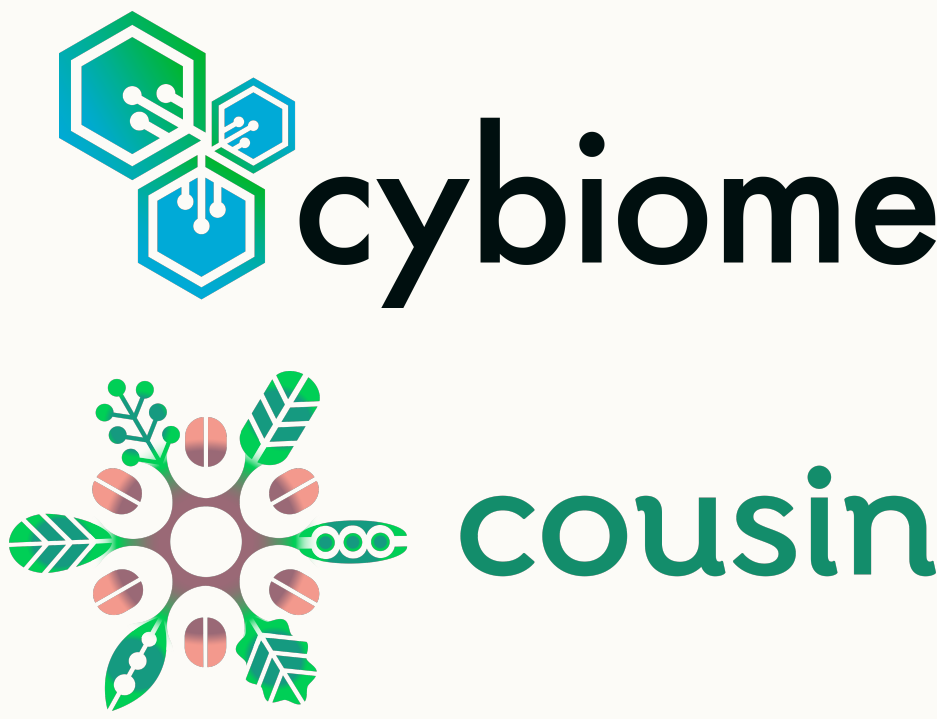




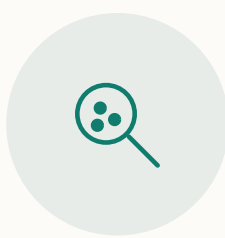
Reading the microbiome to predict the plant.

We turn affordable amplicon data into a toolbox to breed better plants and design precision interventions that improve plant phenotype.

Uriah Daugaard · Alexandre Jousset
Cybiome GmbH, Basel

01 ROLE IN COUSIN

The microbiome is a **diagnostic** and a **target**.



Diagnostic tool

Community composition predicts plant phenotype. Read the microbiome, read the plant.



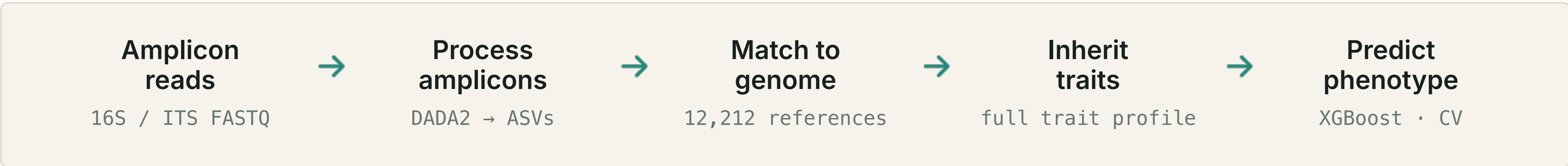
Breeding target

Specific microbial features can be engineered or supplemented to improve outcomes.

02 FROM AMPLICON TO MICROBIAL TRAITS

Reading a microbiome means reading its *traits*.

Amplicon sequencing names microbes cheaply, but a list of names is only useful if we know what each microbe *does*. Our **trait-inference pipeline** pre-computes a rich trait profile (ecology, metabolism, plant-microbe interactions, pathogenicity) for each of 12,212 reference genomes curated from NCBI RefSeq. We match every detected microbe to a reference genome, then assign it the full trait profile.



REFERENCE GENOME DATABASE



12,212

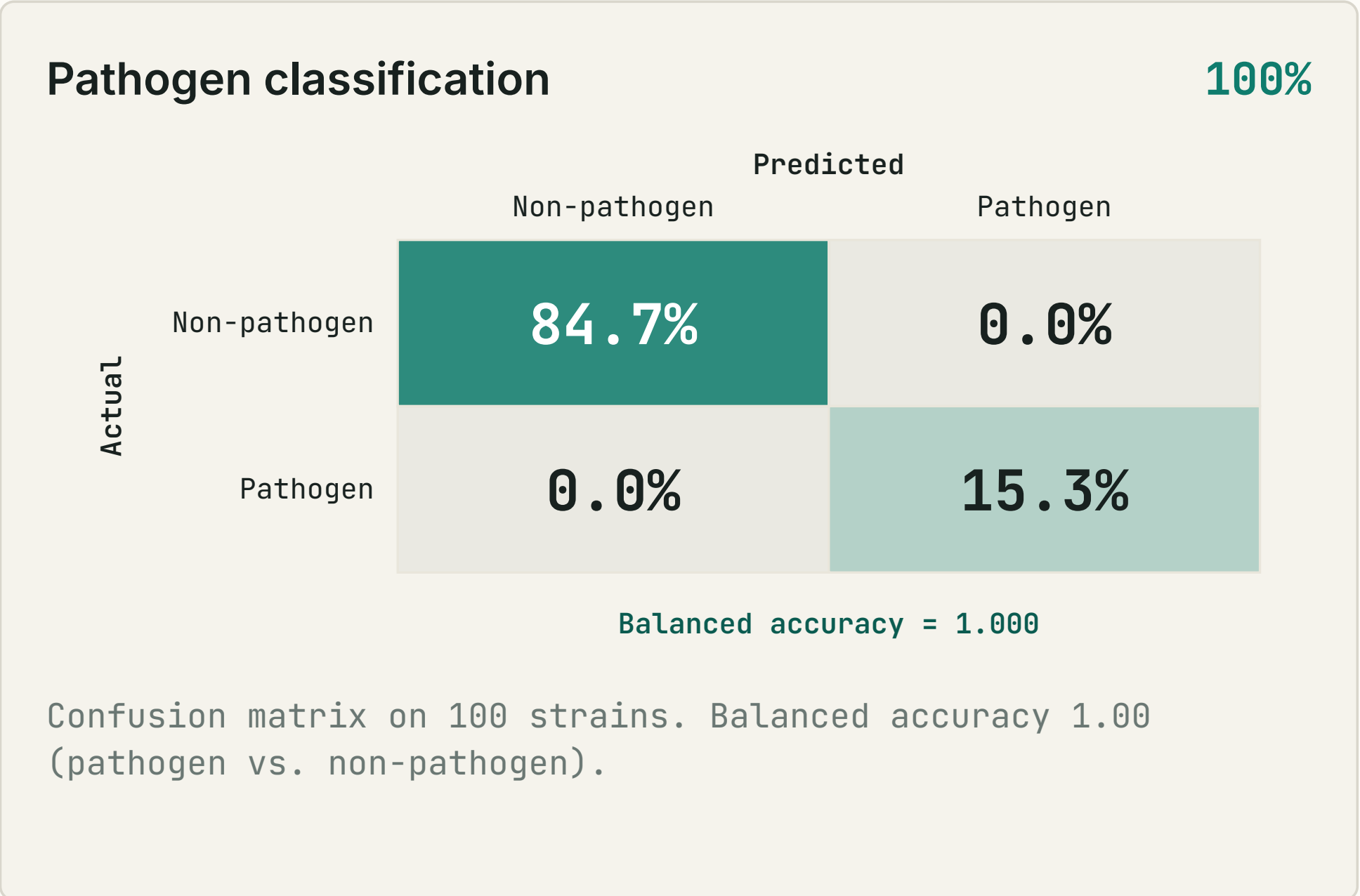
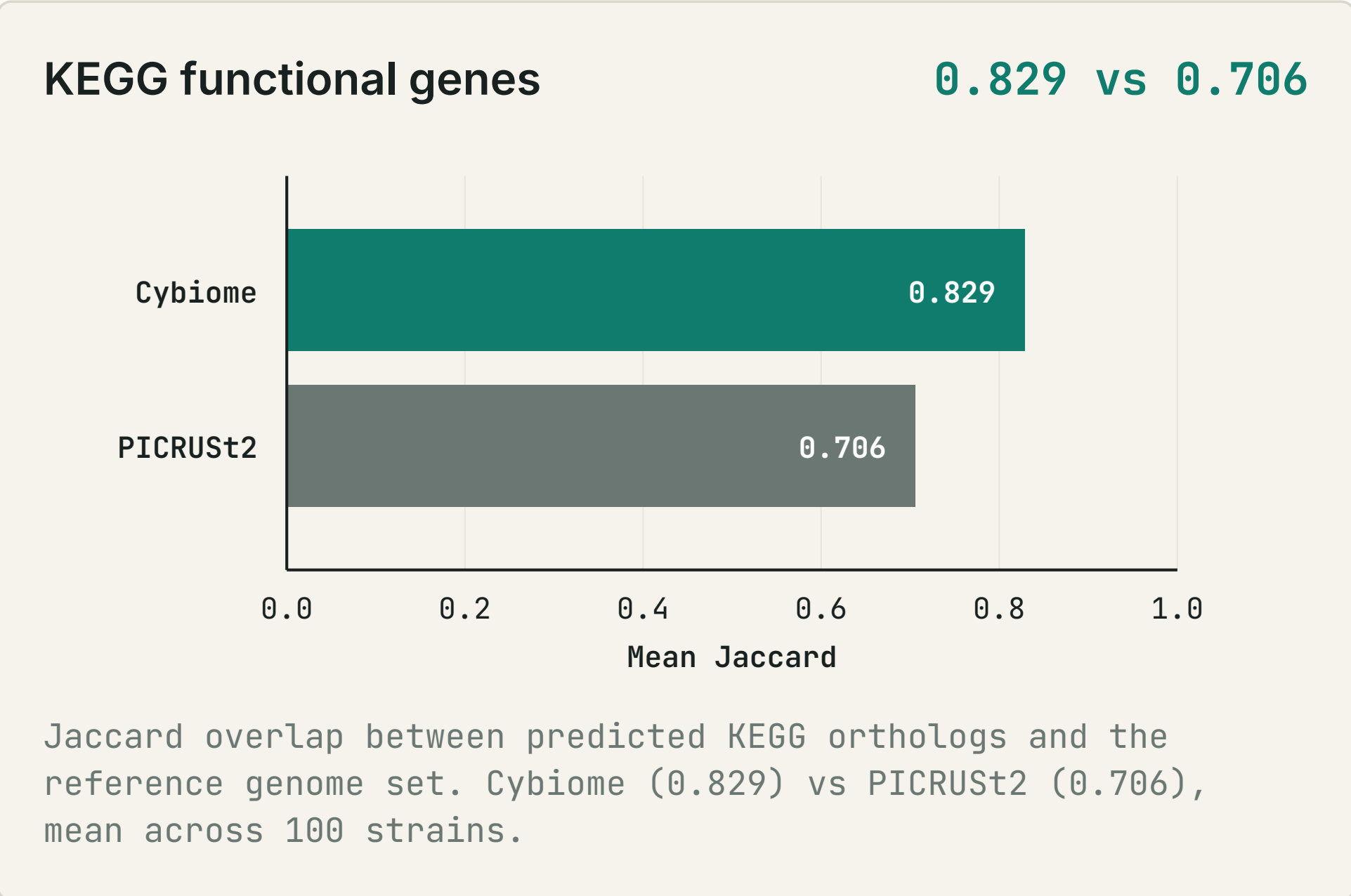
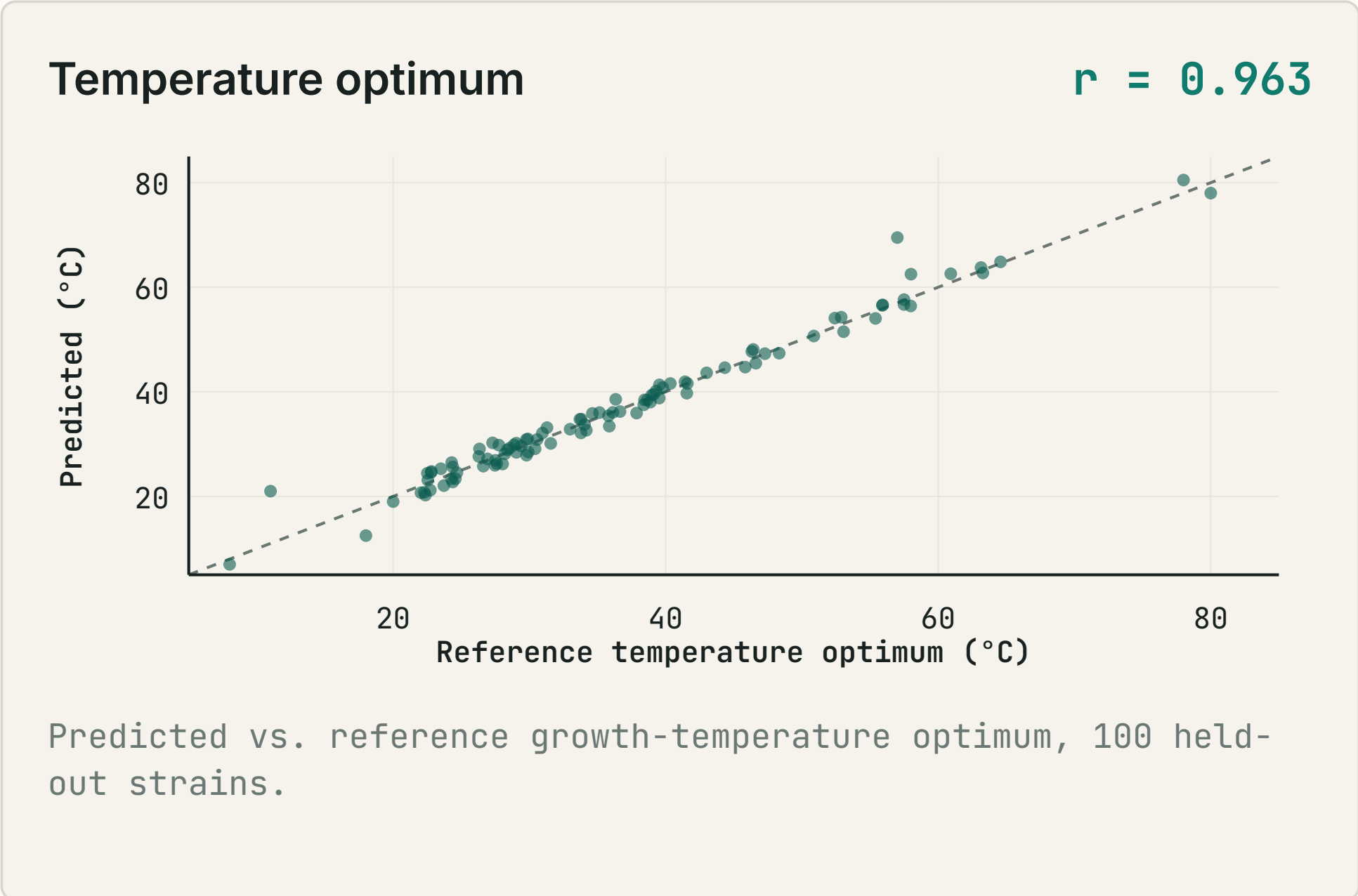
complete bacterial genomes

Trait profile per genome: identity & phylogeny · ecological niche · metabolic capacity · ecological chemistry · biosafety profile.

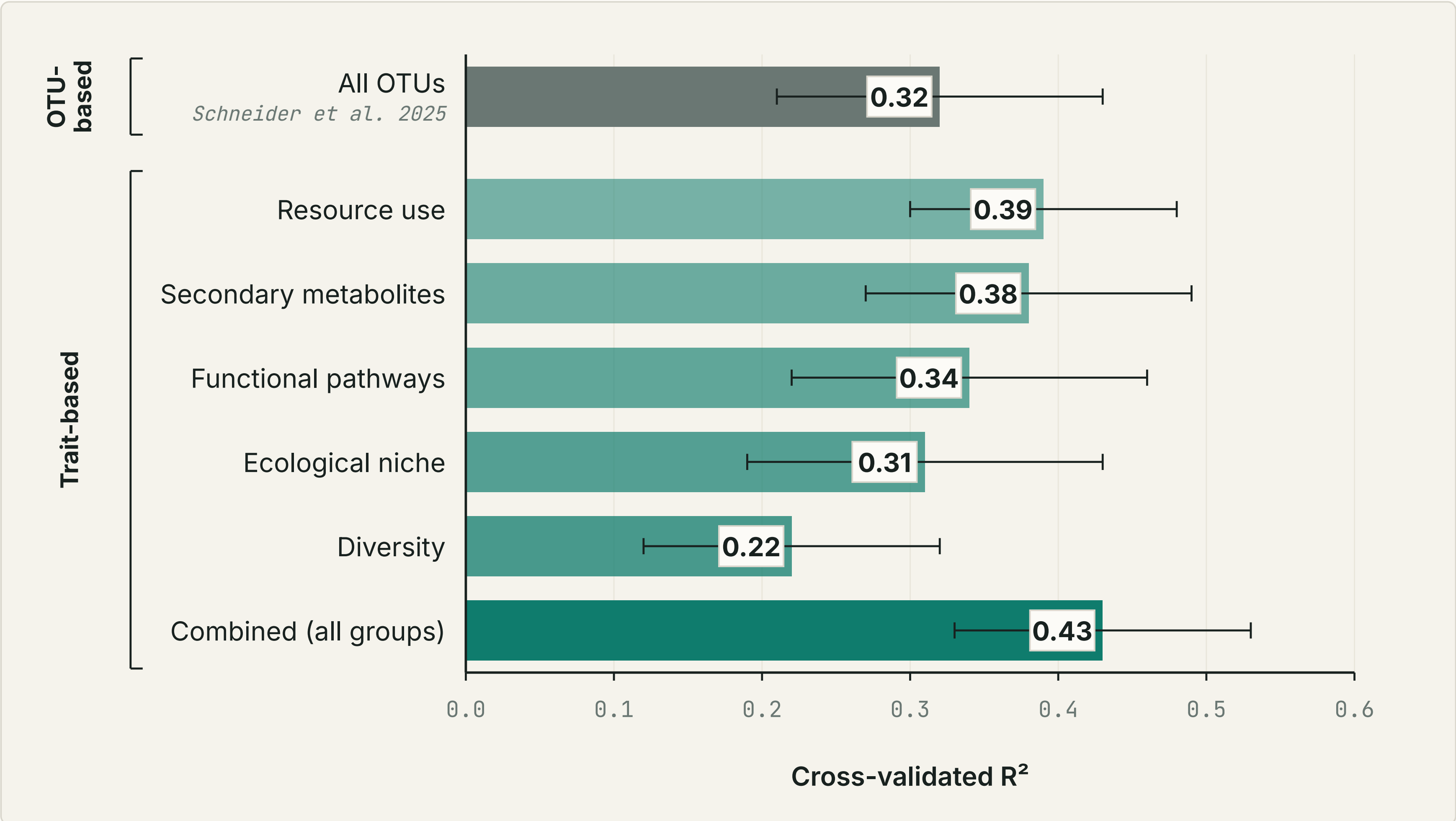
In progress: v2 (50,000 genomes)

Benchmark: Trait inference accuracy on 100 held-out genomes, predicted from synthesized amplicons

~300 bp of 16S rRNA is enough to infer most functional traits accurately. V3–V4 shown; V4 and V5–V7 give near-identical results.



03 FROM MICROBIAL TRAITS TO PLANT PHENOTYPE



n = 252 pea genotypes, naturally infested soil. The taxonomy-based model (Schneider et al. 2025) is re-run with our XGBoost + CV scheme and reproduces their reported $R^2 = 0.32$. Cross-validated R^2 : 5-fold $\times$ 10 reps. Error bars = ± 1 SD.

Trait-based models predict *root rot severity* in pea.

DATA 252 pea genotypes grown in soil naturally infested with the **pea root rot pathogen complex** (Schneider et al. 2025).

APPROACH We predicted Root Rot Index (RRI) from the root microbiome with XGBoost, comparing different trait-based feature sets against the state-of-the-art taxonomy approach (OTUs).

RESULTS Microbial traits predict root rot severity with $R^2 = 0.43$, explaining 43% of the variation. This is a **35% improvement** over the taxonomy baseline (Schneider et al. 2025, $R^2 = 0.32$).

MEANING Because features are biological traits, results are **interpretable** (you can see *which* traits drive a prediction) and **potentially transferable** across studies, crops, and cohorts.

04 OUTLOOK

PREDICT

COUSIN priority traits

Disease resistance, drought tolerance, nutrient-use efficiency, nutritional quality, in barley, wheat, pea, lettuce, and brassica.

SCAN

Crop Wild Relatives

Scan CWR microbiomes to identify candidates for microbiome-assisted breeding, collaboration with **Bonaplanta (BCROP)**.

INTERVENE

Targeted interventions

Design probiotics and tailored microbial consortia to shift specific plant traits.



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UK Research and Innovation

Data. Pea root rot dataset from Schneider et al. (2025), *BMC Plant Biology* 20:89.



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