Introduction of MassARRAY platform and their applications of SNPs genotyping in plant breeding

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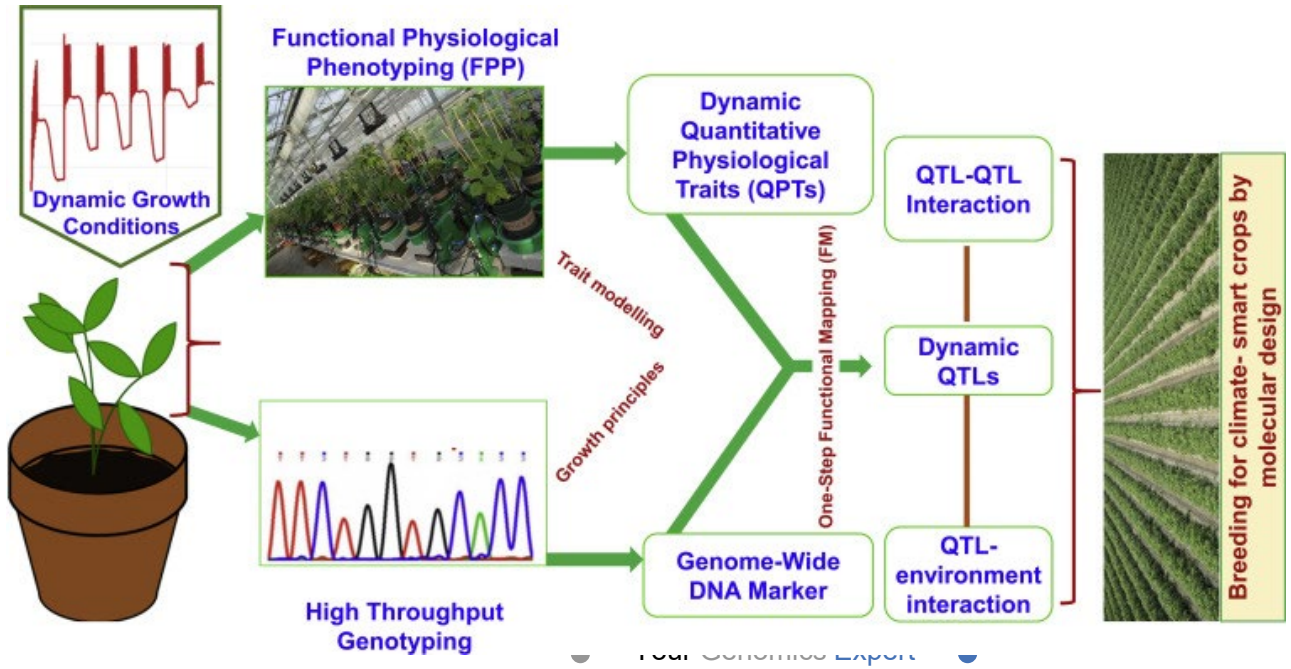
Product specialist, Lifomics Co., LTD

Genotype

- การตรวจสอบรูปแบบดีเอ็นเอ (genotyping)
- การค้นหาความหลากหลายทางพันธุกรรมในบริเวณที่สนใจ (variation analysis)
- รูปแบบความหลากหลายทางพันธุกรรมในปัจจุบัน
  - substitution (SNP), Insertion, Deletion.



Causes for sequence (dis)similarity in biological meaning

```
GCAGCGG----AGCGGGTTGA      Seq1
||  ||||....||||||||||
GCTGCGCCGTGAGCGGGTTGA      Seq2
++-++++----++++++++++      Score
```

mutation: a nucleotide at a certain location is replaced by ***another*** nucleotide (e.g.: ATA → AGA)

insertion: at a certain location one new nucleotide is inserted in between two existing nucleotides (e.g.: AA → A**G**A)

deletion: at a certain location one existing nucleotide is deleted (e.g.: ACTG → AC-G)

indel: an **in**sertion or a **del**etion

Plant/ animal/ microorganism

Genome/ DNA extraction

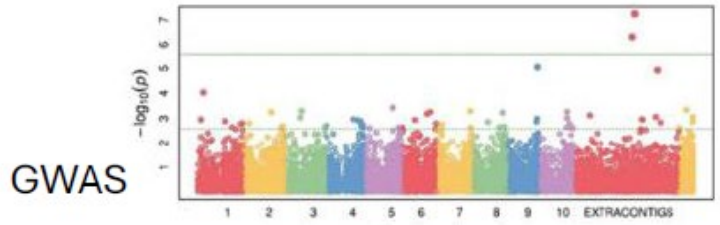
Base calling

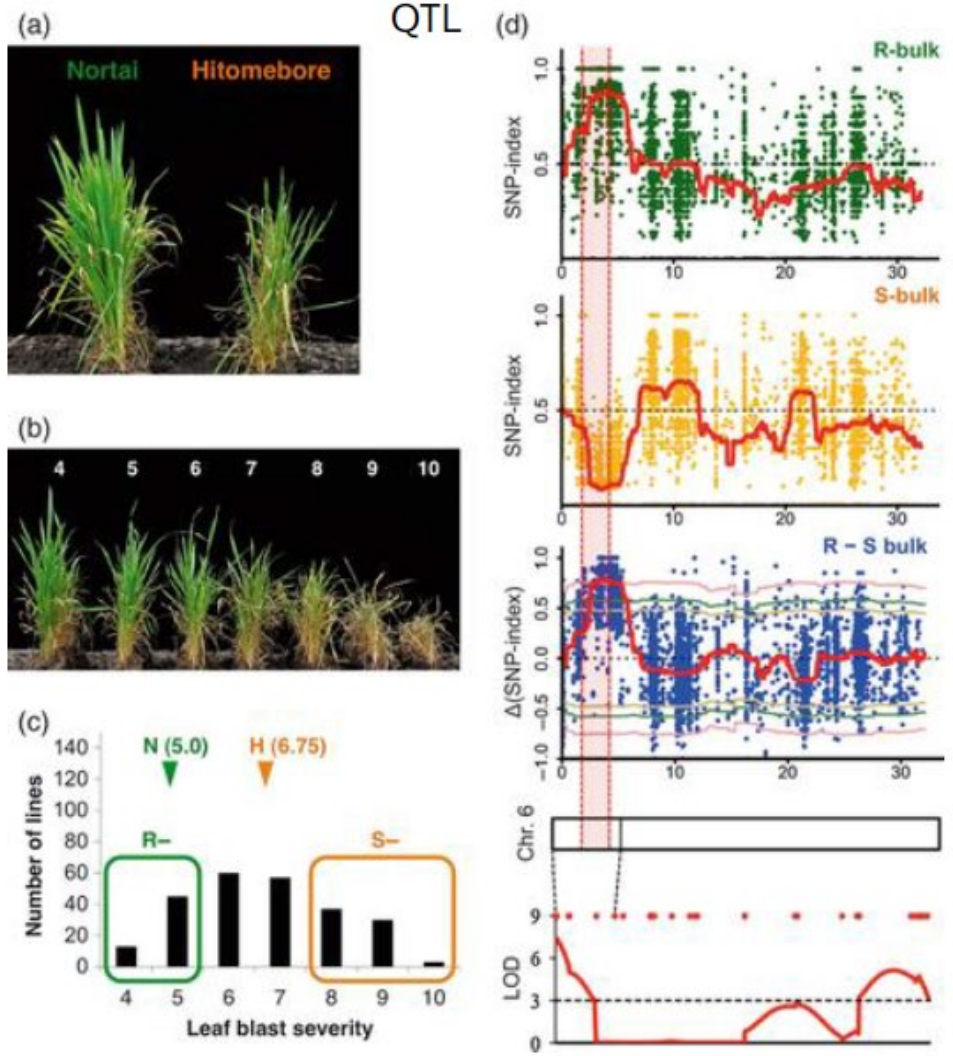
High throughput sequencing technology

Genotype of population

GWAS, QTL

Phenotype

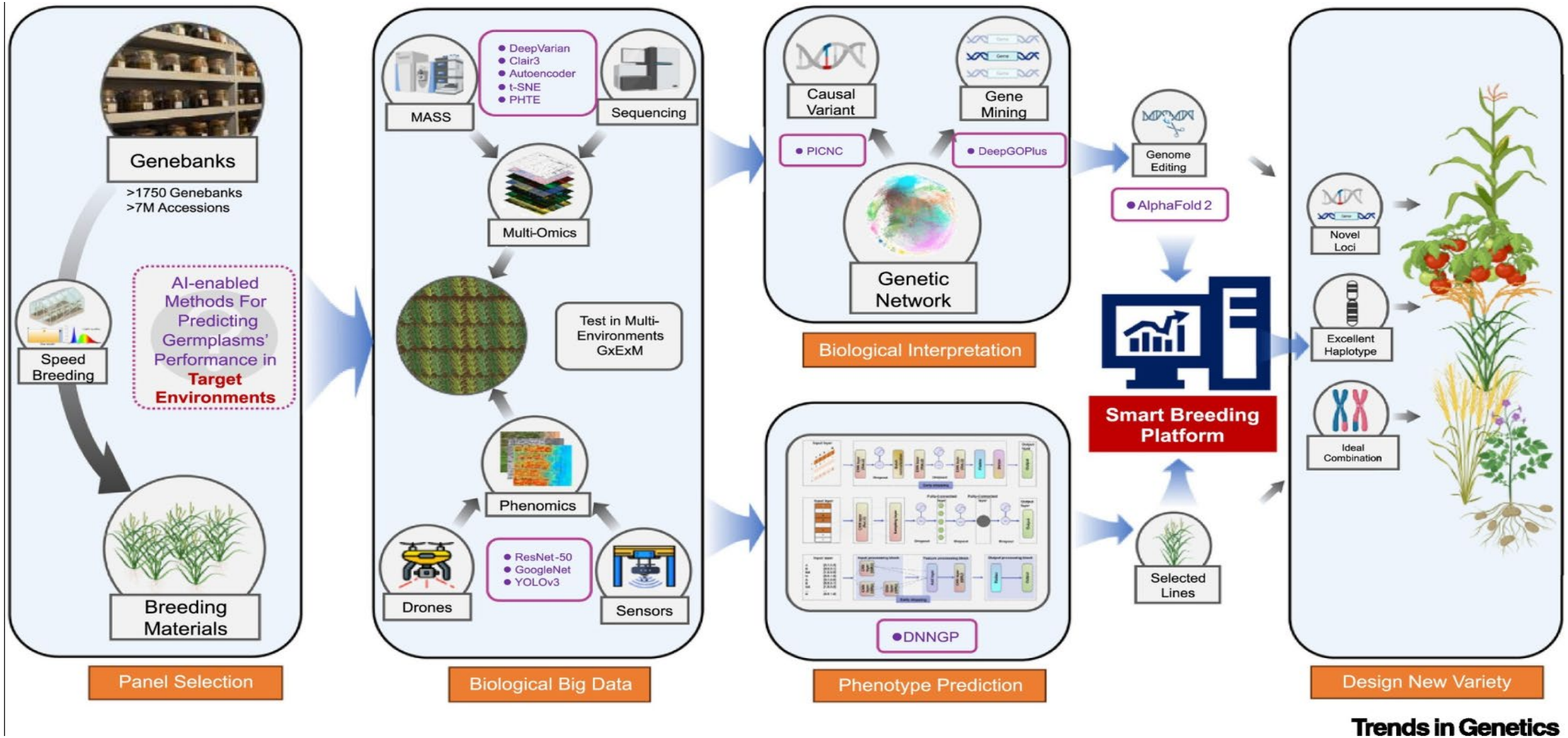




Takagi H, et al., Plant J. 2013 Apr;74(1):174-83.

Advantages of SNP Markers

- Abundant in the genome: SNPs are highly polymorphic, providing numerous markers for analysis.
- High throughput: Modern genotyping technologies allow for efficient and cost-effective SNP analysis.
- Co-dominant inheritance: Both alleles can be detected, providing more precise information.
- Stable: SNPs are generally stable genetic markers.



Farooq, Muhammad Amjad, et al. "Artificial intelligence in plant breeding." *Trends in Genetics* (2024).

https://www.cell.com/trends/genetics/fulltext/S0168-9525%2824%2900167-7#f0005

SNP based marker applications

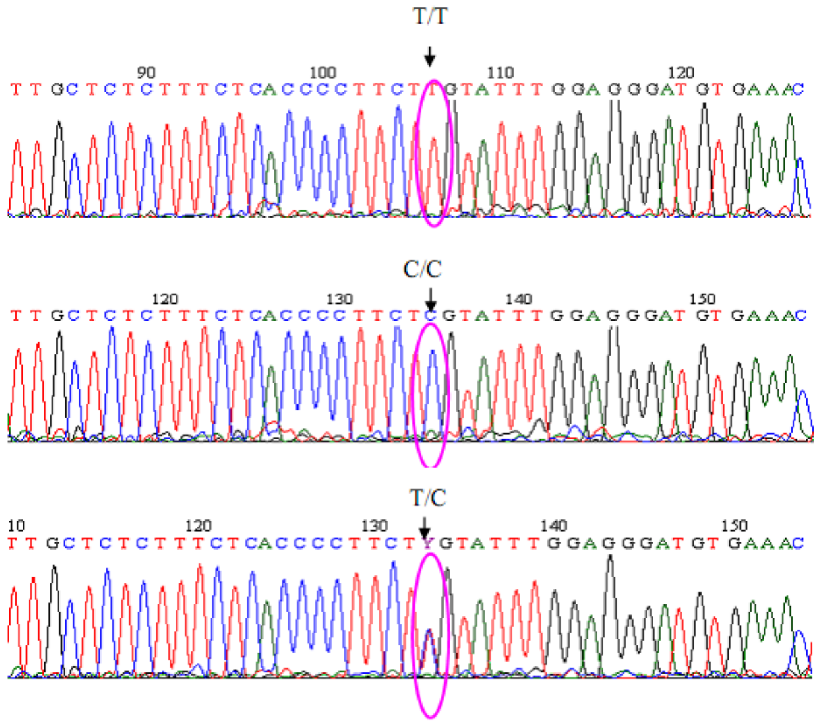
- Cultivar Identification: Hybridity Testing
- Seed Purity Testing
- Germplasm Purity Testing

- Molecular Breeding: Diversity Analysis: Germplasm Fingerprinting
  - Marker-Assisted Selection (MAS): Accelerating and precision in breeding
  - Marker Assisted Backcross (MABC)

- Genetic/QTL Mapping: Identifying gene locations
- Genome-Wide Association Studies (GWAS): Identifying trait associated genetic variants
- Genomic Selection (GS)

Molecular marker (SNP based)

- CAPS : Cleaved Amplified Polymorphic Sequences
- KASP (KASPar) : Kompetitive Allele Specific PCR
- PACE : PCR Allele Competitive Extension
- HRM (High Resolution Melting)
- MassArray
- DNA Sequencing



MASSARRAY TECHNOLOGY

- Introduction
- MassARRAY debrief
- Applications
- Discussion

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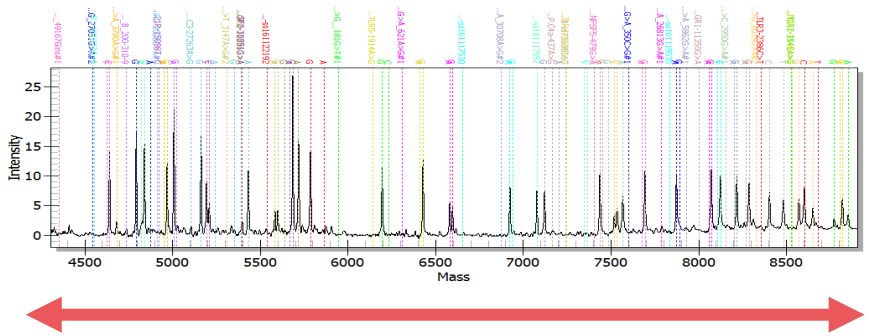
Mass-Detection With The MassARRAY

The MassARRAY is unique technology to detect DNA mutation SNP , Insertion, Deletion

Dalton
Unit of Mass

The Dalton (Da) is a unit of mass widely used in physics and chemistry.

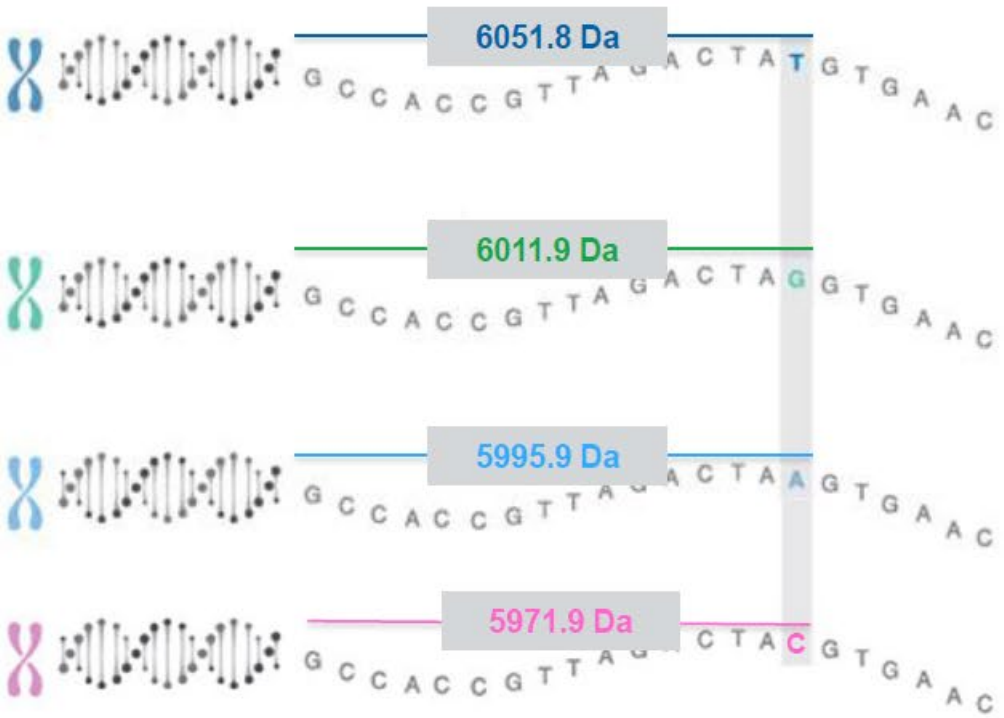


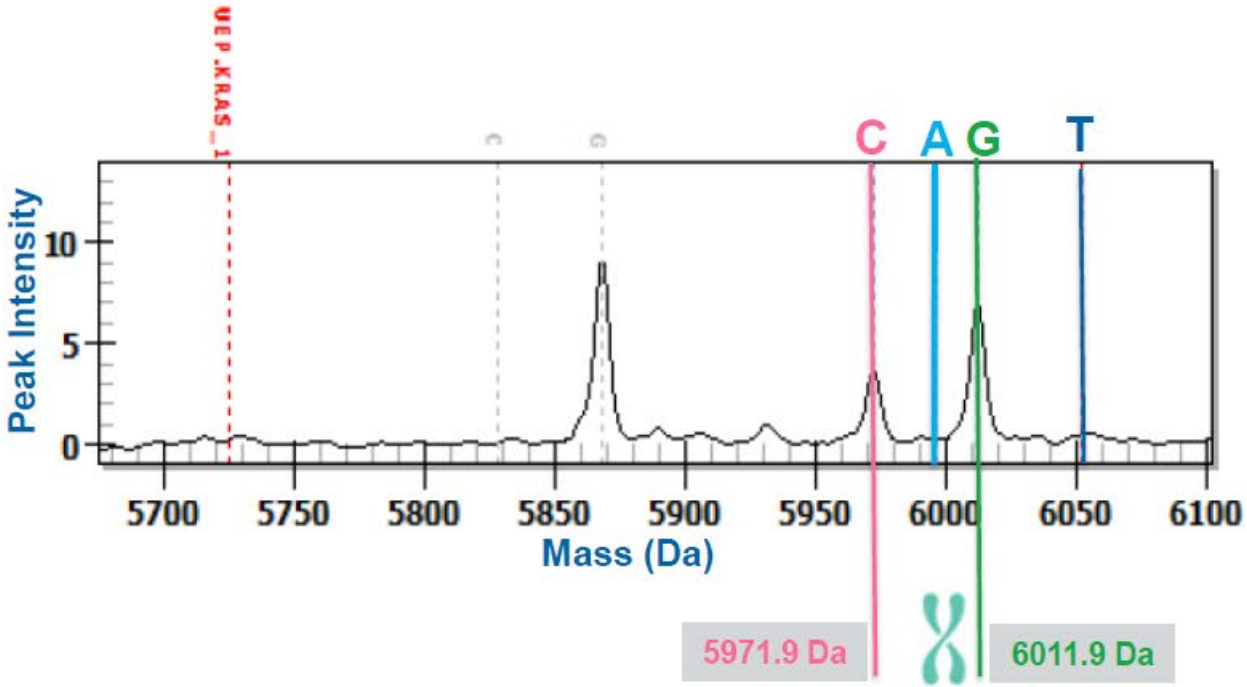
MassARRAY Detection Range 4000 – 9000 Daltons

Mass-Detection With The MassARRAY

SYSTEMS

Single Nucleotide Polymorphism (SNPs)





Heterozygous G/C

Cytosine (C)	Adenine (A)	Guanine (G)	Thymine (T)
247.2 Da	271.2 Da	287.2 Da	327.1 Da

Agena BIOSCIENCE

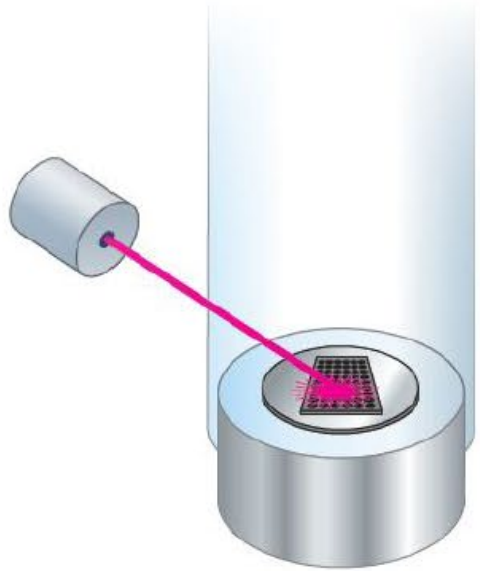
Technology Overview

Matrix-Assisted Laser Desorption Ionization – Time of Flight (MALDI-TOF)

SYSTEMS

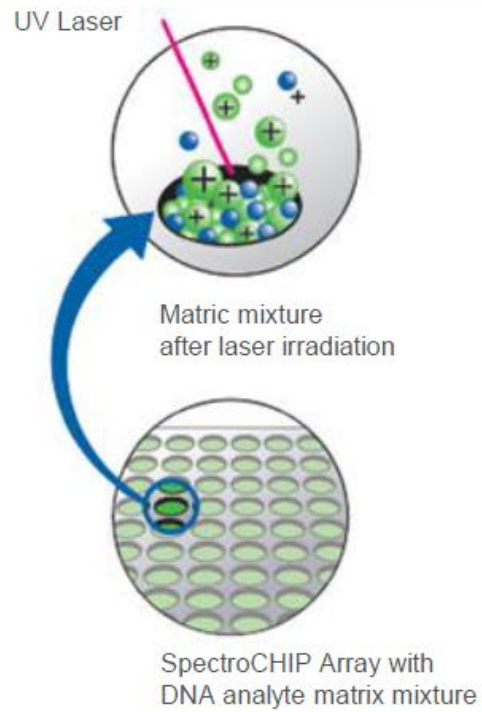
1 DNA Irradiation/Ionization

SpectroCHIP Arrays are placed in the MassARRAY analyzer and the samples are irradiated by a laser.



2 DNA Separation

Samples become ionized (positively charged) and begin to migrate through the vacuum tube



Agena BIOSCIENCE

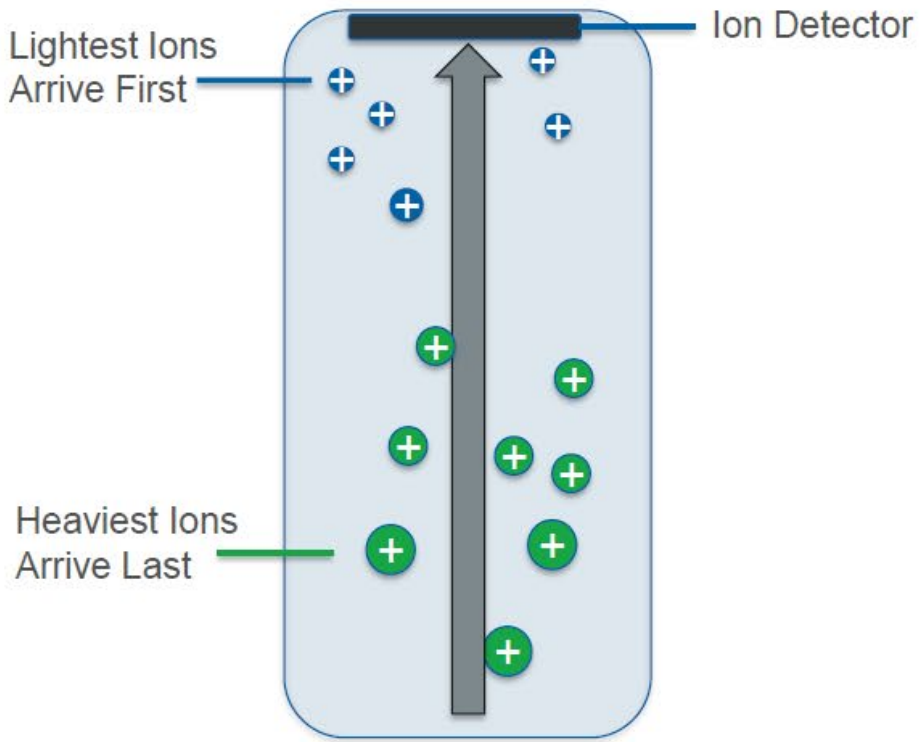
Technology Overview

Matrix-Assisted Laser Desorption Ionization – Time of Flight (MALDI-TOF)

SYSTEMS

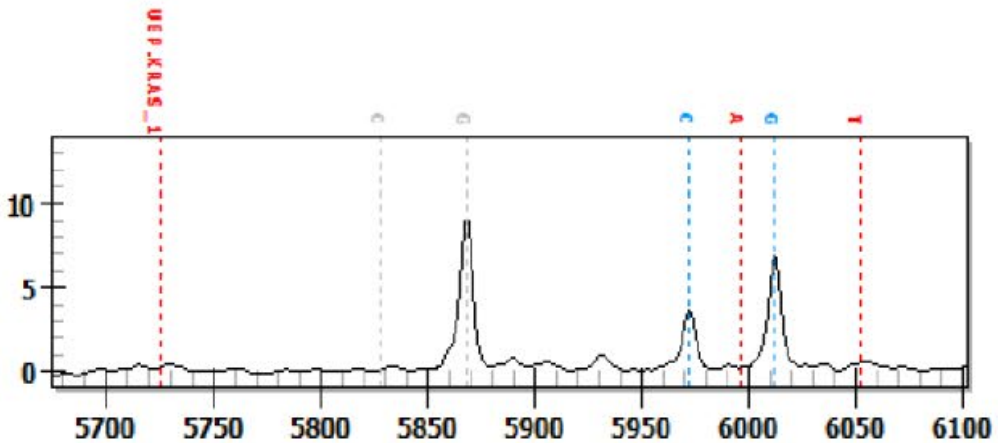
3 Time of Flight

Mass dependent, the DNA analyte ions arrive to the detector at different speeds leading to different arrival times (or times of flight).



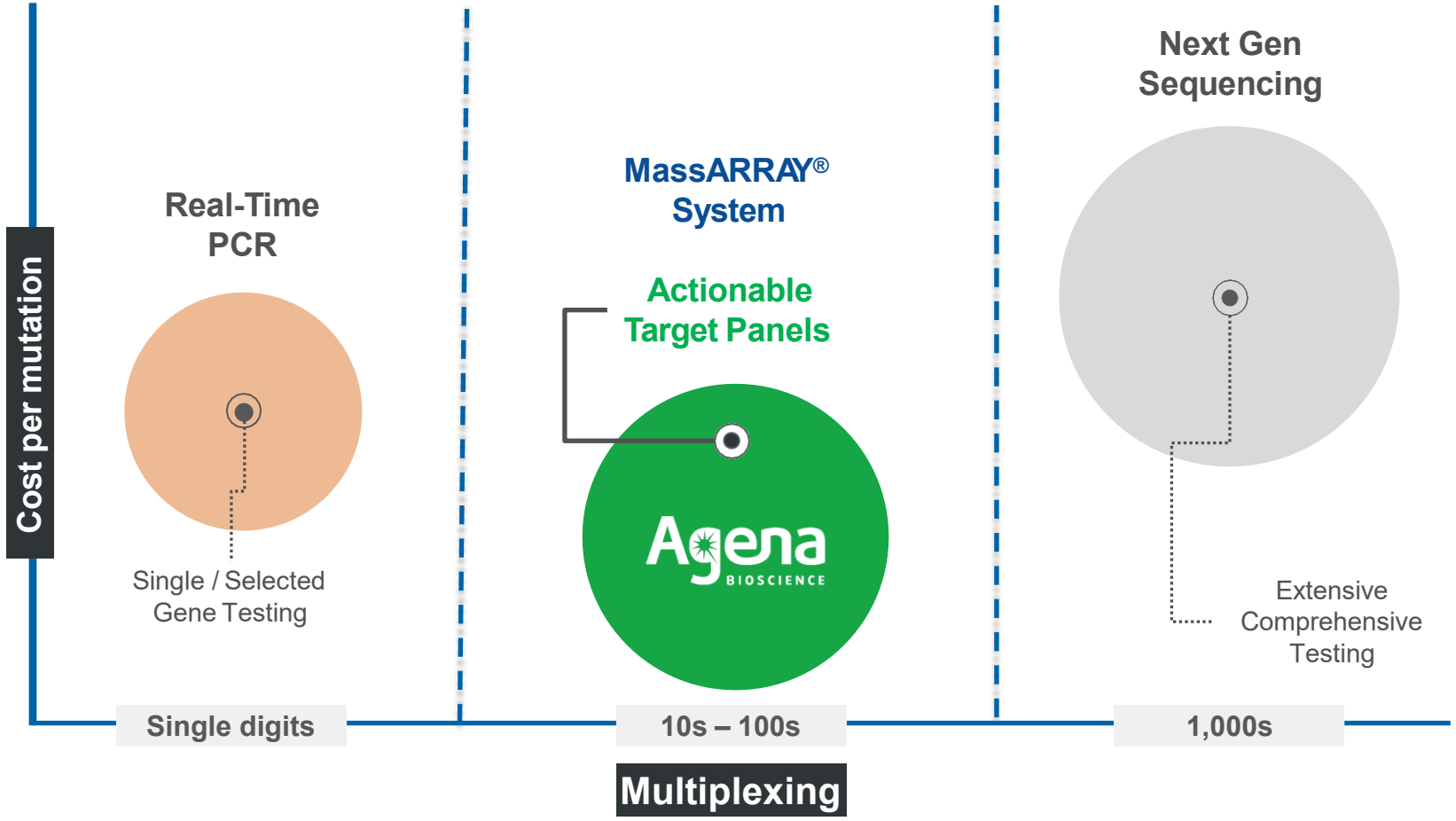
4 DNA Analysis

Using arrival times, the software determines the mass of each DNA ion and generates a mass spectrum to distinguish among the different genetic targets.



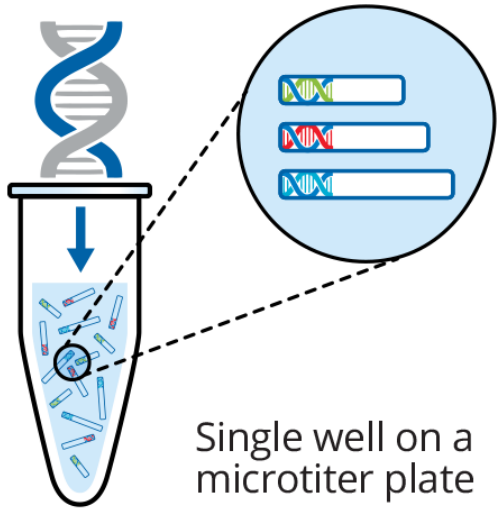
Cost-Effective, Targeted Genetic Analysis

Robust, Flexible, and High Throughput

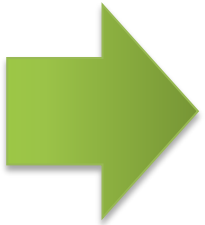


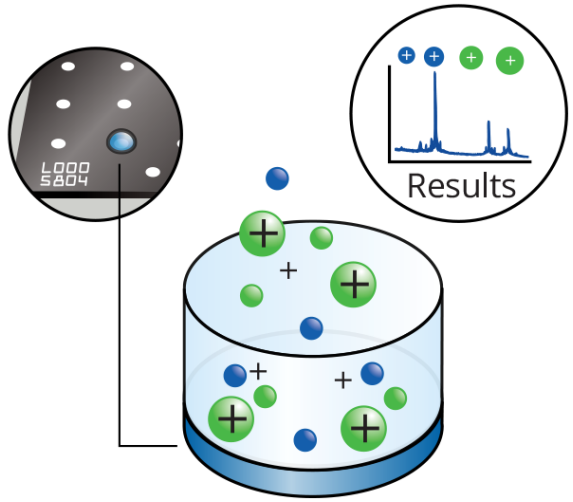
Technology Overview

Matrix-Assisted Laser Desorption Ionization – Time of Flight (MALDI-TOF)



Single well on a microtiter plate





Detection and Analysis

Multiplex PCR

MALDI-TOF Mass

Technology Overview

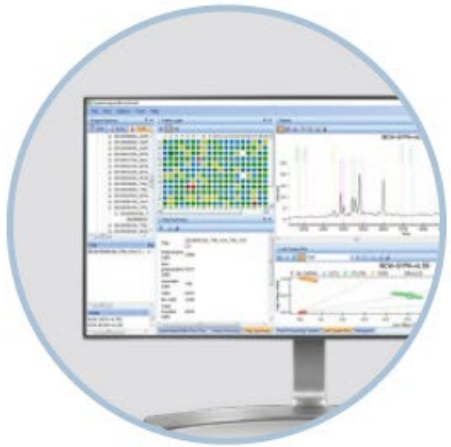
Matrix-Assisted Laser Desorption Ionization – Time of Flight (MALDI-TOF)

PCR/SAP/Extension

Multiplex end-point PCR followed by a single base extension reaction

Target Sequence Detection

Automated analyte transfer and data acquisition



Data Analysis

Data display and report generation

96 FORMAT

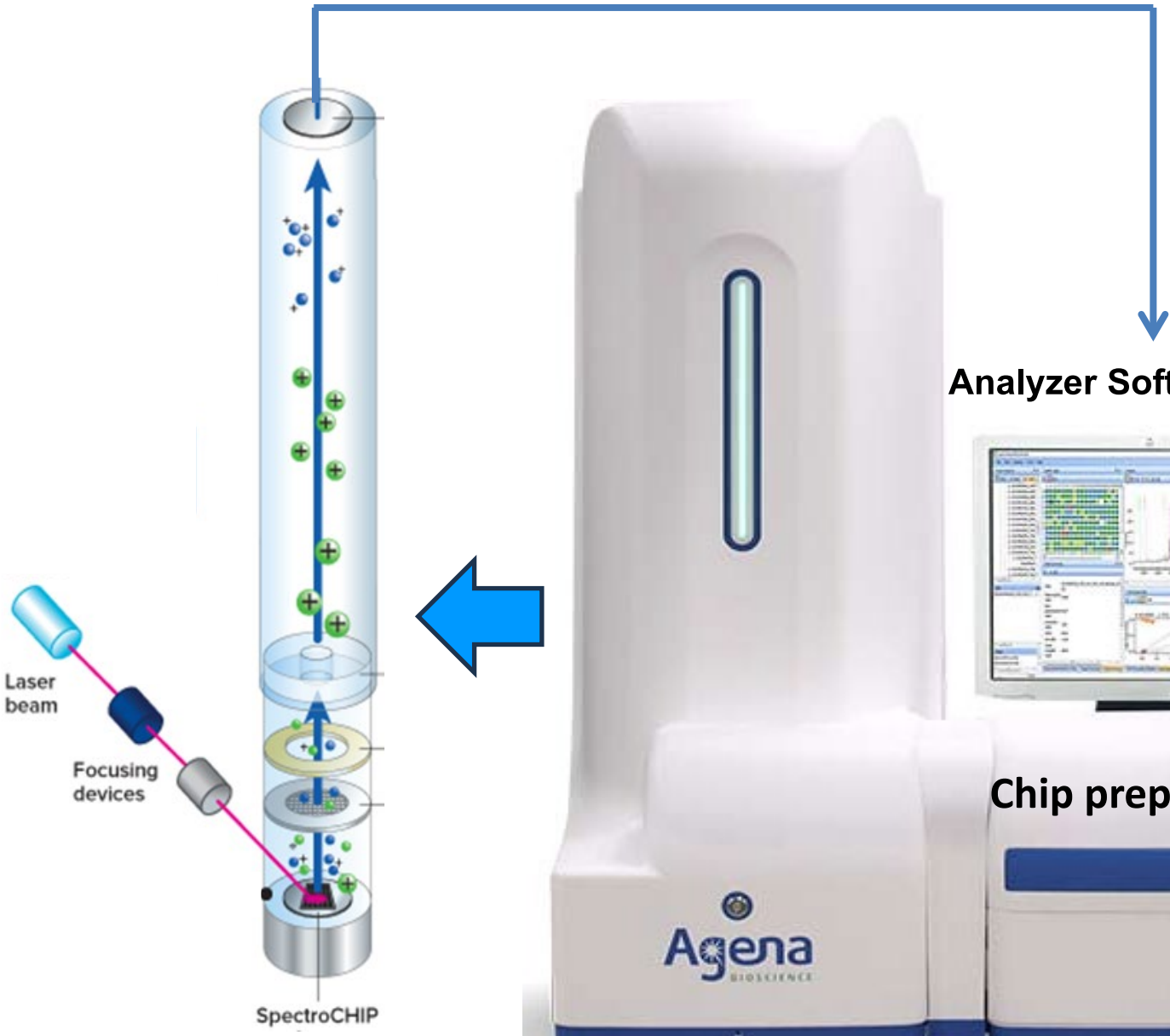
Run Time: 7 Hrs*
Hands-on Time: 23 Min

Run Time: 90 Mins*
Hands-on Time: 5 Min

Hands-on Time:
5-10 Min

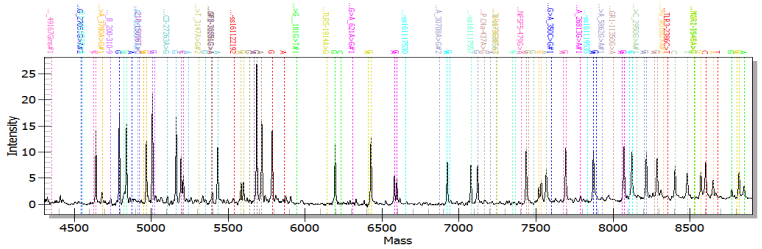
Technology Overview

Matrix-Assisted Laser Desorption Ionization – Time of Flight (MALDI-TOF)



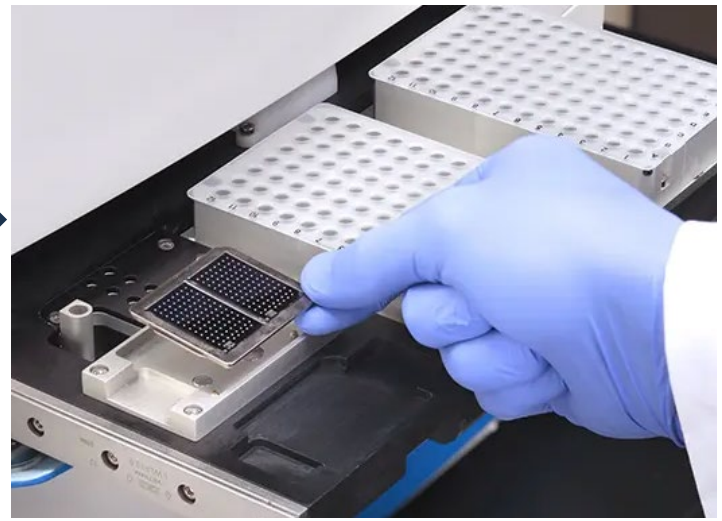
Mass Analyzer

Analyzer Software : TYPER



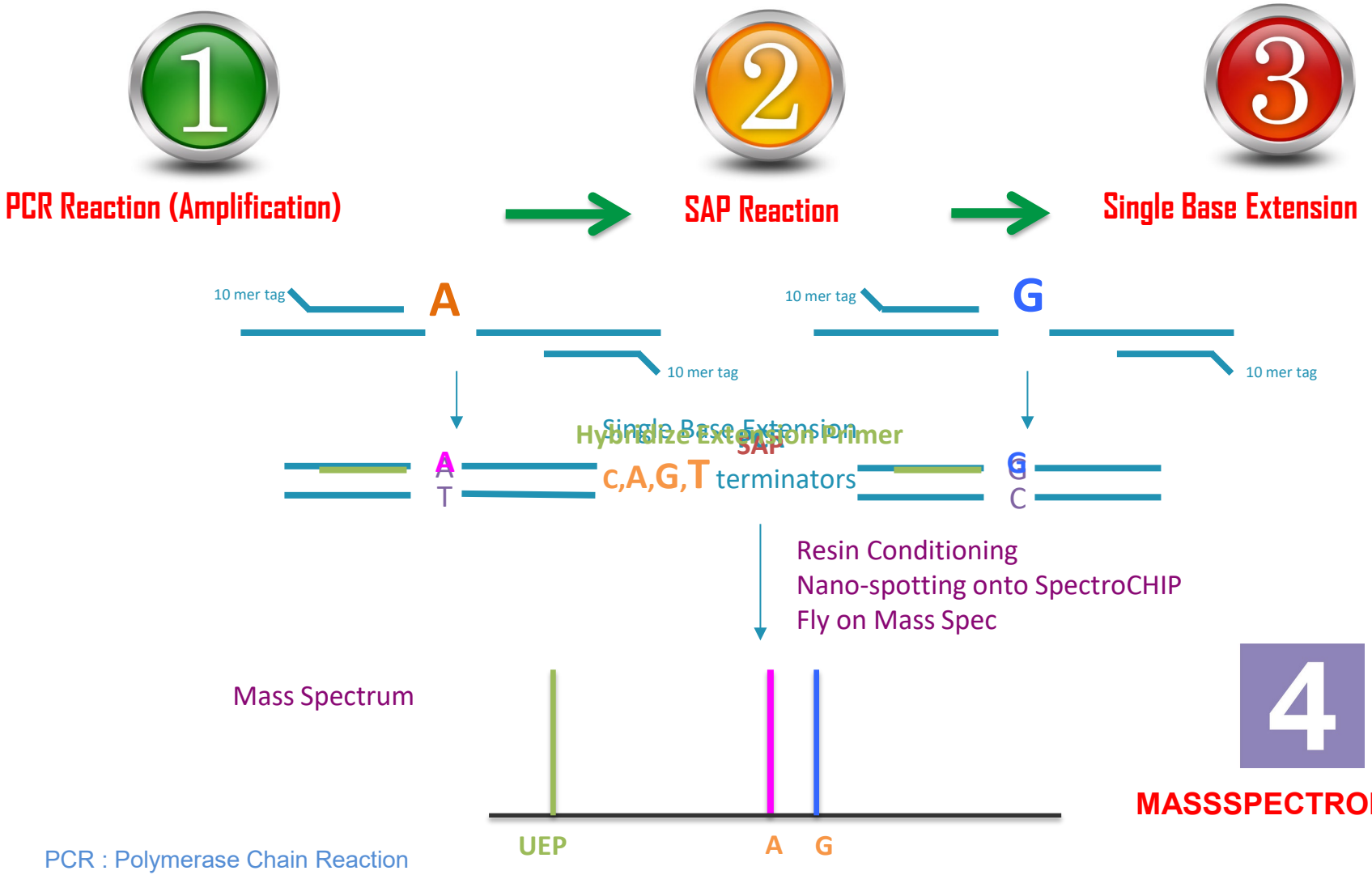
Chip prep Module

Flatform: 96 wells x 2 plates



PATENTED “SPECTROCHIP”

GENOTYPING REACTION : SNP (A/G)



PCR : Polymerase Chain Reaction

SAP : Shrimp Alkaline Phosphatase

UEP : Unextension Primer

1

2

3

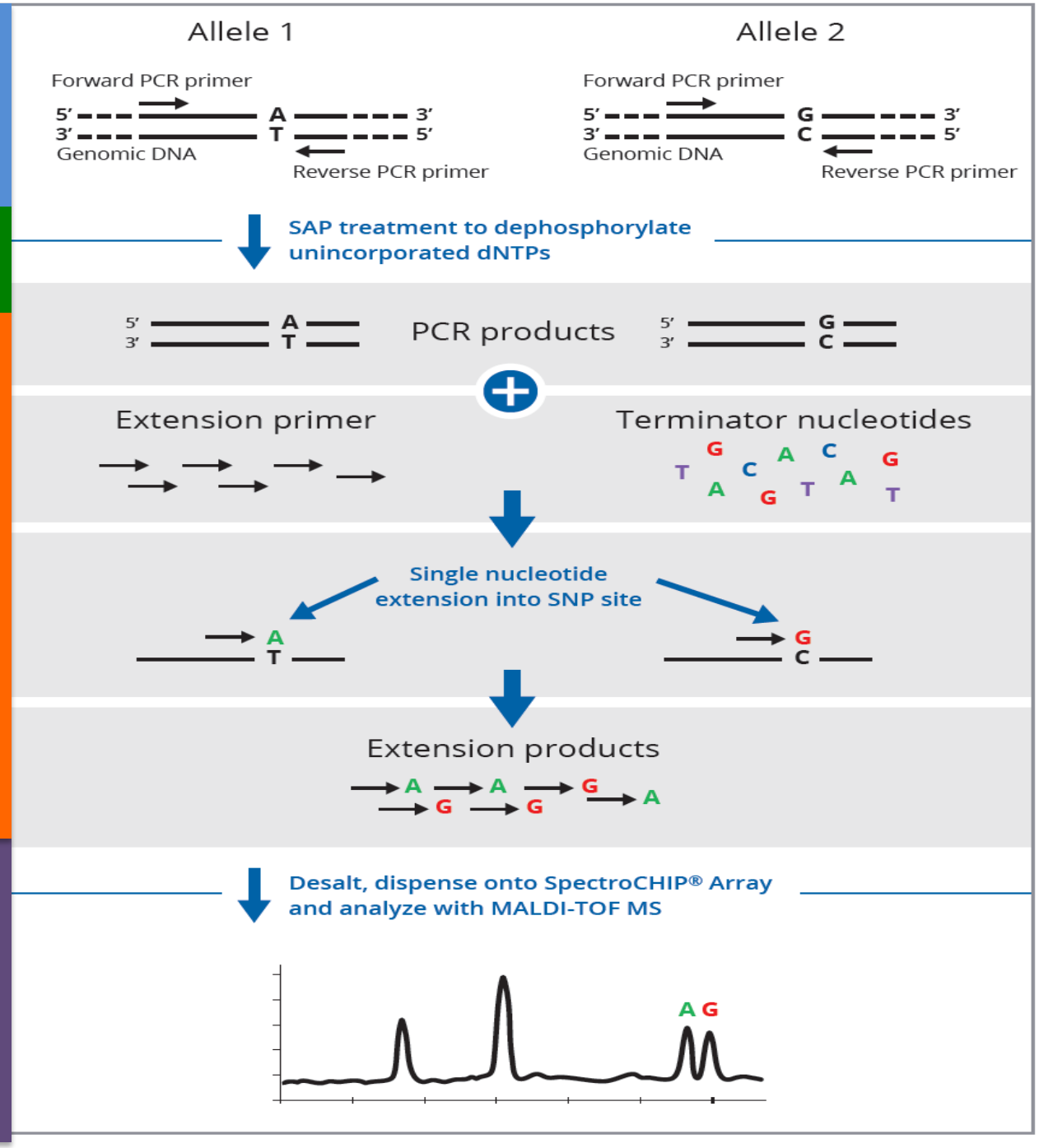
4

PCR REACTION

SAP REACTION

SINGLE BASE EXTENSION

MASSSPEC ANALYSIS



Key Highlight of MassARRAY

“MULTIPLEXING”

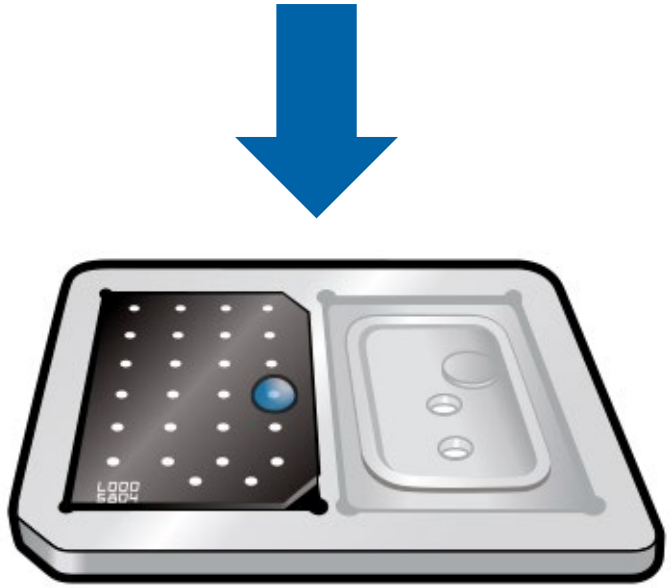
Up to 60 Targets per a Single Reaction…

Simple Workflow

PCR/SAP/Extension

10 Secs / Well (96 Chip)

96 Sample ≥ 15 Mins



PATENTED “SPECTROCHIP”

5-10 ng DNA/ Reaction

High accuracy “99.7%”

270laser shots

(30 x 9 random areas) in a well to optimize Ionization

“MULTIPLE USAGE”

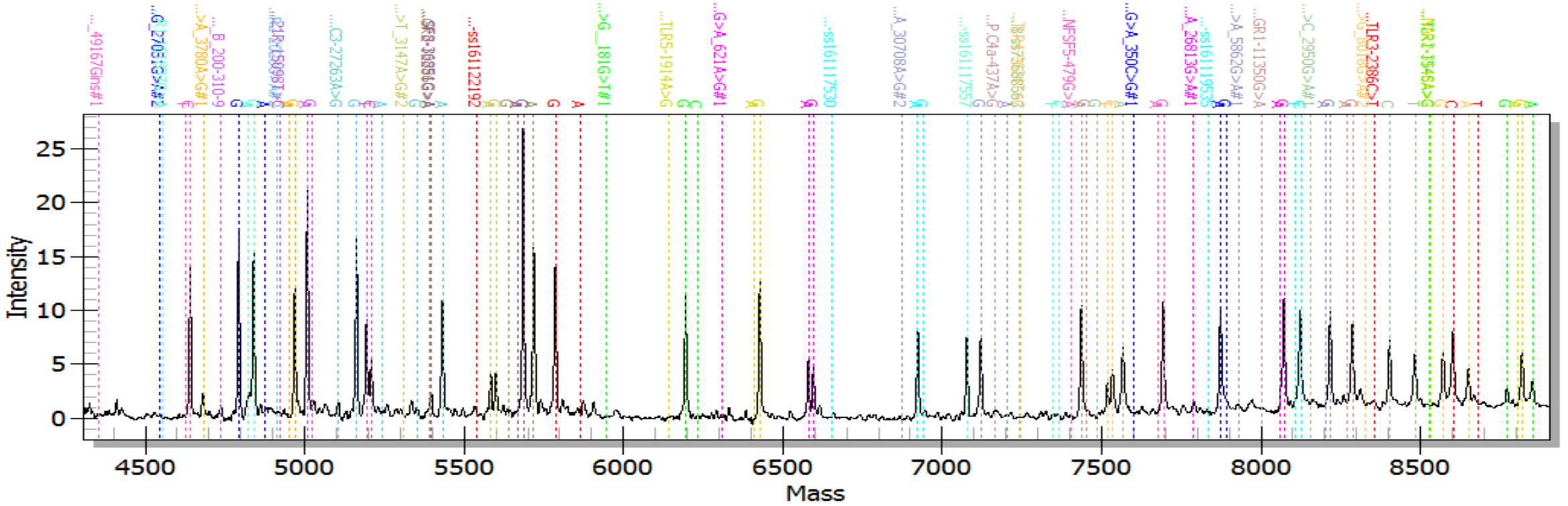
shelf life 1 month
in desiccator/ dry cabinet

Separate run
not require batch run

ADVANCED SOFTWARE : TYPER

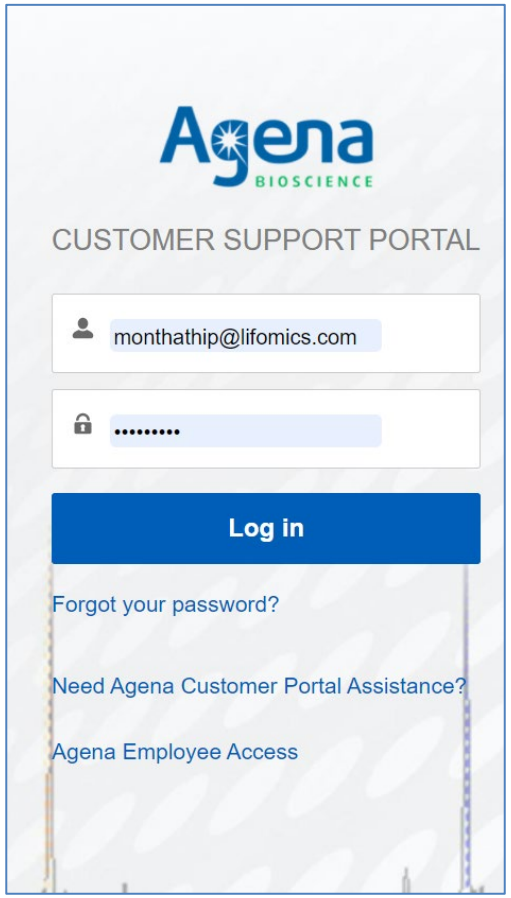
Minimal Bioinformatics Analysis

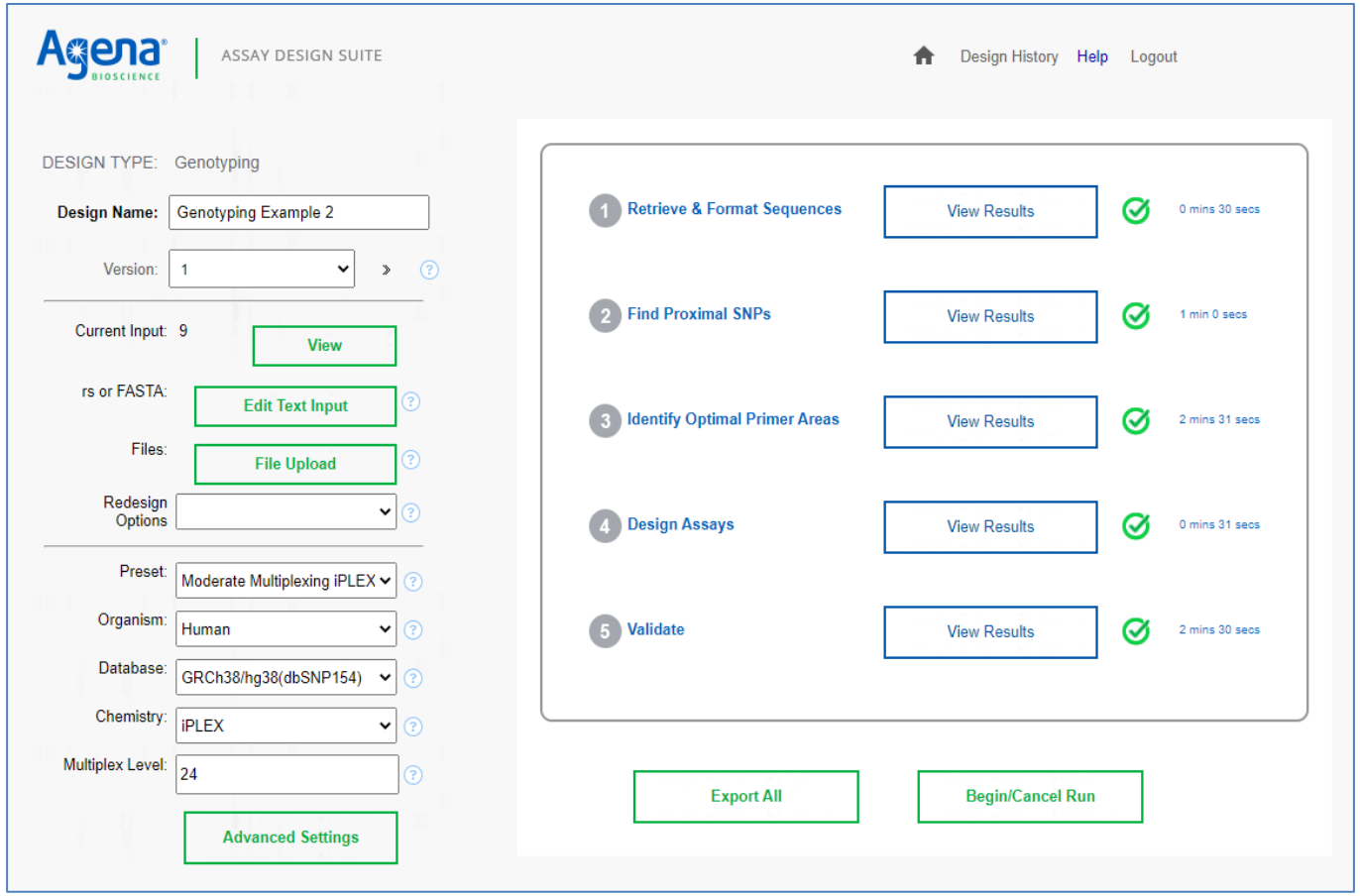
Simplified data analysis and reporting. No complex bioinformatics required.



CUSTOM PANEL

FREE ONLINE ASSISTANT : CUSTOMIZATION

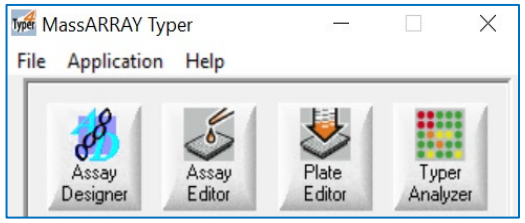


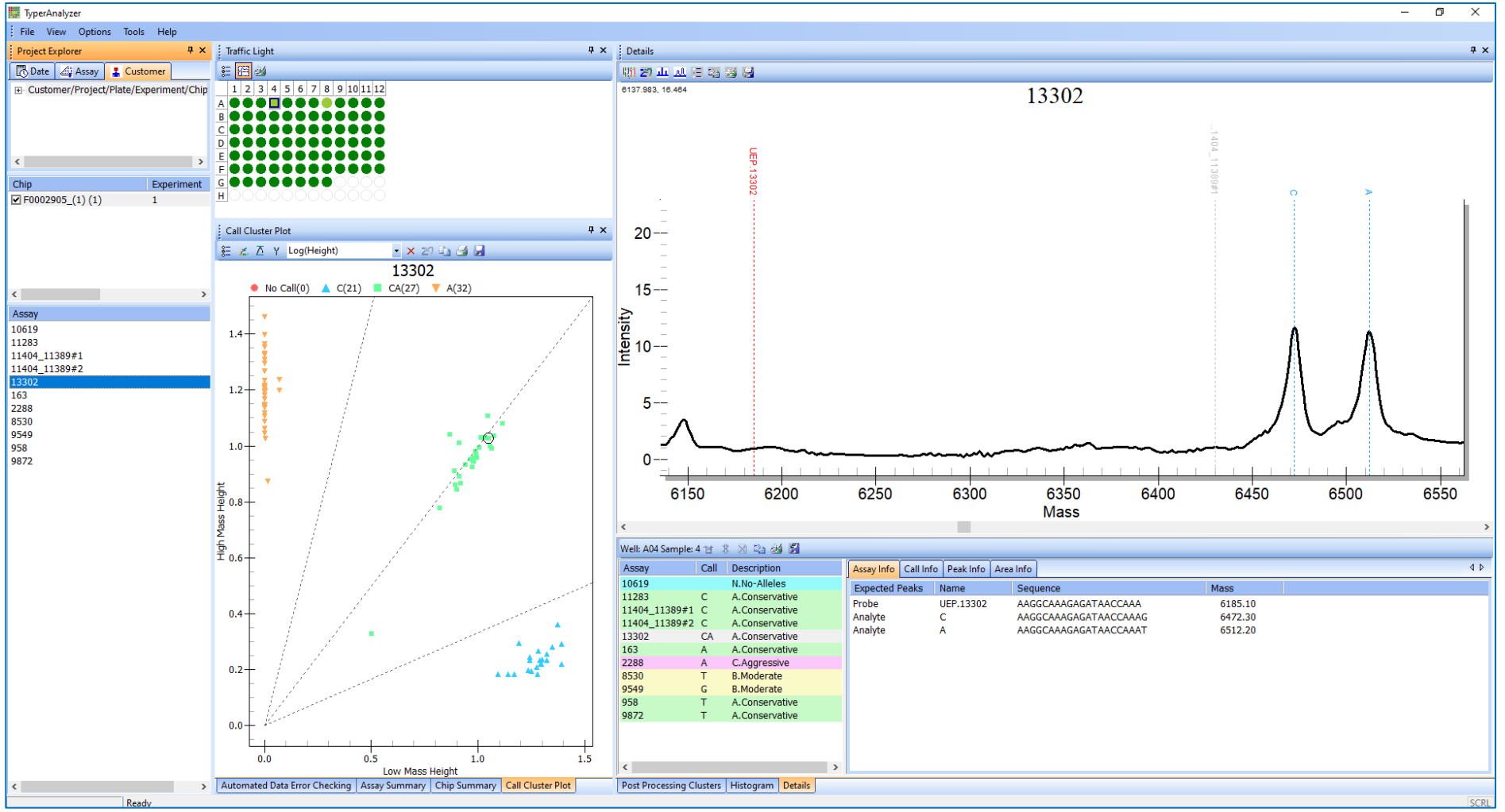


https://agenacx.com/online-tools/

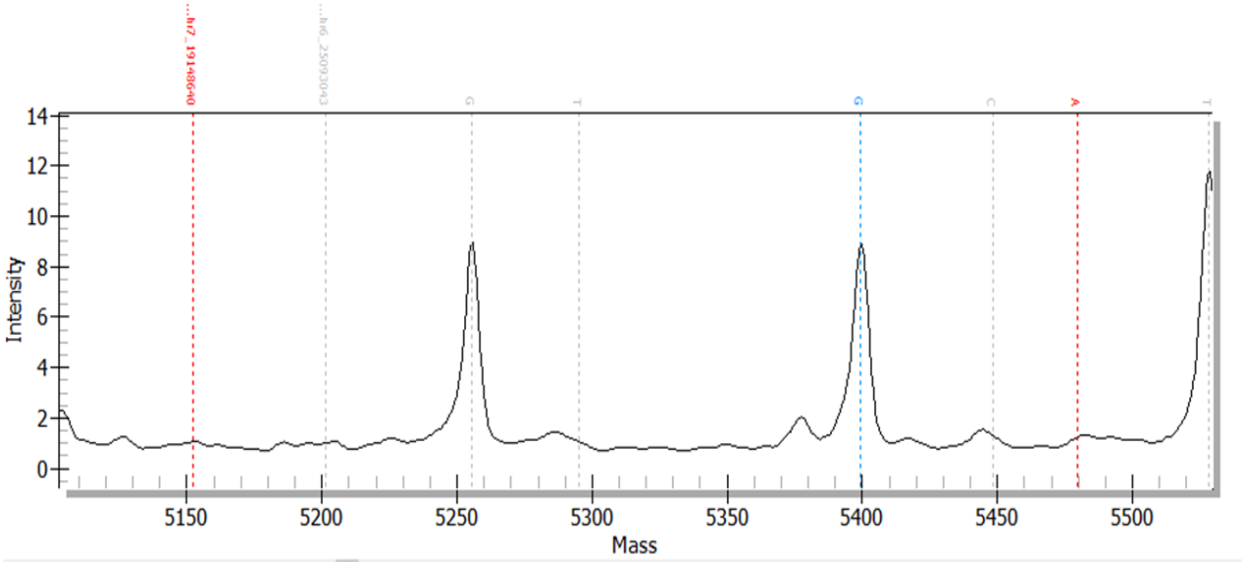
REPORT: EASE INTERPRETATION

TYPER software > Typer Analyzer

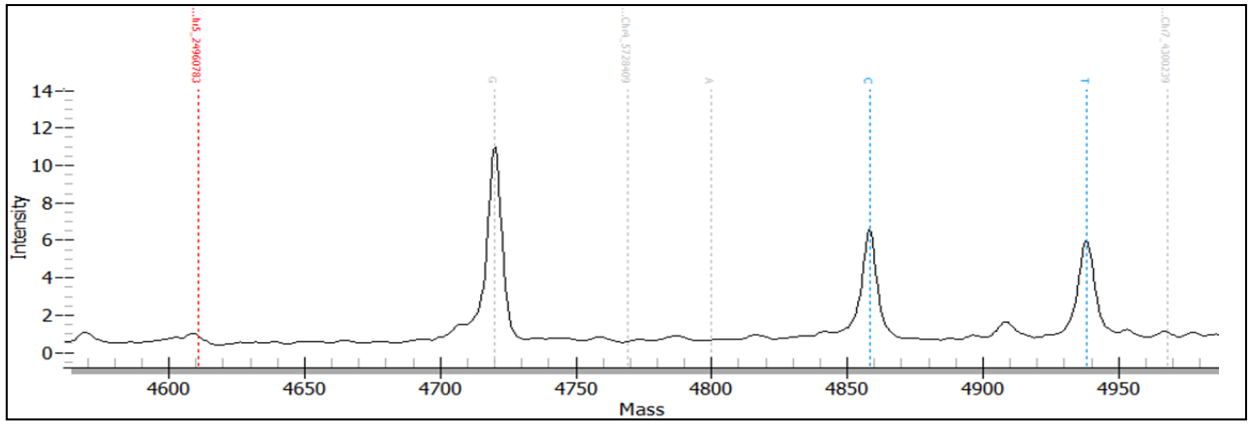




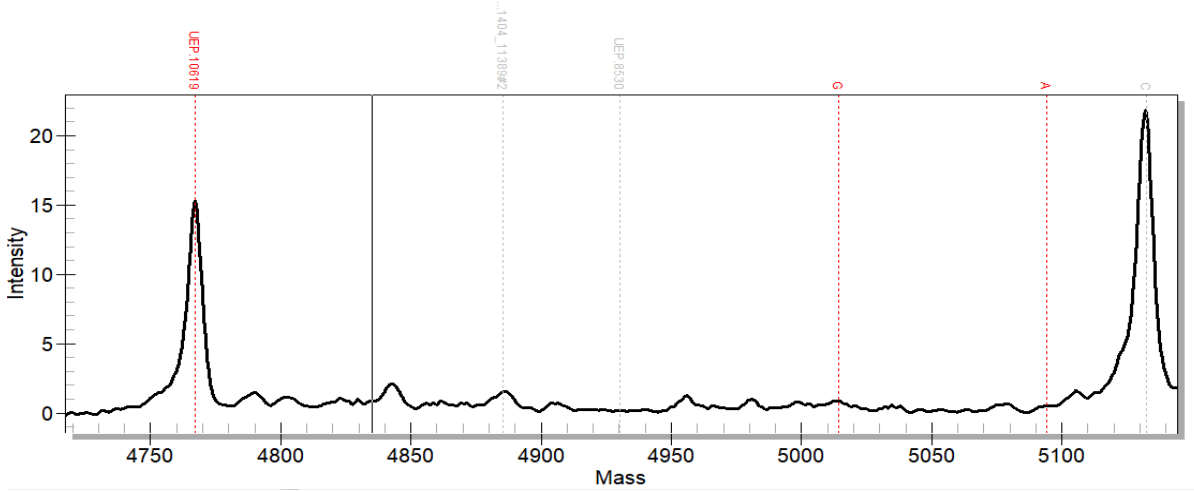
REPORT: Spectrum peak



Call: Homozygous GG



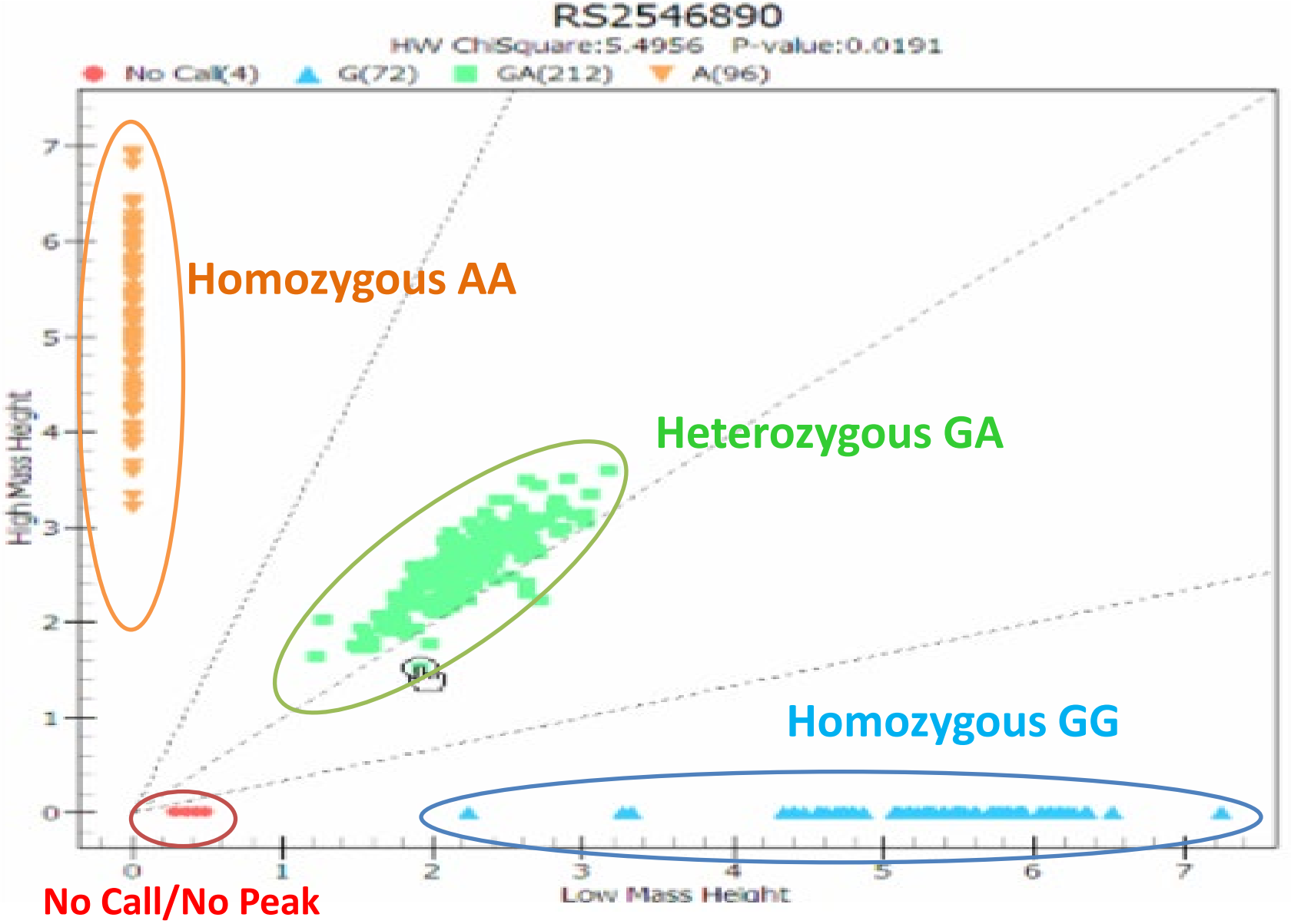
Call: Heterozygous CT



Only UEP Peak

No Call

CALL CLUSTER PLOT



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REPORT OPTION: EXPORT FORMAT

Sample Name

Assay Name

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	SAMPLE_	WELL	Cum_Chr1	Cum_Chr1	Cum_Chr1	Cum_Chr1	Cum_Chr1	Cum_Chr2	Cum_Chr2	Cum_Chr3	Cum_Chr3	Cum_Chr3	Cum_Chr4	Cum_Chr4	Cum_Chr4	Cum_Chr5	Cum_Chr5	Cum_Chr5	Cum_C
2	16016	D04	G	T	C	A	C	A	T	G	G	G	G	T	T	A	C	C	A
3	16017	D05	G	T	C	A	C	A	T	G	G	G	G	T	T	A	C	C	G
4	C-588 F	C04	A	T	T	A	C	A	T	G	G	A	A	T	T	G	C	C	A
5	C-588 F1-1	C06	A	T	T	A	C	A	T	G	G	A	A	T	T	G	C	C	A
6	C-588 M	C05	G	G	C	A	C	A	A	G	G	G	A	T	T	G	C	T	G
7	C-662 F	C01	G	G	C	A	C	G	T	G	T	A	G	T	T	A	T	T	A
8	C-662 F1-1	C03	AG	G	C	G	C	AG	T	G	T	A	G	TA	T	GA	T	T	A
9	C-662 M	C02	A	G	C	G	C	A	T	G	T	A	G	A	T	G	T	T	A
10	C-665 F	B04	G	G	C		C	G	T	G	T	A	G	T	T	A	T	T	A
11	C-665 F1-1	B06			C												T		
12	C-665 M	B05	A	G	C	AG	C	G	T	G	A	G	G	T	T	G	C	T	A
13	C-685 F	D01	G	G	T	A	C	A	T	G	G	G	G	T	T	A	T	T	G
14	C-685 F1-1	D03	AG	GT	T	A	C	A	T	G	G	GA	GA	T	T	GA	CT	TC	AG
15	C-685 M	D02	A	T	T	A	C	A	T	G	G	A	A	T	T	G	C	C	A
16	CU023 F	B01	G	G	G	A	C	A	A	G	T	A	G	A	T	G	T	T	G
17	CU065 M	A06	G	G	C	A	C	A	T	G	G	G	G	T	T	A	C	C	G

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MASSARRAY TECHNOLOGY

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- **Applications**
- Discussion

Applications

Service

Research

Healthcare

Illness / genetic disorder

Wellness

Microorganism detection

Pathogen
Bacteria/ virus / fungi

Food bone pathogen

Agriculture

Genetic selection/ Breeding

Diversity analysis
genetic Classification

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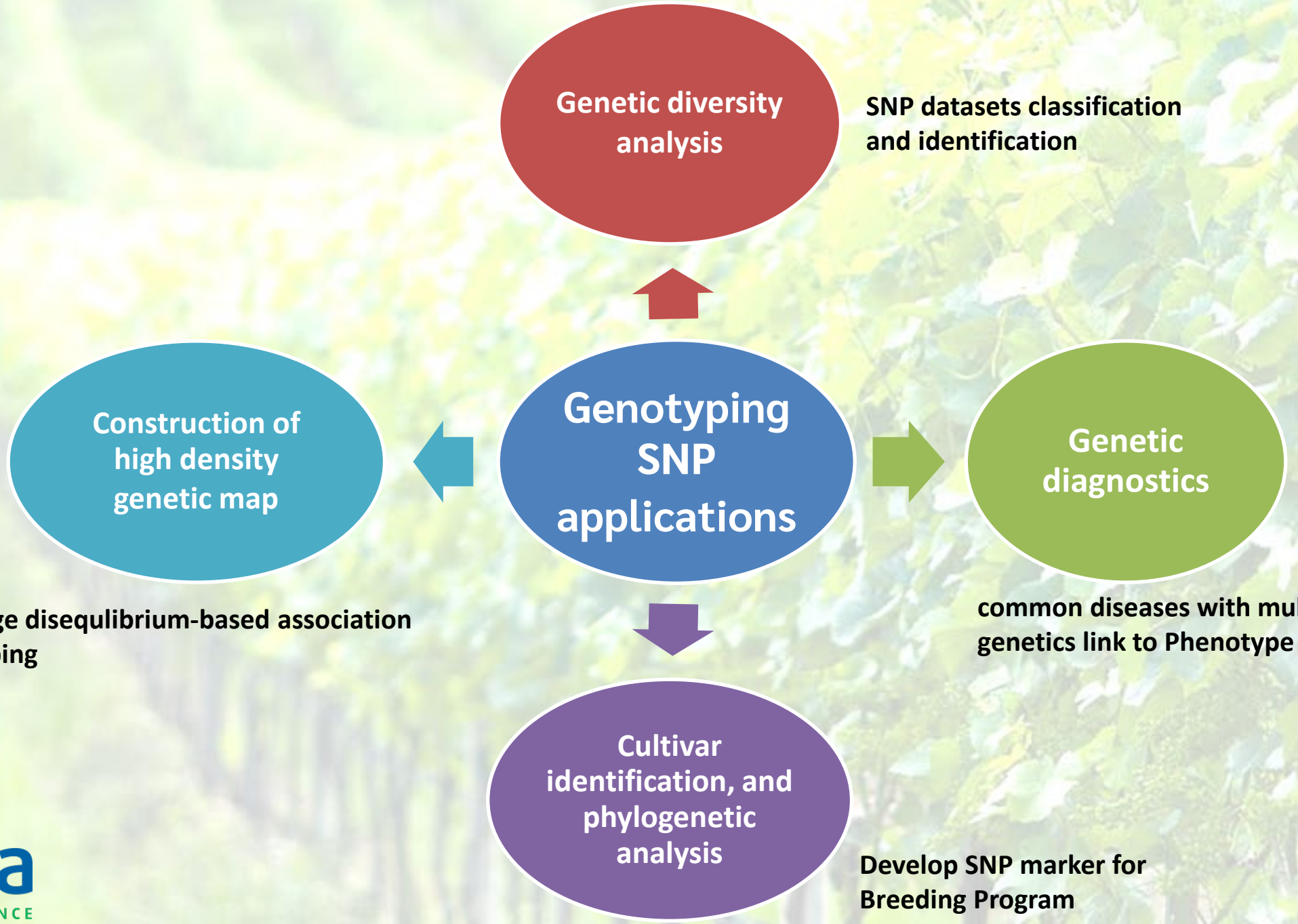
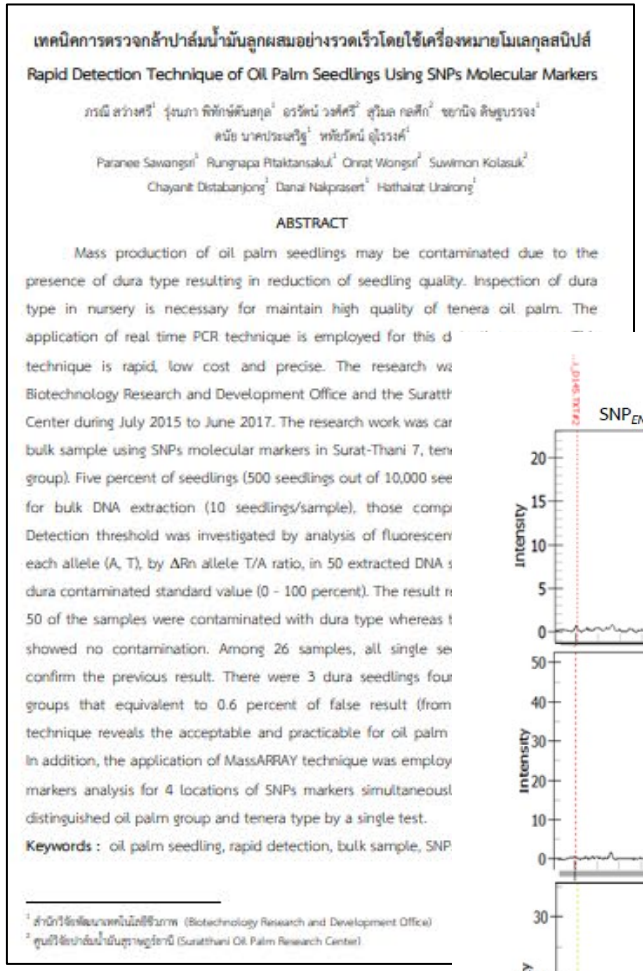

Genetic diversity analysis
SNP datasets classification and identification
Construction of high density genetic map
Genotyping SNP applications
Genetic diagnostics
linkage disequlibrium-based association mapping
common diseases with multifactor genetics link to Phenotype
Cultivar identification, and phylogenetic analysis
Develop SNP marker for Breeding Program

เทคนิคการตรวจกล้าปาล์มน้ำมันลูกผสมอย่างรวดเร็วโดยใช้เครื่องหมายโมเลกุลสนิปส์ Rapid Detection Technique of Oil Palm Seedlings Using SNPs Molecular Markers

ภรณี สว่างศรี และคณะ 2560

ผลงานวิจัยดีเด่น กรมวิชาการเกษตร ปี 2560

สำนักวิจัยพัฒนาเทคโนโลยีชีวภาพ (Biotechnology Research and Development Office) และ ศูนย์วิจัยปาล์มน้ำมันสุราษฎร์ธานี



เทคนิคการตรวจกล้าปาล์มน้ำมันลูกผสมอย่างรวดเร็วโดยใช้เครื่องหมายโมเลกุลสนิปส์

Rapid Detection Technique of Oil Palm Seedlings Using SNPs Molecular Markers

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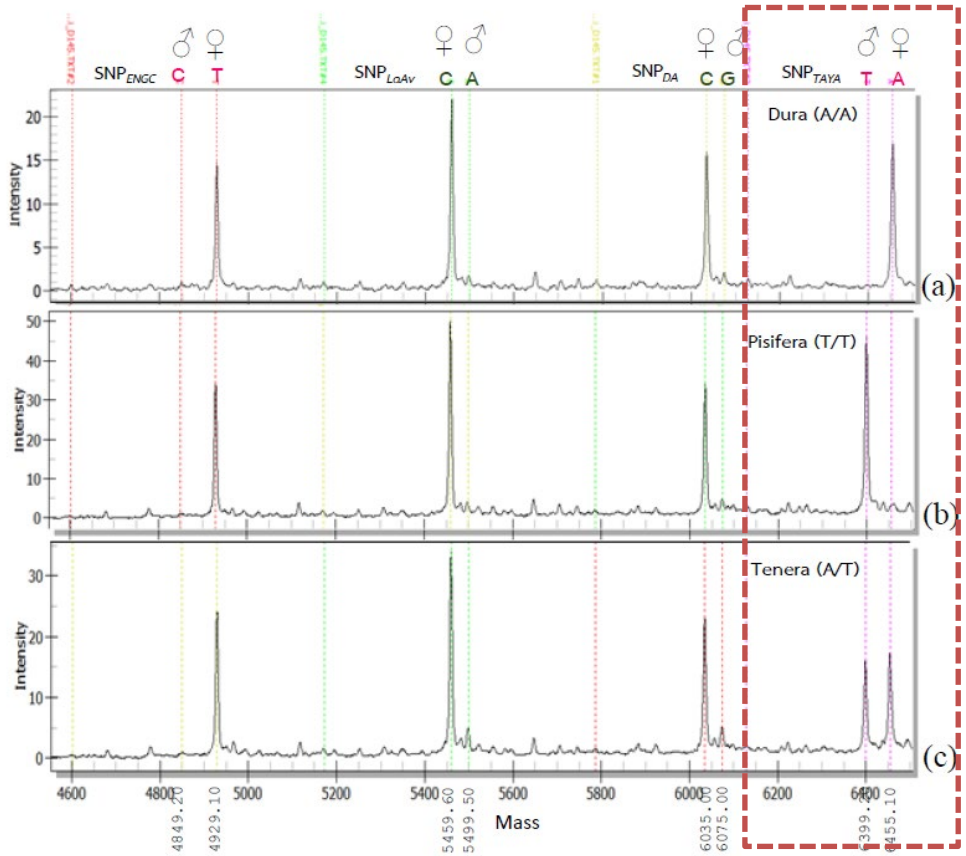
Chayanit Distabanjong[1] Danai Nakprasert[1] Hathairat Urairong[1]

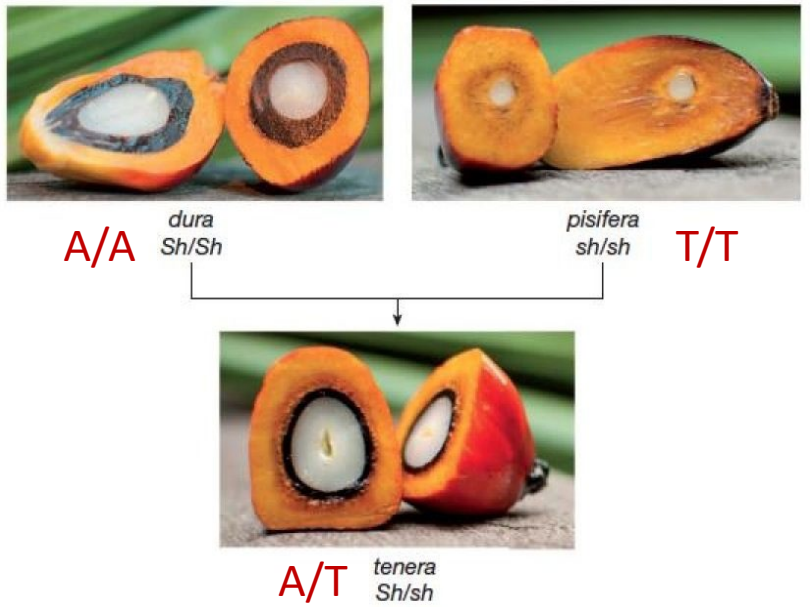
ABSTRACT

Mass production of oil palm seedlings may be contaminated due to the presence of dura type resulting in reduction of seedling quality. Inspection of dura type in nursery is necessary for maintain high quality of tenera oil palm. The application of real time PCR technique is employed for this d technique is rapid, low cost and precise. The research wa Biotechnology Research and Development Office and the Suratth Center during July 2015 to June 2017. The research work was car bulk sample using SNPs molecular markers in Surat-Thani 7, ten group). Five percent of seedlings (500 seedlings out of 10,000 see for bulk DNA extraction (10 seedlings/sample), those compr Detection threshold was investigated by analysis of fluorescen each allele (A, T), by ΔRn allele T/A ratio, in 50 extracted DNA s dura contaminated standard value (0 - 100 percent). The result r 50 of the samples were contaminated with dura type whereas t showed no contamination. Among 26 samples, all single se confirm the previous result. There were 3 dura seedlings four groups that equivalent to 0.6 percent of false result (from technique reveals the acceptable and practicable for oil palm In addition, the application of MassARRAY technique was employ markers analysis for 4 locations of SNPs markers simultaneousl distinguished oil palm group and tenera type by a single test.

Keywords : oil palm seedling, rapid detection, bulk sample, SNP



SNP *TAYA*



ใช้ MassARRAY ตรวจสนิปส์ทั้ง 4 ตำแหน่ง ได้แก่ SNP*ENGC* SNP*LaAv* SNP*DA* และ SNP*TAYA* พบว่าตำแหน่ง SNP*TAYA* แสดง Genotype ที่เป็น polymorphism สอดคล้องกับลักษณะ Phenotype ของผลปาล์ม ที่เมื่อ Genotype เป็น Heterozygous AT แสดงลักษณะผลเปลือกหนากะลาบางซึ่งเป็นที่ต้องการของตลาด ซึ่งสามารถคัดเลือกต้นลูกผสมที่มีลักษณะดังนี้ได้ตั้งแต่ระยะต้นกล้า

Identification of gene associated with sweetness in corn (Zea mays L.) by genome-wide association study (GWAS) and development of a functional SNP marker for predicting sweet corn.

RUANJAICHON, Vinitchan, et al. 2021, Plants,10.6: 1239.

plants MDPI

Article

Identification of Gene Associated with Sweetness in Corn (*Zea mays* L.) by Genome-Wide Association Study (GWAS) and Development of a Functional SNP Marker for Predicting Sweet Corn

Vinitchan Ruanjaichon [1], Kanogporn Khammona [1], Burin Thunnom [1], Khundej Suriharn [2,3], Chalong Kerdsri [4], Wanchana Aesomnuk [1], Arweewut Yongsuwan [1], Naraporn Chaomueang [1], Paradee Thammapichai [5], Siwaret Arikit [6,7], Samart Wanchana [1,*] and Theerayut Toojinda [1,*]

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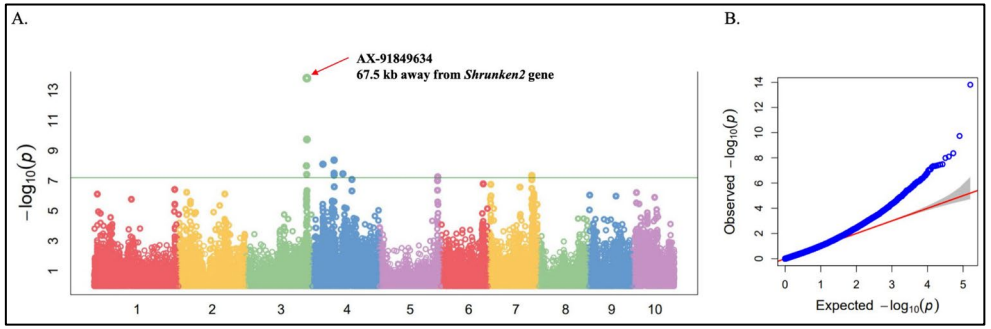
Abstract: Sweetness is an economically important eating quality trait for sweet-corn breeding. To investigate the genetic control of the sweetness trait, we conducted a genome-wide association study (GWAS) in an association panel consisting of 250 sweet corn and waxy corn inbred and recombinant inbred lines (RILs), together with the genotypes obtained from the high-density 600K maize genotyping single-nucleotide polymorphism (SNP) array. GWAS results identified 12 significantly associated SNPs on chromosomes 3, 4, 5, and 7. The most associated SNP, AX_91849634, was found on chromosome 3 with a highly significant *p*-value of $\leq 1.53 \times 10^{-14}$. The candidate gene identified within the linkage disequilibrium (LD) of this marker was *shrunken2* (Zm00001d044129; *sh2*), which encodes ADP-glucose pyrophosphorylase (AGPase), a 60 kDa subunit enzyme that affects starch metabolism in the maize endosperm. Several SNP markers specific to variants in *sh2* were developed and validated. According to the validation in a set of 81 inbred, RIL, and popular corn varieties, marker Sh2_rs844805326, which was developed on the basis of the SNP at the position 154 of exon 1, was highly efficient in classifying *sh2*-based sweet corn from other types of corn. This functional marker is extremely useful for marker-assisted breeding in *sh2*-sweet corn improvement and marketable seed production.

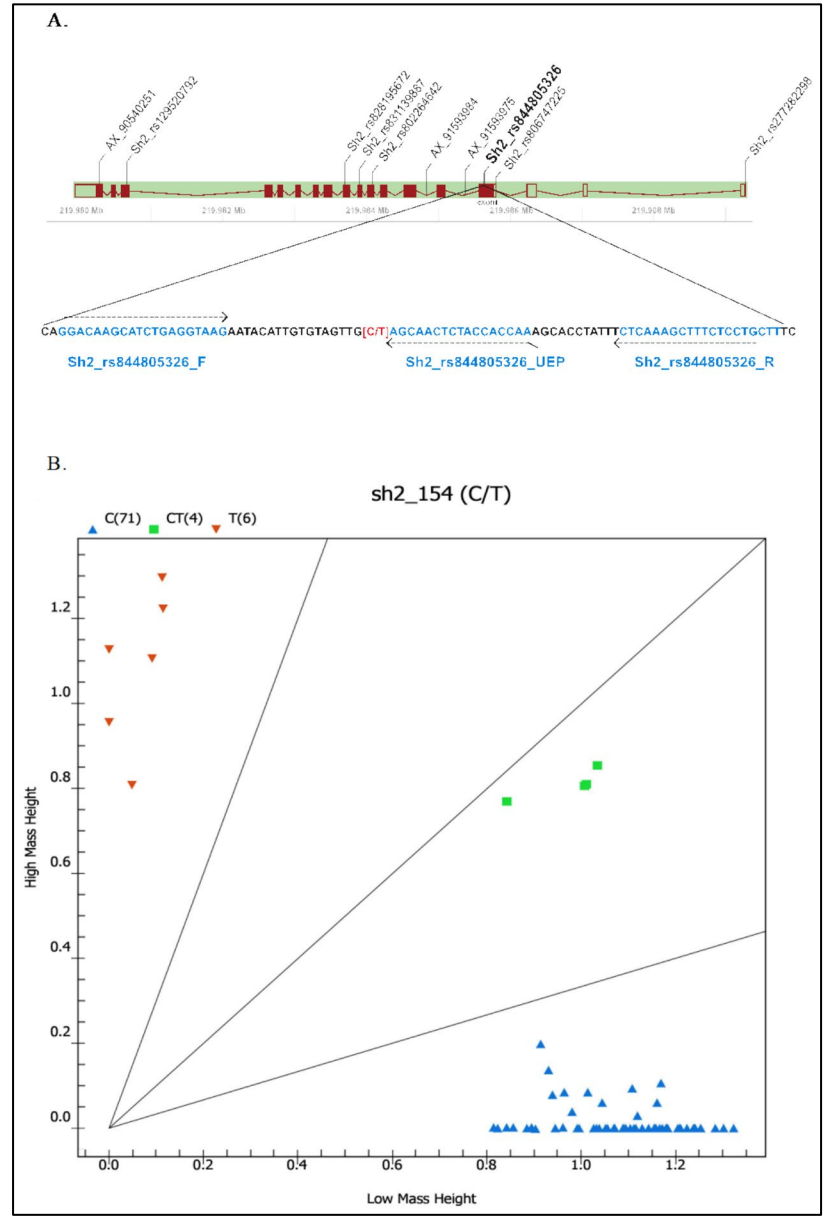
Keywords: maize; kernel sweetness; shrunken2; genome-wide association study (GWAS); single-nucleotide polymorphism (SNP)

1. Introduction

Sweet corn (*Zea mays* L. *var. rugosa* Bonaf.) is globally an economically important crop, and it is widely used for human consumption from both immature and mature kernels as fresh, canned, and frozen due to its high sugar content [1–3]. The demand for sweet corn has been rising on a yearly basis due to enhanced consumption and the increasing



การใช้เทคนิค MassARRAY ในงาน SNP detection เพื่อคัดเลือกหา functional marker ที่เกี่ยวข้องกับยีนที่ควบคุมการสร้างน้ำตาล (shrunken2) ในเมล็ดข้าวโพดหวาน (sweet corn) จากการค้นหา SNP และศึกษา GWAS พบ SNP ตำแหน่ง sh2_154 บนโครโมโซม 3 มีความสัมพันธ์กับความหวานในเมล็ด จึงสามารถใช้ตำแหน่งนี้เพื่อค้นหาต้นที่มีลักษณะที่ต้องการในงานปรับปรุงพันธุ์ต่อไป



https://www.mdpi.com/2223-7747/10/6/1239

National Center for Genetic Engineering and Biotechnology (BIOTEC) and Rice Science Center, Kasetsart University, Kamphaeng Saen Campus, Thailand

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Cereal variety identification using MALDI-TOF mass spectrometry SNP genotyping

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ABSTRACT

Correct identification of cereal varieties is important to food quality, safety
molecular markers have been applied to cereal varietal identification. Tw
wider application of molecular markers in crop plant genetics have been
point. However, in recent years, novel molecular tools, the re-invention/i
nologies, and miniaturisation of technology has both increased through
these costs. Here we have applied Sequenom® MassARRAY® MALDI-T
a collection of recently developed SNPs to facilitate cereal varietal identifi
Sequenom® MassARRAY® mass spectrometry SNP assay targeting 45 lo
Australian barley varieties. Of the 45 loci screened, 33 were informativ
a unique barcode of SNPs for each variety tested. Only one variety could
others due to a high level of varietal heterogeneity. This assay format pro
robust and moderate throughput SNP genotyping method well suited to va
analysis in cereals.

Marker detection for plant breeding

Correct identification of cereal varieties is important to food quality, safety and authenticity and recently, molecular markers have been applied to cereal varietal identification

SNP profile for 35 Australian barley varieties across 33 loci.

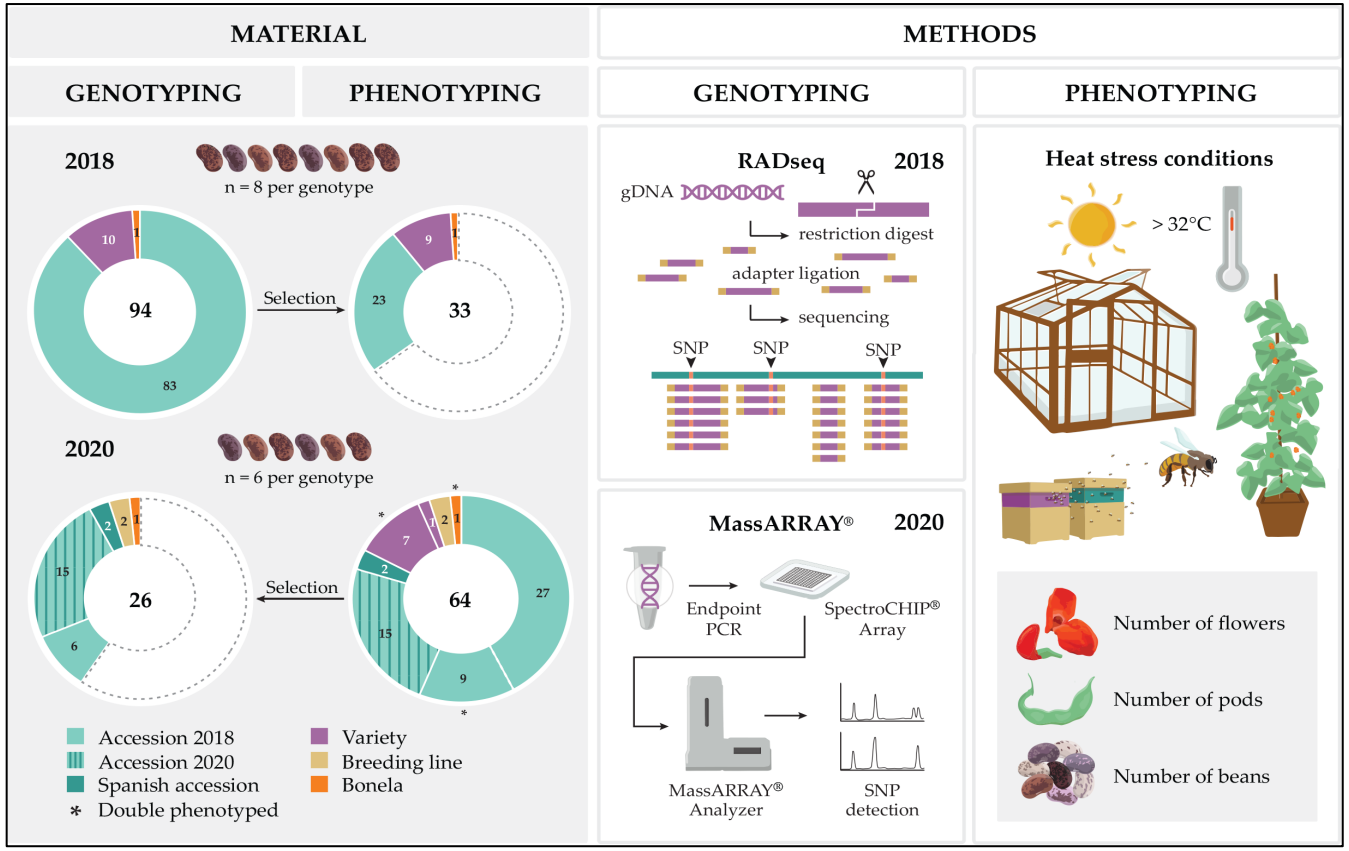
agronomy

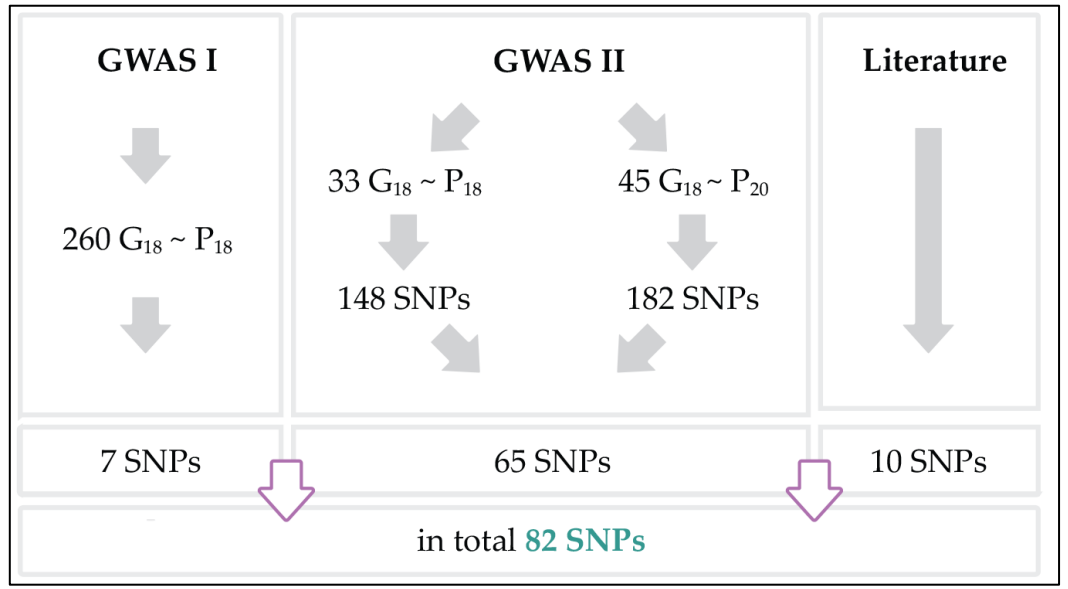
MDPI

Article

Towards Heat Tolerant Runner Bean (*Phaseolus coccineus* L.) by Utilizing Plant Genetic Resources

Svenja Bomers [1,†], Eva M. Sehr [2,†], Eveline Adam [3], Philipp von Gehren [1], Karin Hansel-Hohl [2], Noémie Prat [1] and Alexandra Ribarits [1,*]





Blast result
72
MassARRAY® result
52
Monomorphic
40
Favorable allele identification

18 SNPs

Agronomy 2022, 12(3), 612; https://doi.org/10.3390/agronomy12030612
Received: 1 February 2022 / Revised: 21 February 2022 / Accepted: 24 February 2022 / Published: 28 February 2022

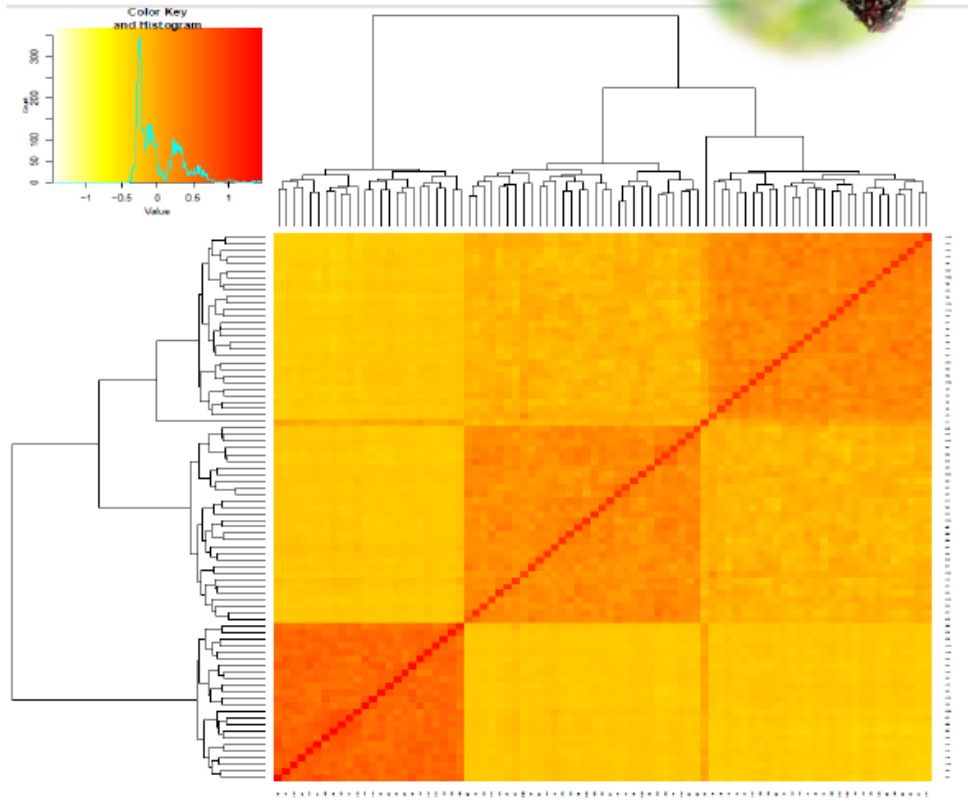
การพัฒนาเครื่องหมายโมเลกุลเพื่อจำแนกเพศในหม่อนผลสด

(DNA marker development for sex classification in *Morus* spp.)

ต้นหม่อน F1

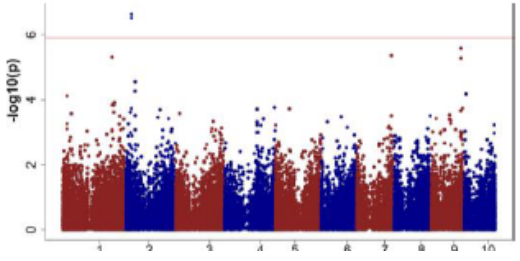
DArT diversity arrays technology

ประชากร	จำนวน SNP	Polymorphic SNP
1. SRC650 x African 1	23,050	2,203
2. SK2802 x น้ำพรม 2	24,041	2,416
3. ขนกลาง 3 x น้ำพรม 2	23,741	1,802



Population diversity illustrated with Kinship

GAPIT



20 highest associated SNP as markers

MassARRAY markers were designed for sex determination in mulberry

SNP ID	Forward Primer ID	Forward Primer Sequence	Reverse Primer ID	Reverse Primer Sequence	Extended Primer ID	Extended Primer Sequence
9872_W1	9872_W1_F	ACGTTGGATGATTGCAGGTACAAGAAGC	9872_W1_R	ACGTTGGATGCATTTCCACATAGCGAGG	9872_W1_E	TGCAGATTGCTTGGG
10619_W1	10619_W1_F	ACGTTGGATGCACAGAATGGCTTGAGAG	10619_W1_R	ACGTTGGATGGTCCGACCTATTAGCATC	10619_W1_E	ACACCATTTGTTCCCT
8530_W1	8530_W1_F	ACGTTGGATGAAGCTTGGGAGCAATCTG	8530_W1_R	ACGTTGGATGTCAAGAGCTCGAAGGAAG	8530_W1_E	GAGCAATCTGCAGGTA
163_W1	163_W1_F	ACGTTGGATGTCCCTGCTCTGTTAAGTG	163_W1_R	ACGTTGGATGAACATTTGGGCT		
9549_W1	9549_W1_F	ACGTTGGATGAGTCTGGTCCACCATTG	9549_W1_R	ACGTTGGATGAATTGCGTGCA		
13302_W1	13302_W1_F	ACGTTGGATGGGCTTCTTTTTTCGTTC	13302_W1_R	ACGTTGGATGGAACAAGCTGC		
2288_W1	2288_W1_F	ACGTTGGTGCCTTGAGTAGGAAAGGTG	2288_W1_R	ACGTTGGATGTGGGAACTTGG		
11283_W1	11283_W1_F	ACGTTGGATGAATCACCAAGTGGAACCC	11283_W1_R	ACGTTGGATGCAACCGTAAAT		
958_W1	958_W1_F	ACGTTGGATGAGGTTTGGTTTGACTGCG	958_W1_R	ACGTTGGATGAGCGGACATGG		
11404_11389 #2_W1	11404_11389 #2_W1_F	ACGTTGGATGATTTCGACAAGCGTAGCC	11404_11389 #2_W1_R	ACGTTGGATGGAATCATGTCA		
11404_11389 #1_W2	11404_11389 #1_W2_F	ACGTTGGATGATTTCGACAAGCGTAGCC	11404_11389 #1_W2_R	ACGTTGGATGGAATCATGTCA		

ลำดับเบสของดีเอ็นเอที่มีความสัมพันธ์กับลักษณะเพศ

ทดสอบในประชากร 80 ต้น

- ตำแหน่งดีเอ็นเอที่เครื่องหมาย 10619_W1

GCTTGAGAGTTTCTGCAGTA[G/A]AGGGAACAAATGGTGTCTTT

ลักษณะพันธุกรรมสอดคล้องกับลักษณะเพศโดย เบส G มีแนวโน้มในการกำหนดลักษณะเพศต้นตัวเมีย เบส A กำหนดลักษณะเพศผู้ที่ 90.70%

- ตำแหน่งดีเอ็นเอที่เครื่องหมาย 9872_W1

GAAGCTGCAGATTGCTTGGG[T/C]GCCGACTGTGTGCCTCGCTA

ลักษณะพันธุกรรมสอดคล้องกับลักษณะเพศโดย เบส T มีแนวโน้มในการกำหนดลักษณะเพศต้นตัวเมีย เบส C กำหนดลักษณะเพศผู้ที่ 73.47%

Rubber tree application

การยางแห่งประเทศไทย
Rubber Authority of Thailand
สถาบันวิจัยยาง

- 376 individuals for DArTseq (2016-2017) DArT diversity arrays technology
- GWAS analysis in Leaf Fall Disease
- 280 samples with 30 markers

- Highly significant in GWAS
- Literature review

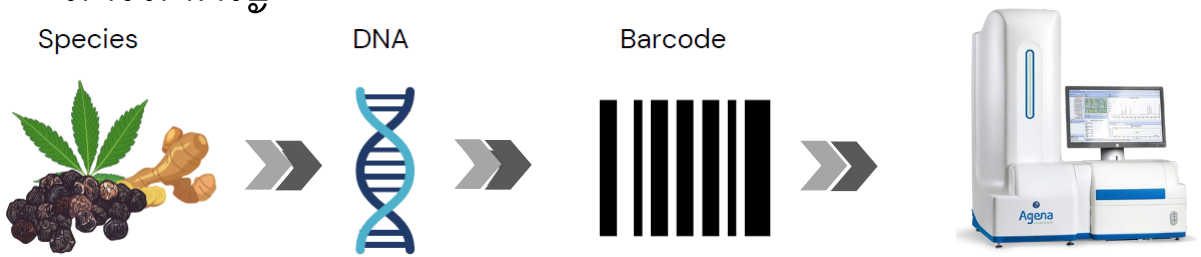
Total SNPs	Average	Min	Max
% Total SNPs	**91.88**	**55.71**	**100.00**
Homo ref. freq	0.57	0.02	0.99
Homo alt. freq	0.29	0.00	0.97
Hetro. Freq	0.15	0.00	0.45

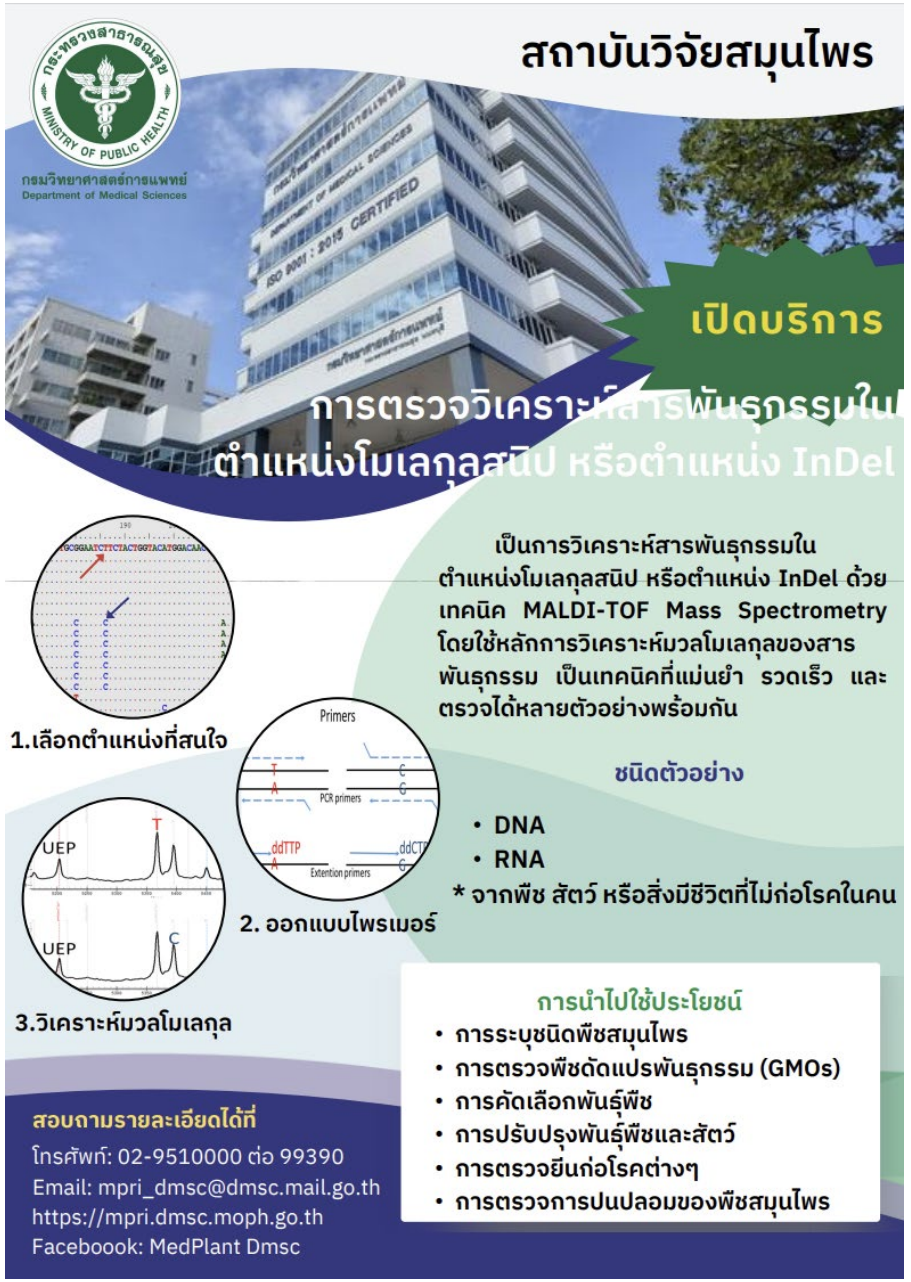
minimizing off-target with Sanger

th.wikipedia.org

Applications for medical plant

- จำแนก และระบุสายพันธุ์พืชสมุนไพร เช่น จำแนกสายพันธุ์กัญชา กลุ่มหมามุ่ย กลุ่มเจตมูลเพลิง ขมิ้นชัน
- ระบุสายพันธุ์พืชปลอมปนในยาผง เช่น การปนพืชสะเดา คะน้า ลงในแคปซูลของฟ้าทะลายโจร
- จำแนกเพศ เช่น พืชกัญชา แยกตัวผู้ ตัวเมีย เป็นต้น
- งานปรับปรุงพันธุ์ ตรวจหา Marker ที่สัมพันธ์กับการผลิตสารสำคัญ





Publications

Design and development of MassARRAY-based bacteriological assay 10 BACTERIAL FOODBORNE PATHOGENS IN A SINGLE REACTION

Primer ID	Bacterial Targets (species)
Bac16_ bac1/2	Bacteria
Eco001N	*E.coli/Shigella spp.*
Ent001	*Enterococcus faecalis*
Ent003	*Enterococcus faecium*
Clos001	*Clostridium perfringens*
Cmp002	*Campylobacter jujuni*
Cmp005 Cmp006	*Campylobacter coli*
Lis001	*Listeria monocytogenes*
Stp001	*Staphylococcus aureus*
Sal002	*Salmonella spp.*

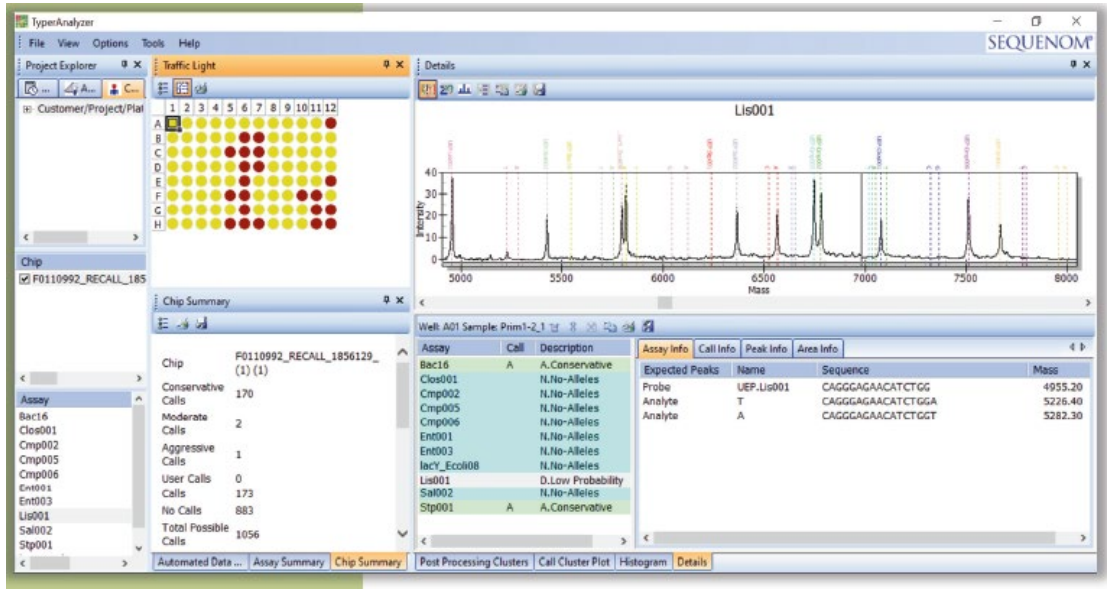


Figure 4 : TyperAnalyzer software for analysis of multiplexing reaction correlated to specific well on SpectroChip.

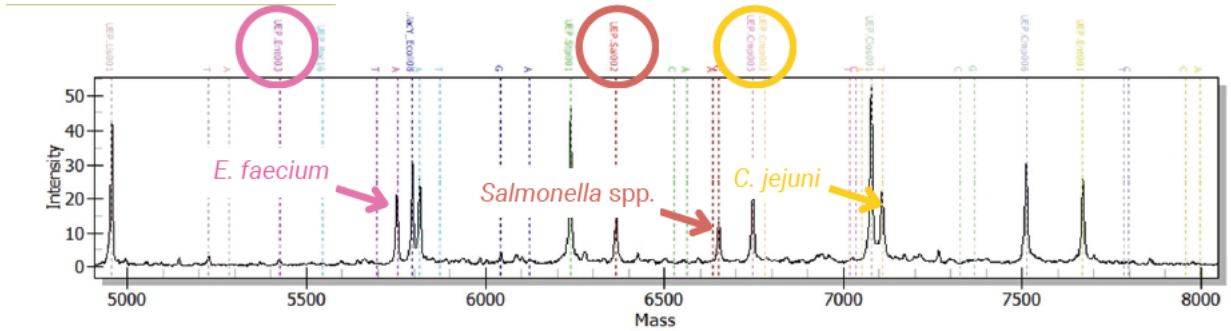


Figure 5 : *Enterococcus faecium*, *Salmonella* spp., and *Campylobacter jejuni* were identified in a single assay. The circles represent the mass-to-charge ratio (m/z) of unextended primers (UEP), while the arrows indicate the mass spectral peak corresponding to the extended base, facilitating bacterial identification.

BIOTEC
a member of NSTDA

MassARRAY System workflow

AgenaCx Account

1	2	3	4	5
Select Target Markers	Design primer	Optimize & validation	Sample run	Analyze data & Report
1-4 week	1 week	Run Time: 7 Hrs* Hands-on Time: 23 Min	**Run Time: 90 Mins*** Hands-on Time: 5 Min	Hands-on Time: 5-10 Min

MassARRAY system in Thailand

ศูนย์จีโนมทางการแพทย์
Center for Medical Genomics

คณะแพทยศาสตร์

Mahidol University
Research EXperts

ศูนย์โอมิกส์แห่งชาติ
(National Omics Center)

กรมวิชาการเกษตร

กรมวิทยาศาสตร์การแพทย์
Department of Medical Sciences

Lifomics Co., Ltd.

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ทีมวิจัยนวัตกรรมด้านเทคโนโลยีชีวภาพพืชและการเกษตรแบบแม่นยำ

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