How to exclude New GMOs in Non-GMO value chains?

Excluding New GMOs in value chains: State of play in the development of detection methods

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Non-GMO Summit 2026

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NEW GENOMIC TECHNIQUES
NEW FOOD SYSTEMS

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Connects health, science and society

How to deal with New GMOs in Non-GMO feed and food chains – Non-GMO Summit 2026 – Frankfurt, Germany – 13 May 2026

Genetic fingerprints derived from genome database mining allow accurate identification of genome-edited rice in the food chain

Dr. Fraiture Marie-Alice

Transversal Activities in applied Genomics (TAG), Sciensano, Belgium

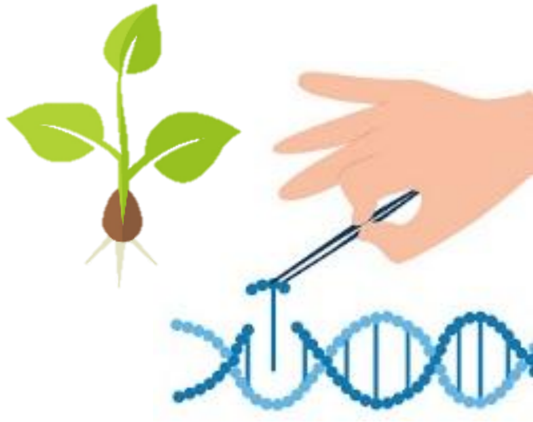
Funded by the European Union

Context

Court of Justice 2018

Organisms produced by **genome editing**

Directive 2001/18/EC
Deliberate release of GMO into the environment



Commercialization on the EU market → **Traceability/Labelling**
EC 2003/1829-1830

Methods for **control**
ENGL Minimum performance for GMO

Large insertion of several nucleotides

→ Classical event-specific methods (qPCR, ddPCR)

Modification of few nucleotides ⚠

→ Detection challenging at the analytical and interpretation levels

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Identification of GE organisms with SNVs → Challenging!

- Detection of the SNV introduced by genome-editing ≠ to determine if the SNV was introduced by genome editing techniques
  - SNV can also occurs naturally or through random mutagenesis

- Detection of only **SNVs introduced by genome-editing** is not sufficient to unambiguously identify a GE line from other lines → Need to **simultaneously** detect multiple key genetic elements in the same line

  → **A specific key for each GE line !**

Unique genetic fingerprint for each GE line

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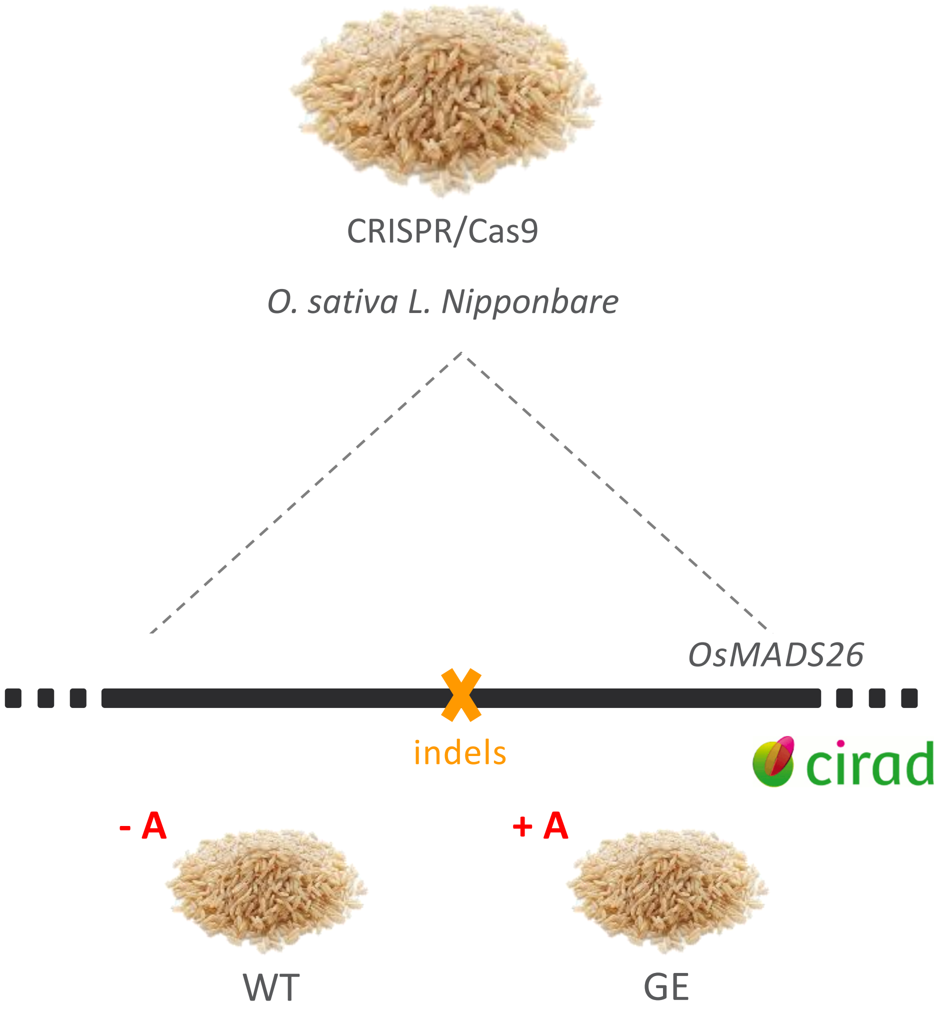
Proof-of-concept

Rice is a **model plant**:

- → Major crop
- → Small genome size
- → Diploid
- → One of the most characterized crops, including genomic level



SNV → Gene inactivation to increase biotic resistance and stress tolerance

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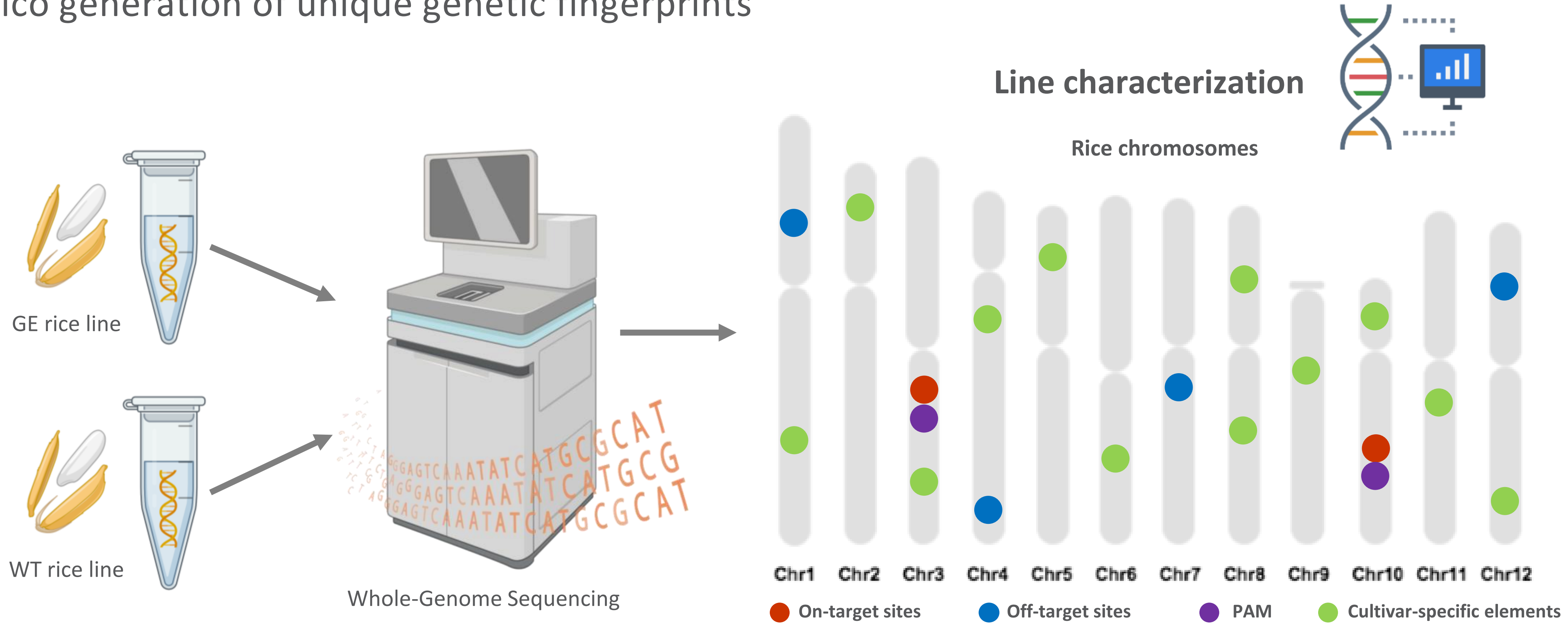
Unique genetic fingerprints to discriminate a specific GE line

- In-silico generation of unique genetic fingerprints



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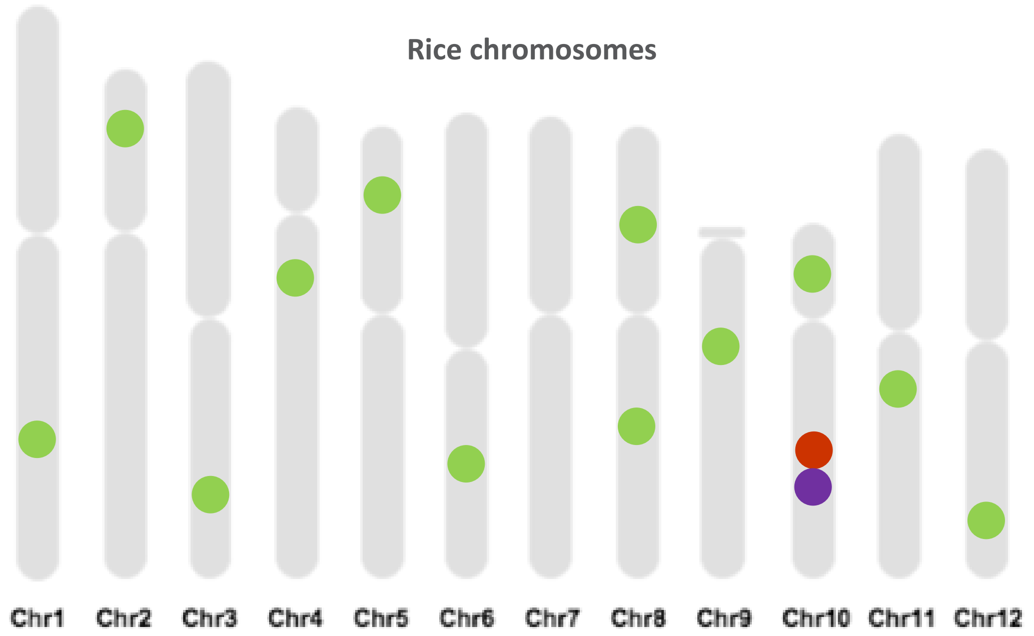
Unique genetic fingerprints to discriminate a specific GE line

- In-silico generation of unique genetic fingerprints

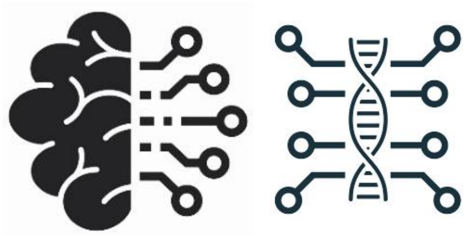
Characterized GE rice line



On-target sites Off-target sites PAM Cultivar-specific elements

Not observed in the tested GE rice line
→ Consistent with optimization of GE technologies

High-quality available database encompassing natural species diversity



Data mining, machine learning and bioinformatics tools and software

Unique genetic fingerprint

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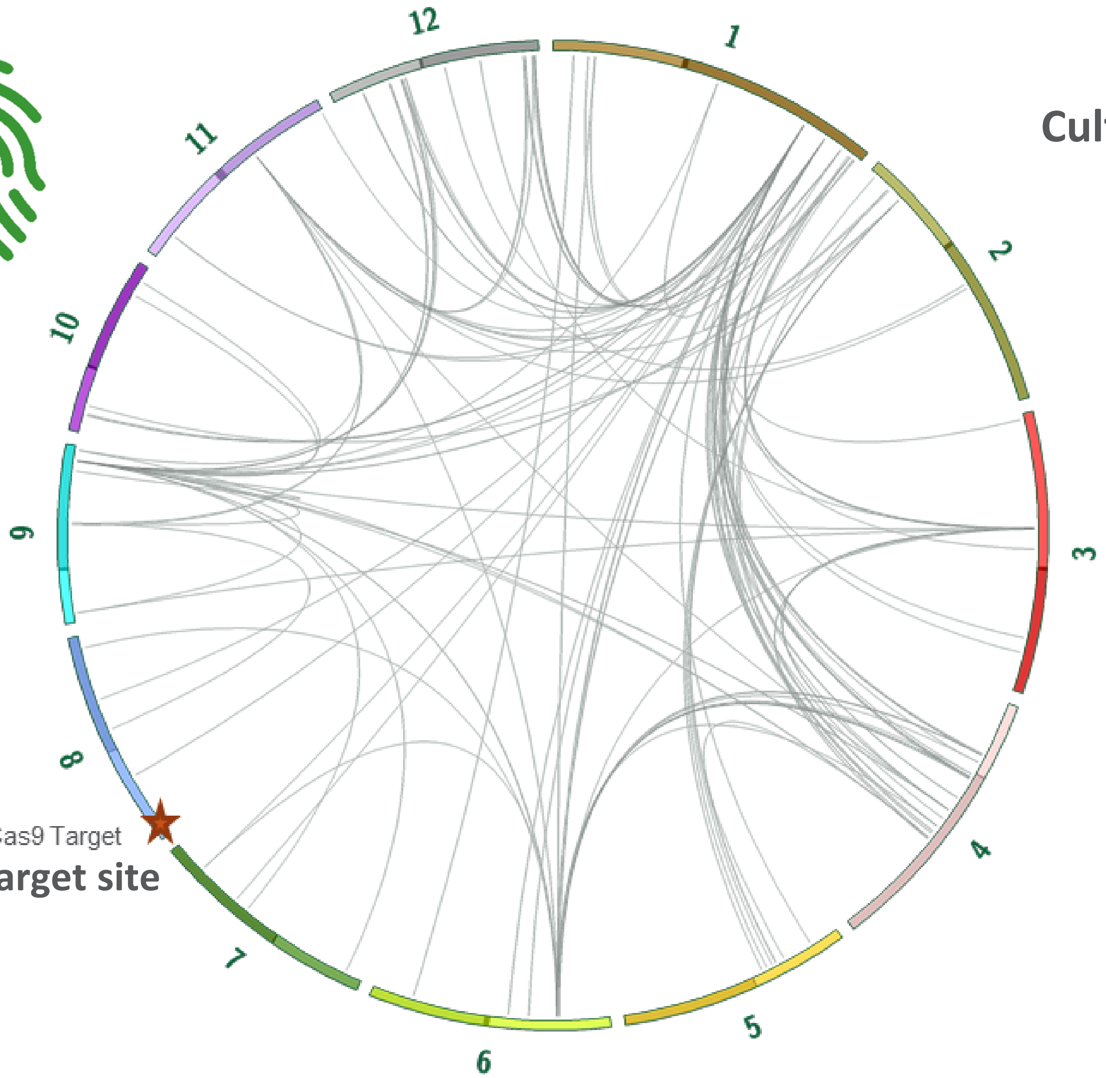
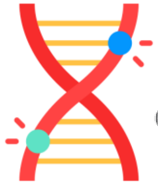
Unique genetic fingerprints to discriminate a specific GE line



Cultivar-specific marker

→ A set of ≠ redundant barcodes

2 869743 695423
79359426436872
8452379
842536939647
7 29394556487
7 93574264958
79357426495872396
754395967238
793574264958723968573
842536939



Crispr/Cas9 Target

On-target site

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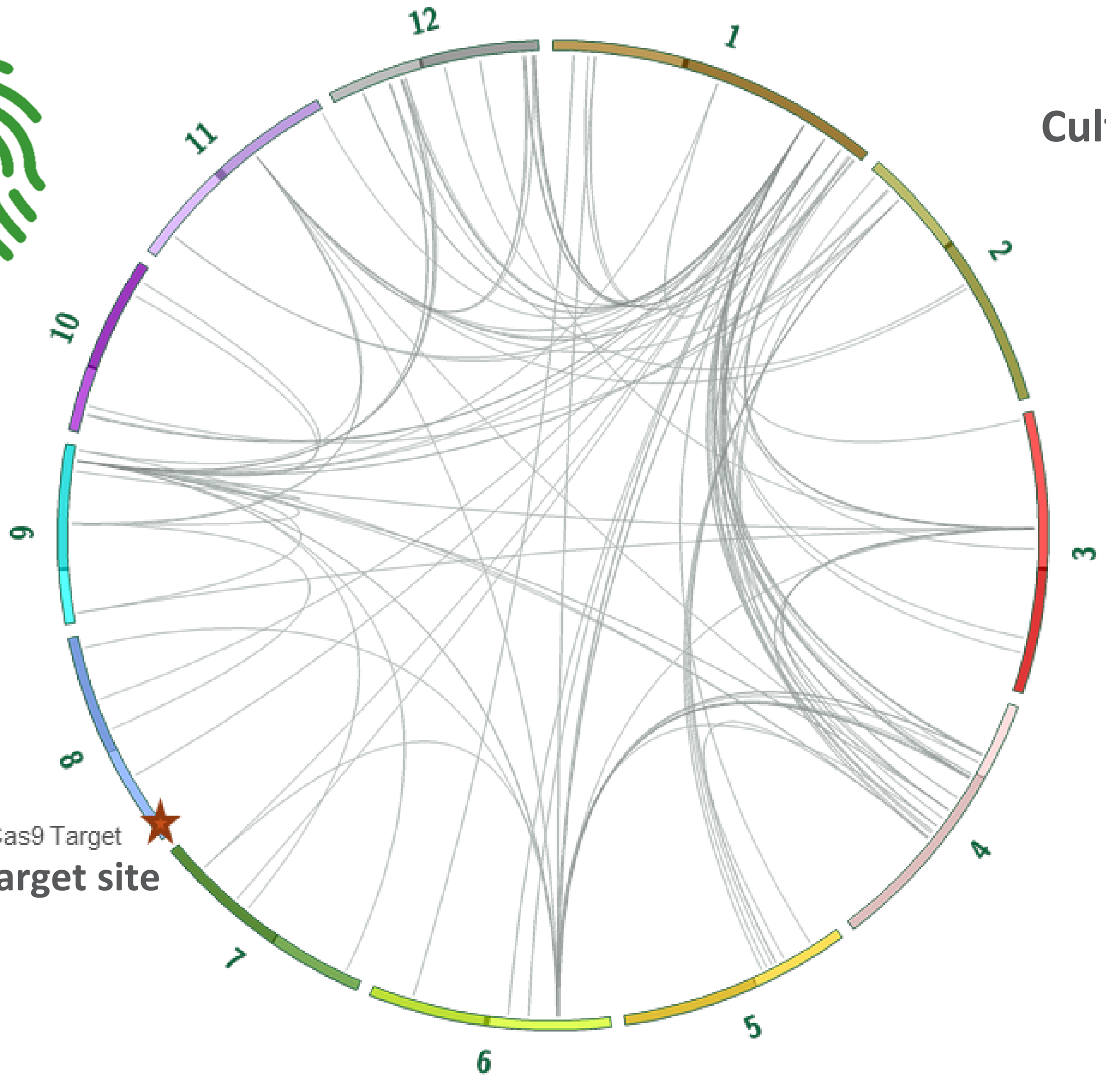
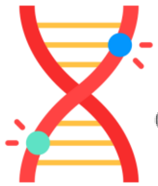
Unique genetic fingerprints to discriminate a specific GE line





Crispr/Cas9 Target
On-target site

Cultivar-specific marker

→ A set of ≠ redundant barcodes

1 234567 890128

A unique 2-SNV barcode
→ Combination of 2 ≠ SNVs specific to a cultivar

SNV	CHR	POS	REF	ALT
1	9	21,176,062	T	G
2	2	3,247,472	G	C
3	1	37,778,084	T	C
4	1	41,879,706	G	A

Barcode-1 (SNV 1–2)

Barcode-2 (SNV 3–4)

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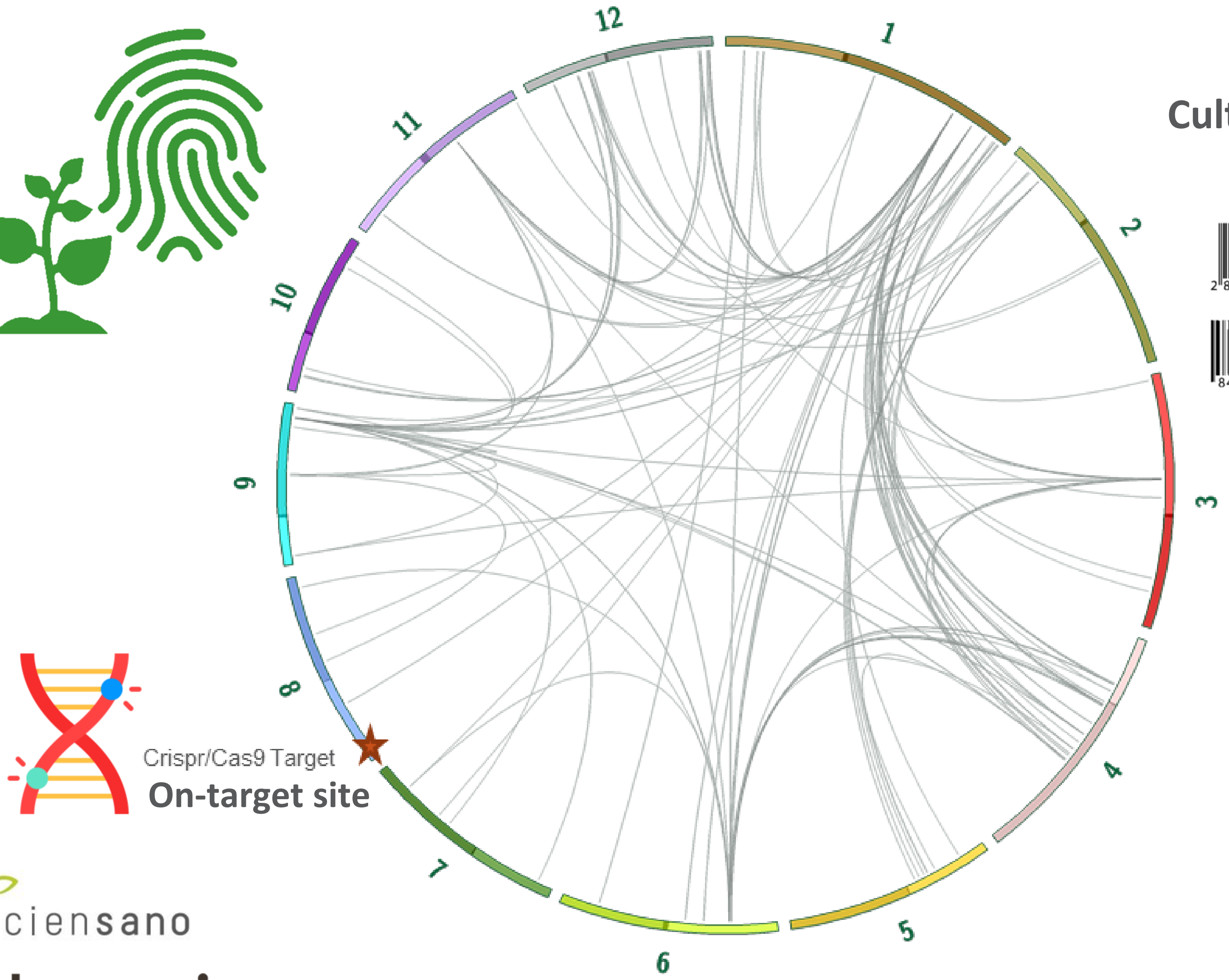
Unique genetic fingerprints to discriminate a specific GE line



Cultivar-specific marker

→ A set of ≠ redundant barcodes

In theory, a single 2-SNV unique barcode is sufficient BUT genome-wide coverage and redundancy are highly recommended:

- High specificity: very unlikely to occur through commercial breeding or natural events in any other rice line
- Tolerance for missing data leading to incomplete fingerprint, due to e.g. (1) potential mutations in the target SNVs that may appear in GE lines through natural occurrence; (2) at experimental level, partial coverage of all 2-SNV barcodes

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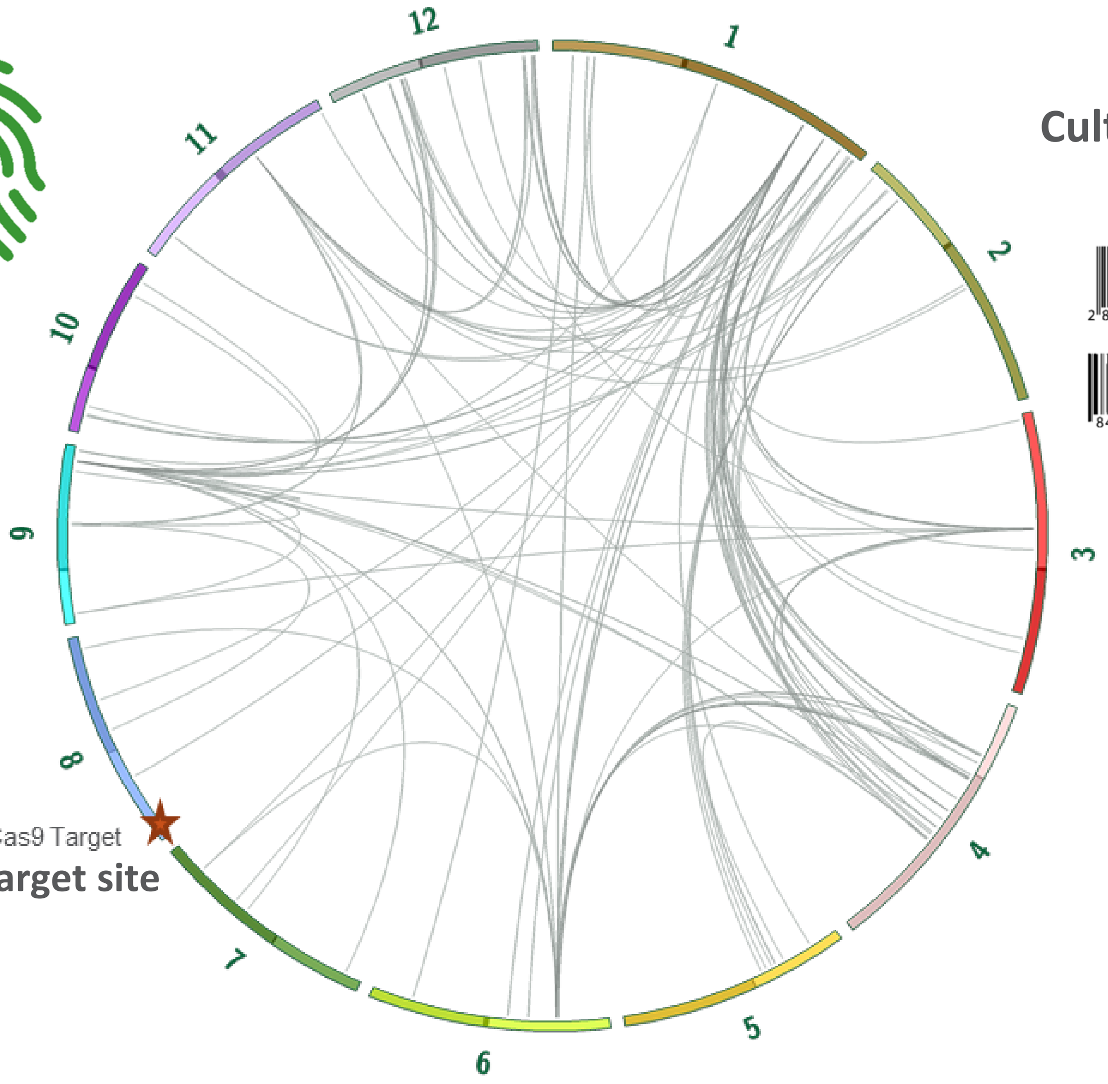
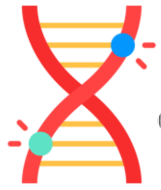
Unique genetic fingerprints to discriminate a specific GE line





Crispr/Cas9 Target
On-target site

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Cultivar-specific marker

→ A set of ≠ redundant barcodes

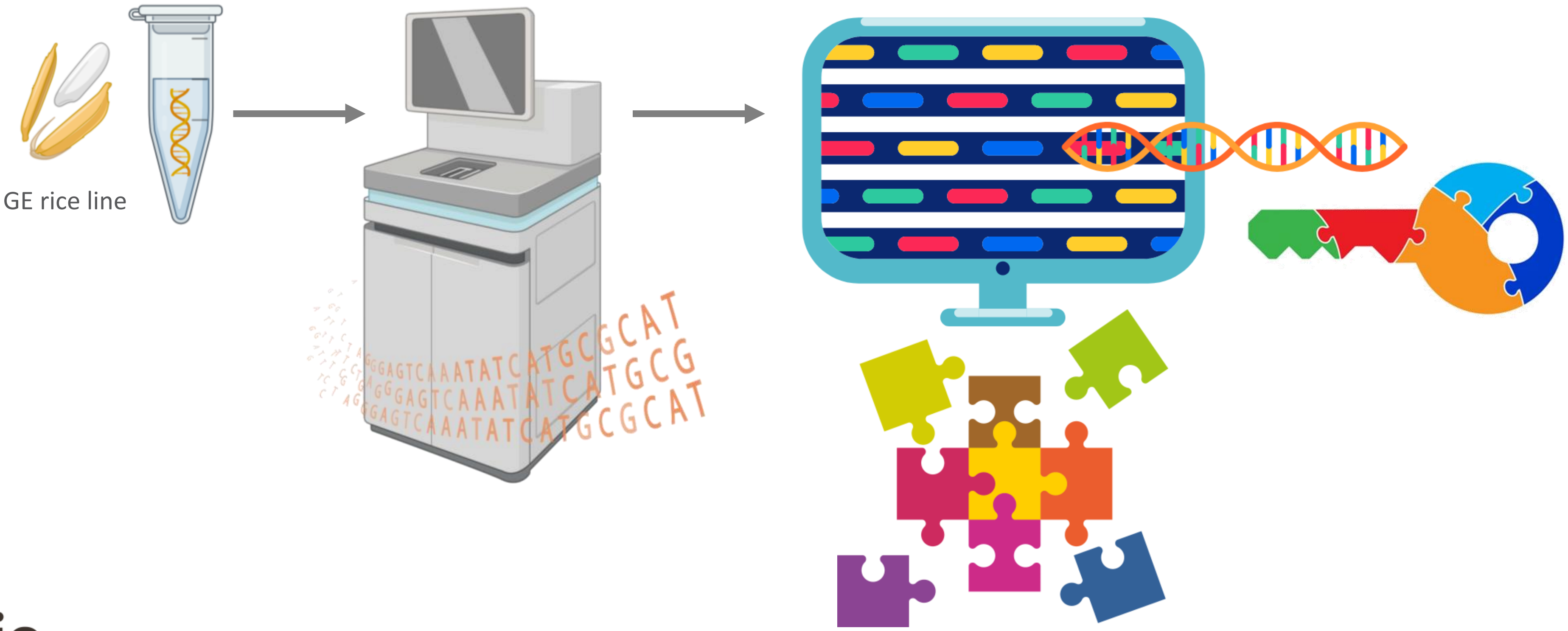
2869743695423 79359426436872 8452379 79357426495872396 754395967238
842536939647 7 29394556487 7 93574264958 7935742649587239685 73 842536939

Ex. Nipponbare cultivar:
- ✓ 145 redundant 2-SNV barcodes, including 99 ≠ SNVs
- ✓ covers almost all rice genome chromosomal arms

Genetic fingerprint detection for unambiguous NGT identification

- Examples of different analytical approaches to detect a genetic fingerprint

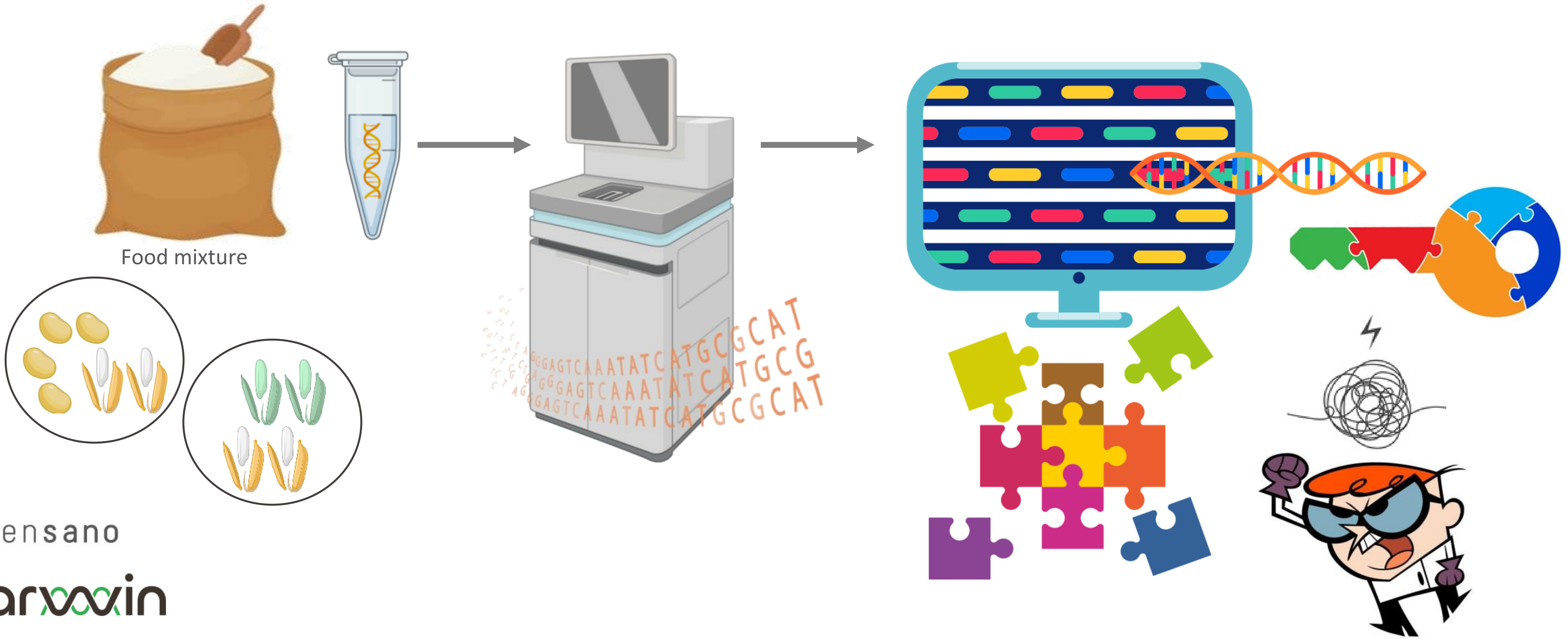
→ Whole-genome sequencing for a pure/single line



Genetic fingerprint detection for unambiguous NGT identification

- Examples of different analytical approaches to detect a genetic fingerprint

→ Shotgun metagenomics for mixture



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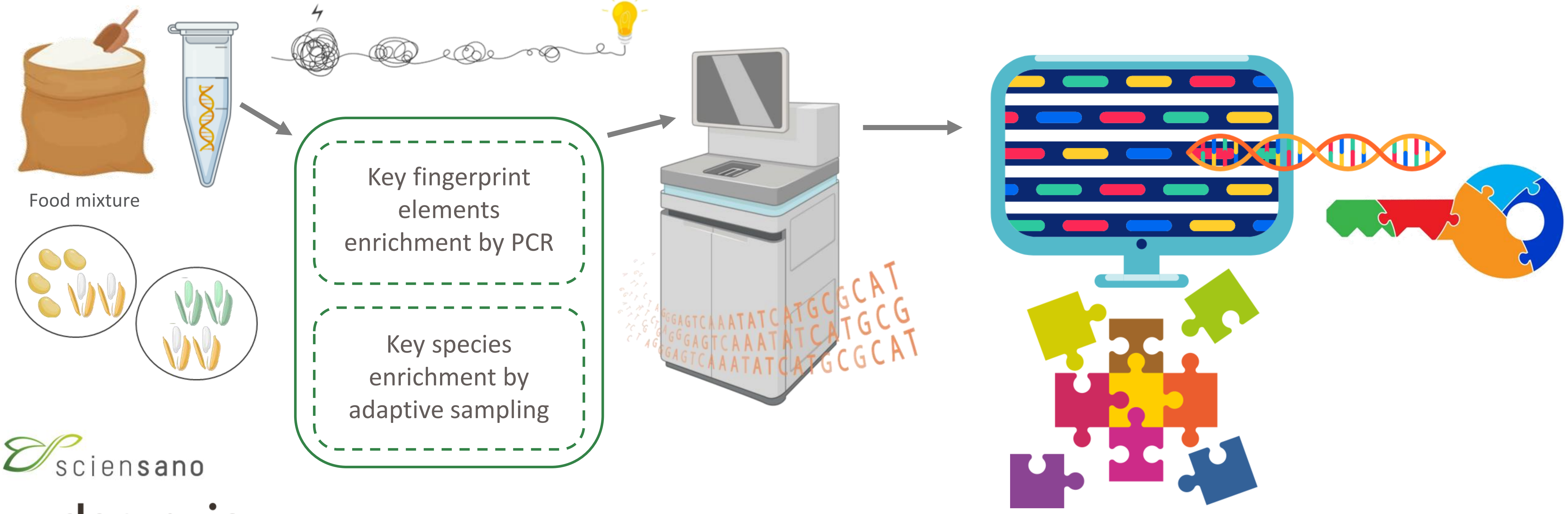
Genetic fingerprint detection for unambiguous NGT identification

- Examples of different analytical approaches to detect a genetic fingerprint

  → Metagenomics with prior enrichment



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Conclusion

- Identification of GE lines is technically possible
- But current approaches used for classical GMOs are NOK
- Novel approach for unambiguous identification of a specific GE line by detecting its genetic fingerprint:
  - On-target site(s) introduced by genome editing technologies
  - Cultivar-specific marker → a set of several redundant 2-SNV barcodes
- Different analytical approaches are available for fingerprint detection using sequencing, with or without prior enrichment

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Available peer-reviewed publications on NGT detection

ELSEVIER
Food Research International
Volume 221, Part 1, December 2025, 117218

Genetic fingerprints derived from genome database mining allow accurate identification of genome-edited rice in the food chain via targeted high-throughput sequencing

Marie-Alice Fraiture [a,1], Jolien D'aes [a,1], Andrea Gobbo [a], Maud Delvoye [a], Anne-Cécile Meunier [b,c], Julien Frouin [b,c], Emmanuel Guiderdoni [b,c], Dieter Deforce [d], Charlotte De Vogelaere [a], Sigrid C.J. De Keersmaecker [a], Kevin Vanneste [a,2], Nancy H.C. Roosens [a,2]

npj | science of food
Published in partnership with Beijing Technology and Business University & International Union of Food Science and Technology
Article
https://doi.org/10.1038/s41538-026-00846-z

Enhancing low-level genome-edited crop detection and identification in food mixtures using nanopore adaptive sampling: Rice-Soybean mixture as proof-of-concept

Arno Stuyts[1,2,5], Amin Zolfaghari[1,2,5], Jolien D'aes[1], Kevin Vanneste[1], Anne-Cécile Meunier[3,4], Alexandre Soriano[3,4], Sigrid C. J. De Keersmaecker[1], Dieter Deforce[2], Nancy H. C. Roosens[1,6] &
Marie-Alice Fraiture[1,6]

Check for updates

ELSEVIER
Food Control
Volume 137, July 2022, 108904

ddPCR strategy to detect a gene-edited plant carrying a single variation point: Technical feasibility and interpretation issues

Marie-Alice Fraiture [a], Emmanuel Guiderdoni [b,c], Anne-Cécile Meunier [b,c], Nina Papazova [a], Nancy H.C. Roosens [a]

foods
MDPI
Article

Targeted High-Throughput Sequencing Enables the Detection of Single Nucleotide Variations in CRISPR/Cas9 Gene-Edited Organisms

Marie-Alice Fraiture [1,†], Jolien D'aes [1,†], Emmanuel Guiderdoni [2,3], Anne-Cécile Meunier [2,3], Thomas Delcourt [1], Stefan Hoffman [1], Els Vandermassen [1], Sigrid C. J. De Keersmaecker [1], Kevin Vanneste [1,‡] and Nancy H. C. Roosens [1,*,‡]

+ others ongoing

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Dr. Anne-Cécile Meunier
Dr. Julien Frouin

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Ghent University

Dr. Dieter Deforce

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