtech



Who we are

Combining expertise in plant sciences, target discovery & machine learning



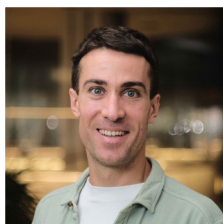
Cecily Price, Co-founder & CEO

- Oxford Biological Sciences specialising in Genetics
- Drug manufacturing at GSK, market access strategy consulting for gene-editing technologies
- Imperial MSc, ML & AI specialising in graph ML for biological modelling



Dominic Hall PhD, Co-founder & CTO

- Cambridge Masters, Maths, Stem cell Biology
- Cambridge PhD, Computational Genomics focusing on graph ML for gene regulation prediction
- Graph ML research for gene discovery in cancer cell lines at Relation Therapeutics



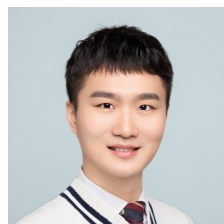
Paride Antinucci PhD
ML Engineer

Molecular Biology PhD (King's College London); BenevolentAI graph ML for target ID



Guy Aglionby PhD
ML Engineer

PhD in Natural Language Processing using graph ML (Cambridge)



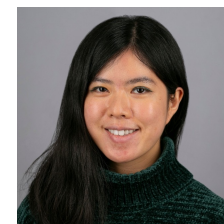
Linhao Luo
ML Researcher

Computer Science PhD (Monash) focussed on LLMs, knowledge graphs & graph ML



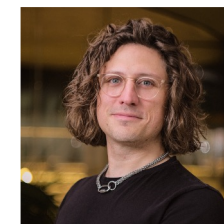
Felix Homma PhD
Plant Scientist

Plant disease resistance gene ID - PhD, Postdoc (Oxford) & industry (BASF & KWS)



Victoria Auyeung
Computational Biologist

Metabolomics PhD (Cambridge); plant disease resistance research (Sainsbury Lab)



Dennis Schwartz
Data Engineer

Bioinformatics MSc (TU Munich); 7+ years data engineering for graph-based target ID

Thank you



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Thank you