



FERRIS
GENOMICS

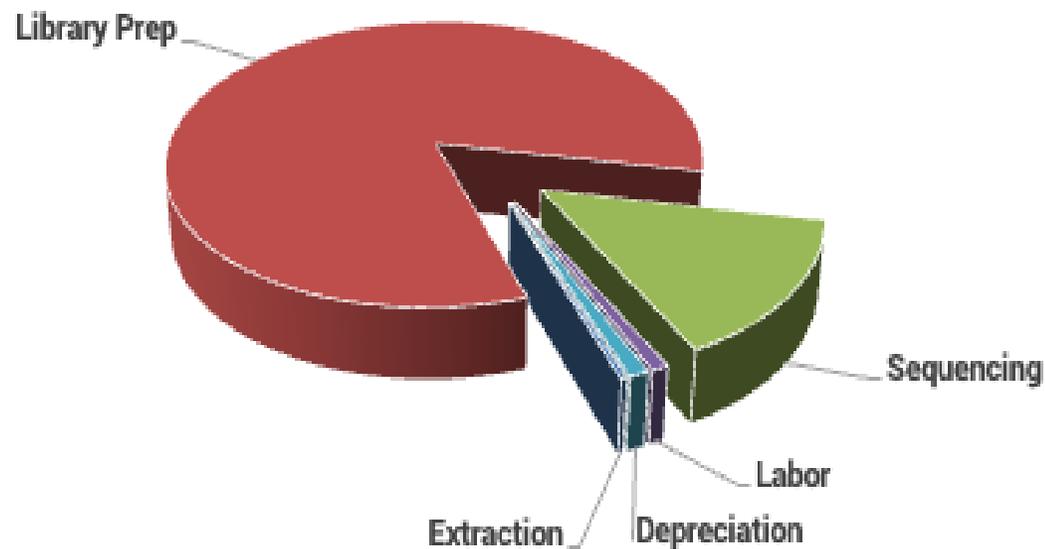
The Power of More.

Key Drivers

Cost per Genome



Whole Genome Sequencing - Mfg Guidance



Introducing AMRA Technology

Our AMRA process enables microfluidic miniaturization and reaction efficiency, enabling faster delivery of more quality data, with lower costs for whole genome sequencing library preparation.

More than next generation, AMRA represents an advancement with the potential to shift the whole genome sequencing paradigm.



Introducing AMRA Technology



ADAPTIVE

Our flexible process delivers on wide-ranging genomic samples and reagents in a mostly consumable free environment.



MOLECULAR

We are specialists in the execution of commercially significant genomic protocols.



REACTION

Droplet-based reactions are stabilized within a unique environment.



ASSEMBLY

Our process delivers flexibility in “addition-only” steps in a suitable microenvironment to perform cutting-edge genomic research.



Services and Tools

SAMPLE COLLECTION

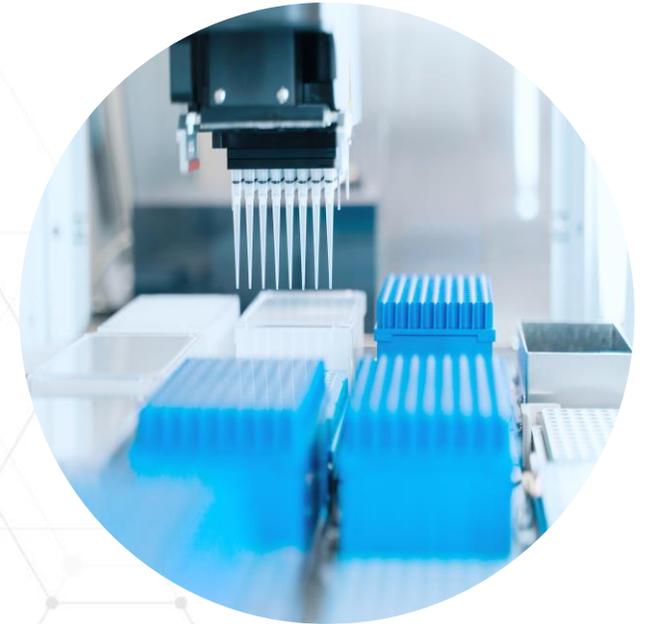
Speed Breed kit shortens turnaround time by providing a way to more effectively track and transfer sample identities to demultiplexed data files or reports. Our Speed Breed kit provides all collection materials needed, including a return box and shipping labels. Leaf tissue sample collection is simple and turnaround time is fast— data returned in as soon as five days or up to a maximum of 10 days from plate receipt.



Services and Tools

PLANT AND ANIMAL DNA EXTRACTION

Our experience in handling diverse samples makes us the perfect partner to work with your samples. Not all source material is the same, so we recommend the right extraction process for your sample type. We also are adept at removing or limiting the effects of inhibitors such as polysaccharides, proteins, polyphenols, oils, and other chelators. The result is high-quality RNA/DNA that leads to better libraries, sequencing, data, analysis, and ultimately, better decisions.



Services and Tools

WHOLE GENOME LIBRARY PREPARATION

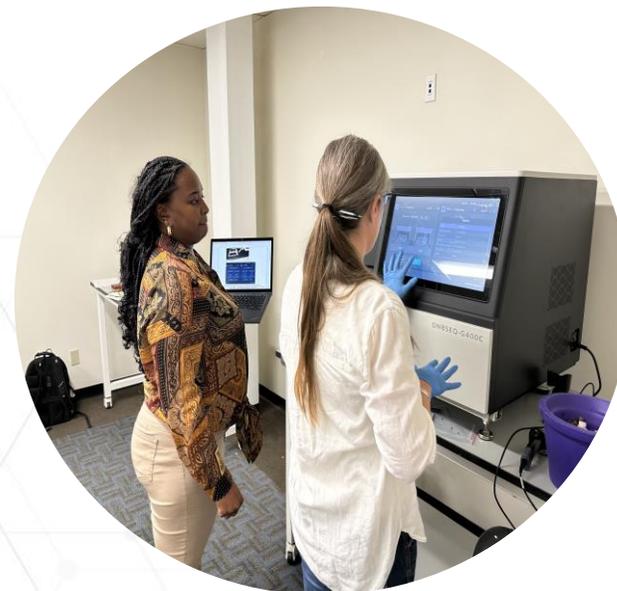
Our experience utilizing the AMRA process enables us to best prepare high quality libraries for sequencing. Whether your samples are destined for lowpass skim sequence to help you make breeding decisions, or hybrid capture, our process helps enrich your samples and deliver more data with higher discovery power.



Services and Tools

SEQUENCING

We are driven to provide a quality-controlled data set in your preferred format. Whether you need a trimmed FASTQ for feeding into your analysis pipeline, or a VCF file and/or report to load into your predictive breeding analysis pipeline, we can deliver your data the way you need it.





Skim Sequencing Facilitates Speed Breeding

Wanfang Fu, Ph.D.

Ferris Genomics

PAG, 2024

Keep the price affordable and gain more data

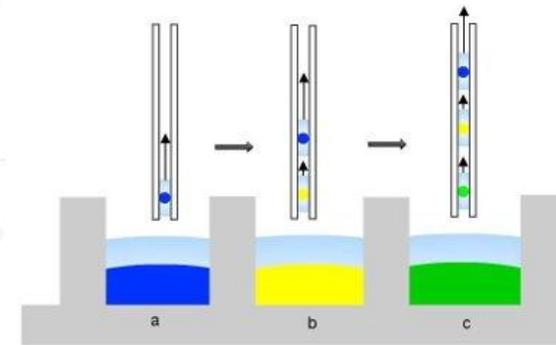
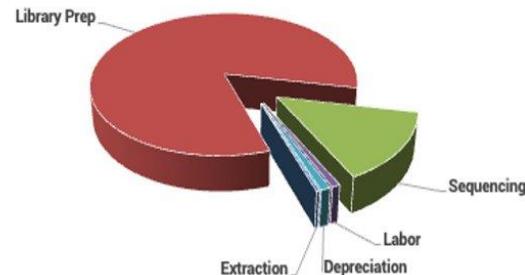
- **Reduce the cost of library prep**

- Reagents input
- Cost of time and labor
- AMRA technology

- **Increase number of samples per run**

- Skim/low pass sequencing
- Imputation

Whole Genome Sequencing - Mfg Guidance



Speed breeding kit

Sampling



We provide all tools that needed for sample collection.

- Simple
- Flexible
- Effectively track

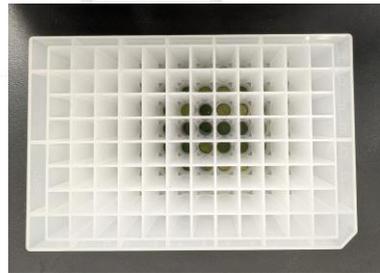


Extraction



Rapid and high-quality DNA extraction.

- High throughput
- Accommodate to different species and tissue types

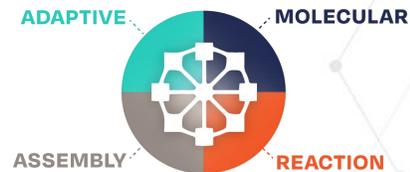


Library creation



Utilize the AMRA technology to enable high quality library construction.

- High efficiency
- Low cost



Sequencing



Skim/ low-pass sequencing coupled with imputation pipeline.

- Fast turnaround
- 5 – 10 days from sample receipt



Data delivery



Deliver your data in the way you need it.

- Fastq files
 - Demultiplexed raw fastq
 - Trimmed fastq
- BAM files
- VCF files
- etc.

Pilot study – using soy as an example

- **Plant material**

- 96 soy sample: Wm82 and IL 3025

- **Skim / Low pass sequencing**

- 0.1 ~ 0.4X: Complete Genomics DNBSEQ-G99, PE 150
- 5 ~ 10X: Complete Genomics DNBSEQ-G400, PE 150
- Missing SNP calls for low pass sequencing data were imputed using Gencove's imputation platform

- **AMRA micro reaction library preparation**

- Pooled DNA sample of all 48 IL3025 samples were used
- 4 different reaction treatment
 - Control: 1X reaction volume, no AMRA microreactor
 - Treatment 1: 1X reaction volume, add AMRA microreactor
 - Treatment 2: 0.1X reaction volume, no AMRA microreactor
 - Treatment 3: 0.1X reaction volume, add AMRA microreactor



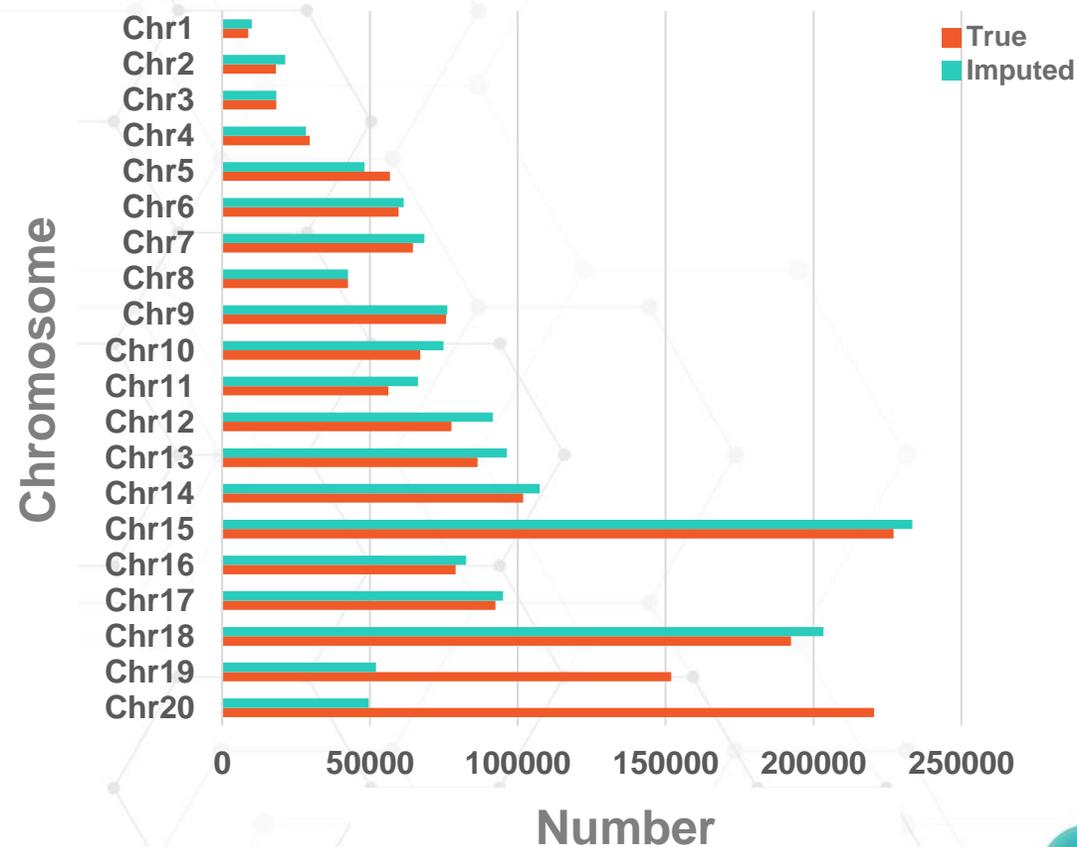
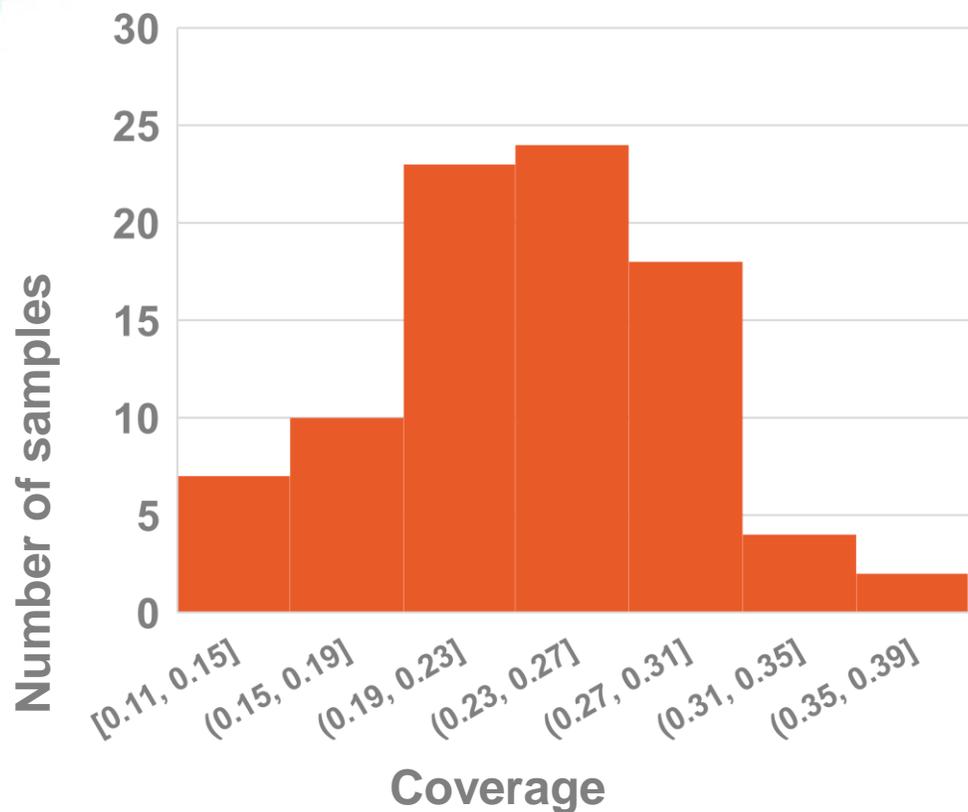
DNBSEQ-G99



DNBSEQ-G400

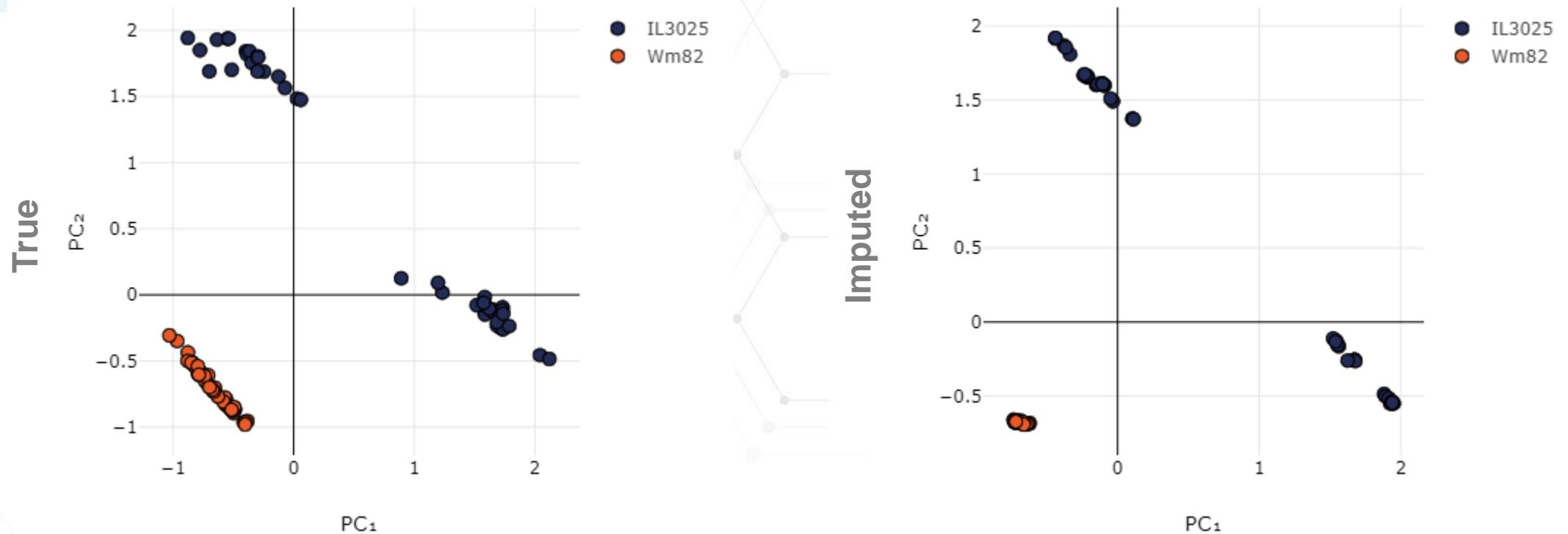


Results – skim sequencing



- Overall, using high depth sequencing data, ~1.7M SNPs were identified across the whole genome.
- Gencove imputation platform return ~1.5M SNPs (~5500 SNPs without imputation).

Results – skim sequencing



- Using the imputed SNP data, we are able to correctly identify the subgroups in the analyzed material



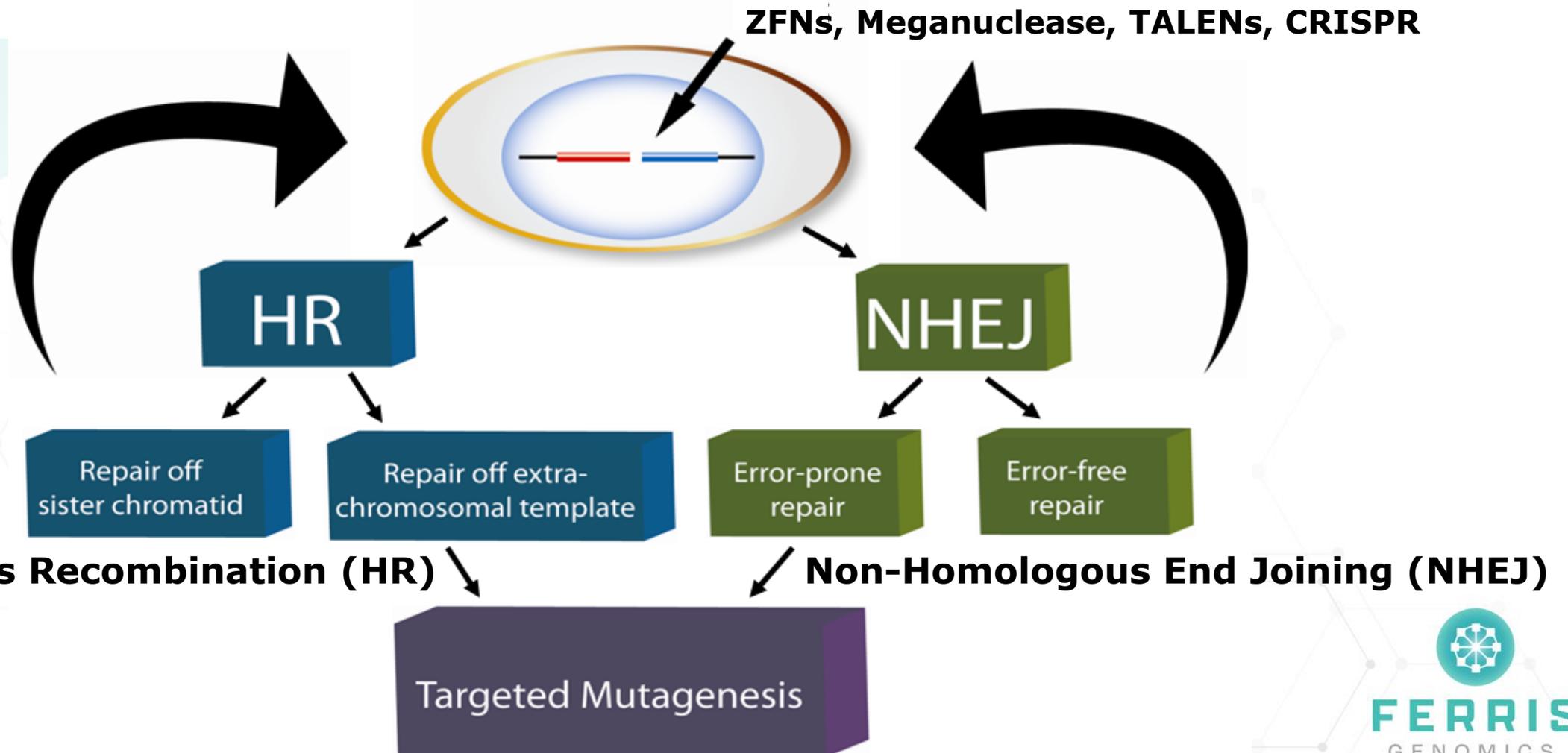
In Vivo Gene Editing Strategies

Pat Sullivan

Ferris Genomics

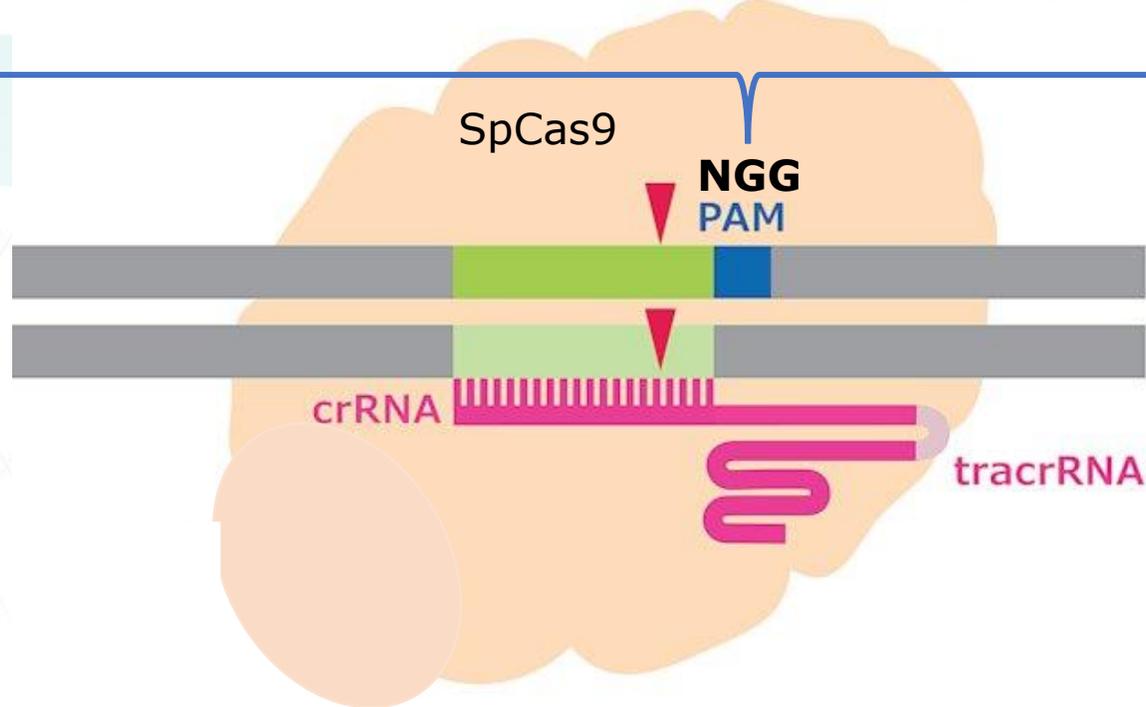
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Gene Editing: The Process



CRISPR Design Challenges for *In Vivo* Editing

Exact PAM sequence match is required to get genomic DNA cutting



Physical Design Challenges

Genetic Variations in the Patient Population

Epigenetic Variations in different cell types

Skim Sequencing to Identify Off-Target Integrations



[Brief Bioinform.](#) 2023 May; 24(3): bbad131.

PMCID: PMC10199778

Published online 2023 Apr 20. doi: [10.1093/bib/bbad131](https://doi.org/10.1093/bib/bbad131)

PMID: [37080758](https://pubmed.ncbi.nlm.nih.gov/37080758/)

Using traditional machine learning and deep learning methods for on- and off-target prediction in CRISPR/Cas9: a review

[Zeinab Sherkatghanad](#), [Moloud Abdar](#), [Jeremy Charlier](#), and [Vladimir Makarenkov](#)[✉]

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EDISON

AGROSCIENCES

Domestic Natural Rubber. From Sunflower.

December 2023

Natural Rubber: Extreme Supply Risk

Unfortunately, 100% of this strategic raw material is grown over 10,000 miles away and harvested manually from a tree species that's already been wiped from its native continent by disease.

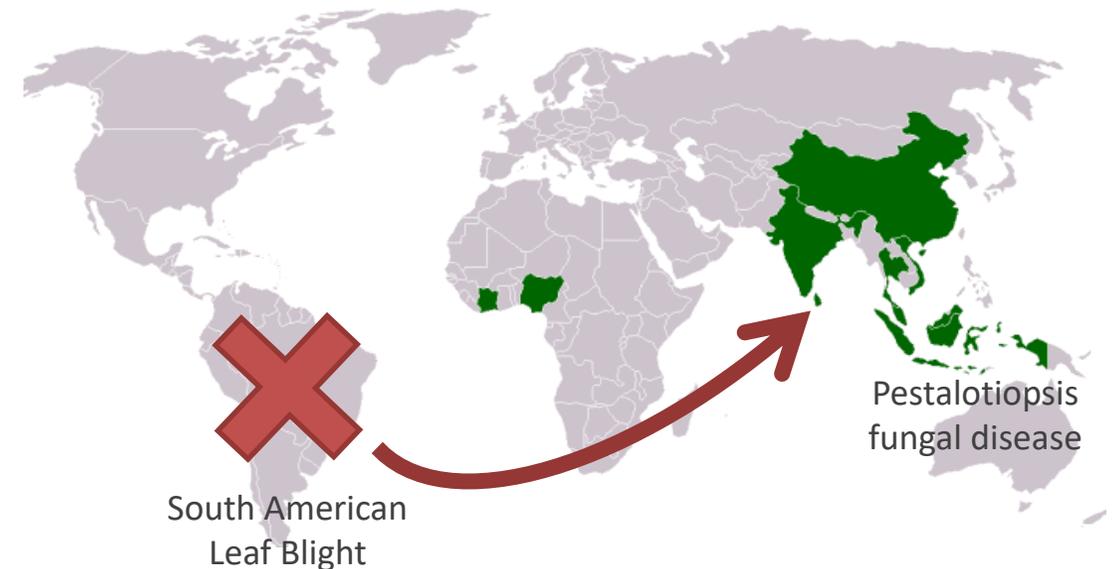
Geographic Concentration

Nearly 90% of natural rubber production occurs in South and East Asia. None is produced in North America.



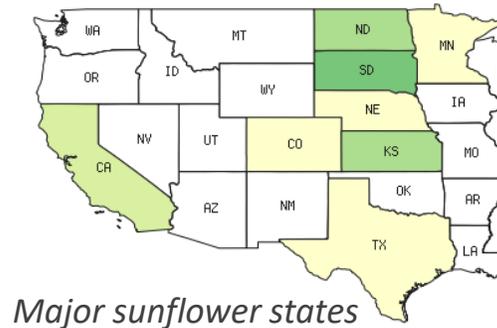
Disease Susceptibility

Most rubber plantations consist of trees that are clones of those wiped out by disease in South America in the early 1900's.

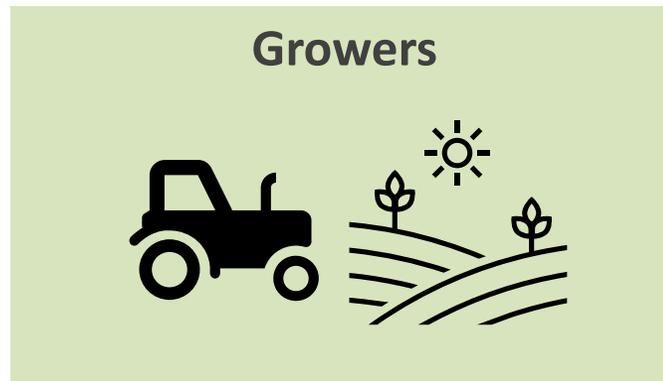


Our Solution: An Existing Domestic Source of Natural Rubber

U.S. sunflower fields annually produce over 50,000 tons of natural rubber in the plant leaves (4% of U.S. demand), but the concentration is too low for economical collection and extraction.

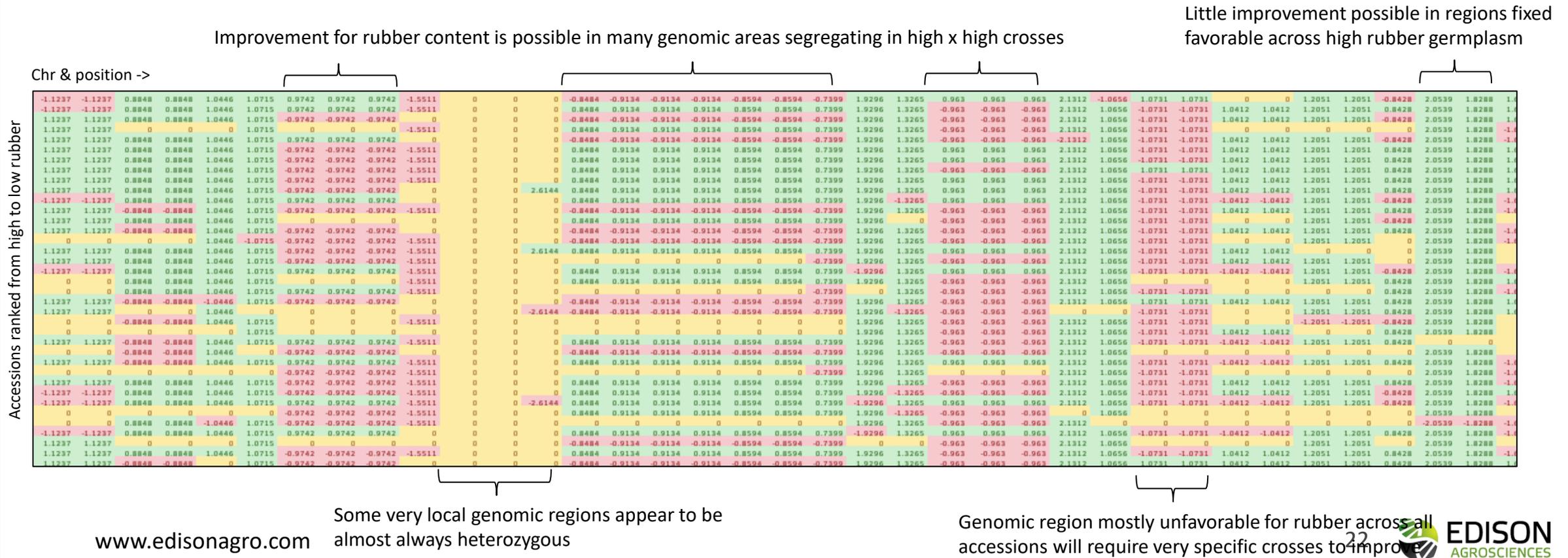


- Edison is leveraging standard biotechnology to increase the levels of natural rubber already present in **sunflower** to benefit:



Genomic analysis shows rubber variation is controlled by many gene effects distributed across the sunflower genome

- Visualizing the distribution of positive (green), negative (red) and heterozygous locus effects (yellow) on rubber content across the genome and across germplasm using graphical genotypes
 - Only 2% of the genome is represented here for the top 37 lines from the 2021 experiment

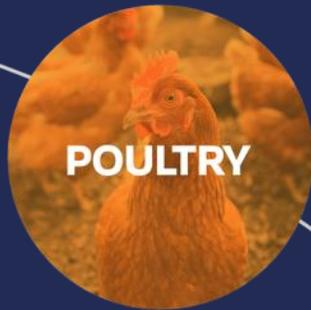


More data is better but ... how?

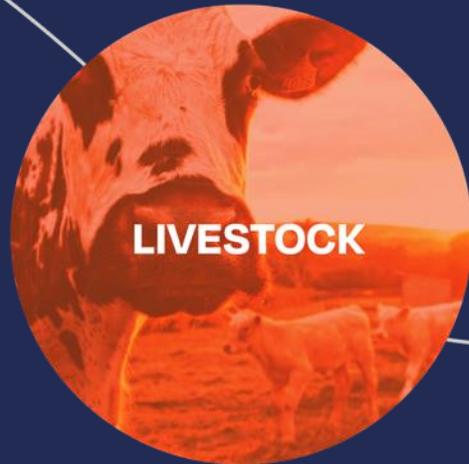
Whole genome skim seq

- More data is better ... but each additional data point has less value
 - How can we drive up the amount of data while reducing the cost per data point to near zero?
 - Traditional genotyping approaches are fairly expensive (>\$15 / sample)
- Whole genome sequencing drives the cost per data point down enabling the value and leverage from “more” data but sample cost is high
- Skim seq makes whole genome information cheap!
 - In a sense all sequencing is skim sequencing ... just at what depth?
 - Skim drops average sequencing depth below 1x to as low as 0.1x
 - Reduced coverage reduces cost
 - Computation and prediction is used to improve data quality and fill in gaps
- Whole genome sequencing applied to the breeding pipeline forms a natural bridge to a genome editing strategy for product development

Get More, Where You Need It Most.



POULTRY



LIVESTOCK



**AQUA
CULTURE**



**SPECIALTY
CROPS**



**ROW
CROPS**