Application of Molecular Breeding Technologies in Commercial Crop Breeding

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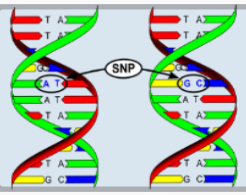
HUAZHI RICE BIO-TECH CO., LTD.

Outline

Molecular breeding and seed industry development — Monsanto as an example



SNP marker development

Molecular breeding technologies

Trend of molecular breeding

Monsanto — the rise of multi-national seed Industry giant

Prior to 1996: had agricultural biotech, pharmaceutical, chemical, and nutrition business segments, not a seed company

1996: acquired Agracetus (soybean、corn seed company)

1997: acquired Holden's Foundation Seeds L.L.C. and Corn States Hybrid Service L.L.C (corn seed company)

1998: acquired DeKalb Genetics Corp (corn and soyben seed company)

2005: acquired Seminis, Inc. (vegetable seed company)

2007: acquired Delta and Pine Land Company (cotton seed company)

2008: acquired De Ruiter Seeds breeds Group (vegetable seed company)，Semillas Cristiani Burkard (corn hybrid seed production company), CanaVialis S.A. and Alellyx S.A (sugarcane company)

2009: acquired Westbred (wheat seed company)

2017: multi-national seed Industry giant, annual seed sale of > $10.9B, ~20% of the world seed market share

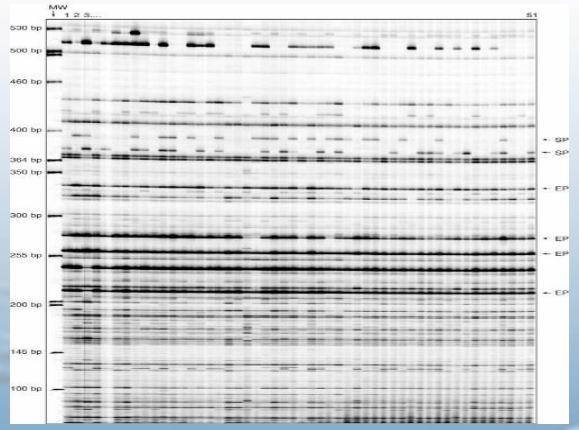
10/18/2000: IPO as a pure agriculture company, market cap of $4B

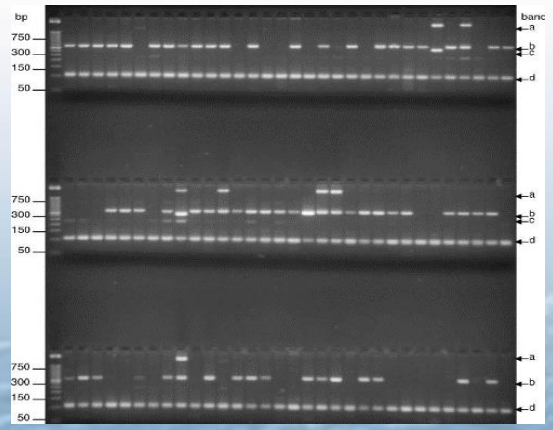
June 7, 2018: sold to Bayer for $65B

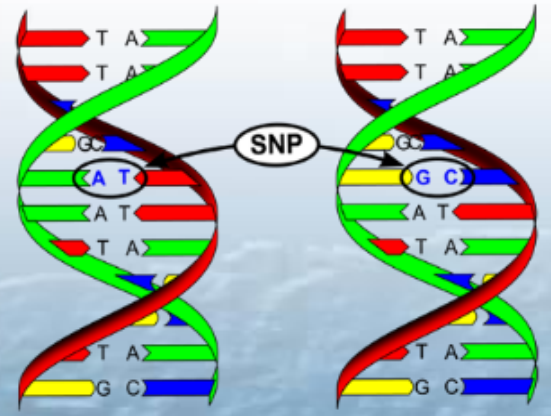
Two core technologies made Monsanto become the world seed industry giant

Insect-resistance, herbicide-tolerance transgenic technology (R&D initiated in 1980)

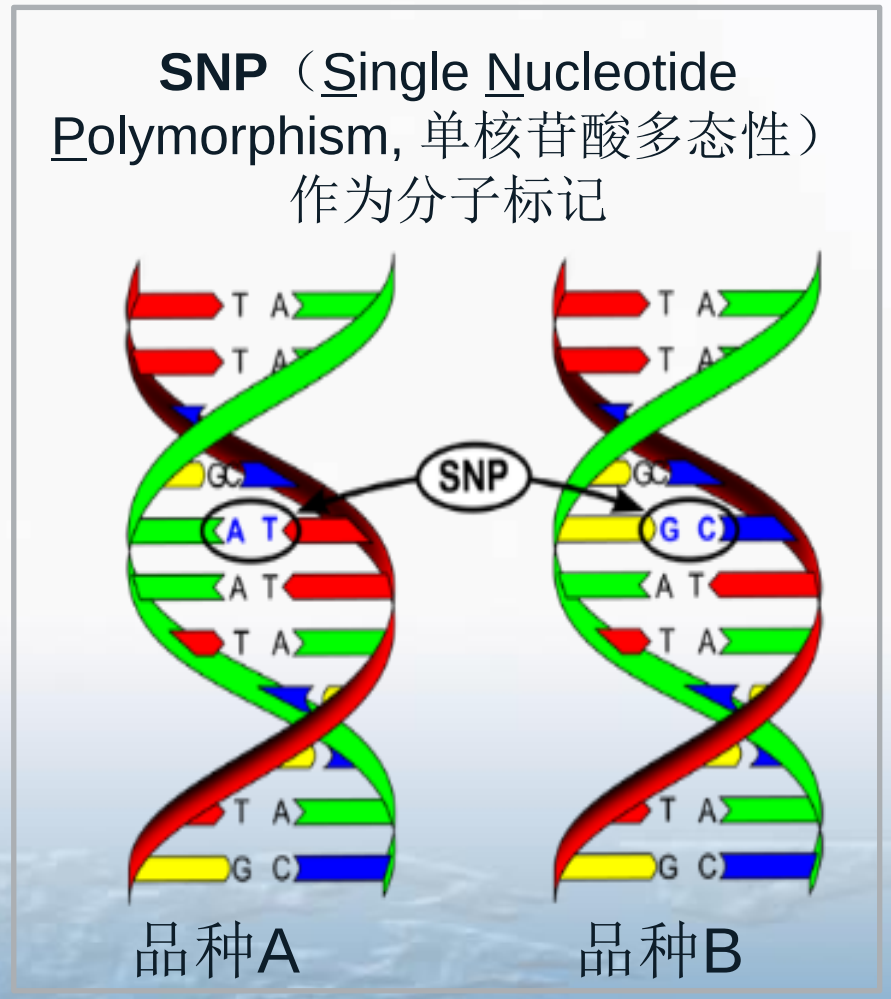
Molecular breeding (started in 1996)







Molecular breeding



- a new field emerging in early 1990s developed from plant genomics, molecular biology, molecular genetics, quantitative genetics, and breeding
- applications of molecular markers and genomics tools in plant breeding
- innovation in breeding methodologies
- discovery/creation of novel genetic variation
- core competitive advantages of multi-national seed industry giants

Outline

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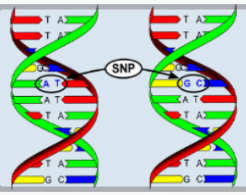

SNP marker development

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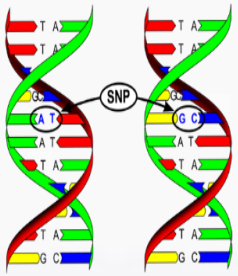
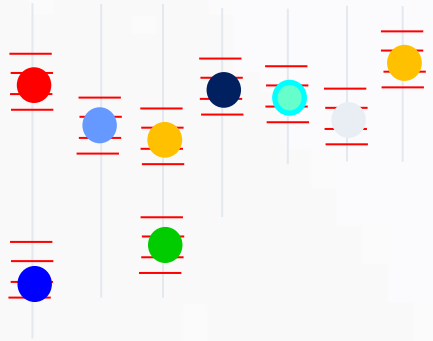
From DNA sequences to molecular breeding: Overview

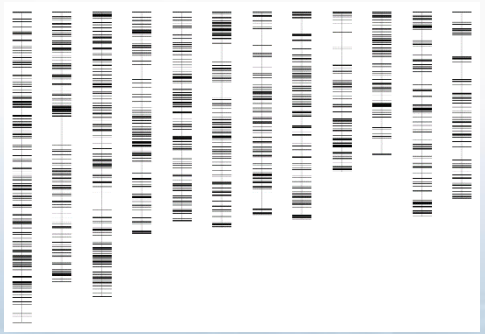
DNA sequences



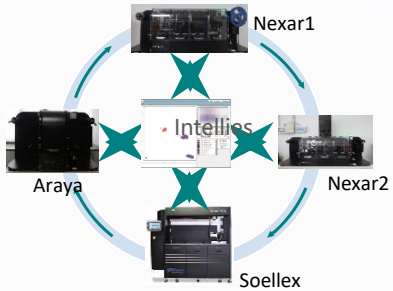
SNP



Target trait SNP markers



Genome-wide SNP markers



- Genetic diversity assessment
- Parental line selection
- Cross design
- F1 hybrid confirmation
- MAS
- Linkage drag elimination
- MARS
- MABC
- GWS
- Seed genetic purity assessment
- Variety IP protection

SNP discovery

SNP marker development

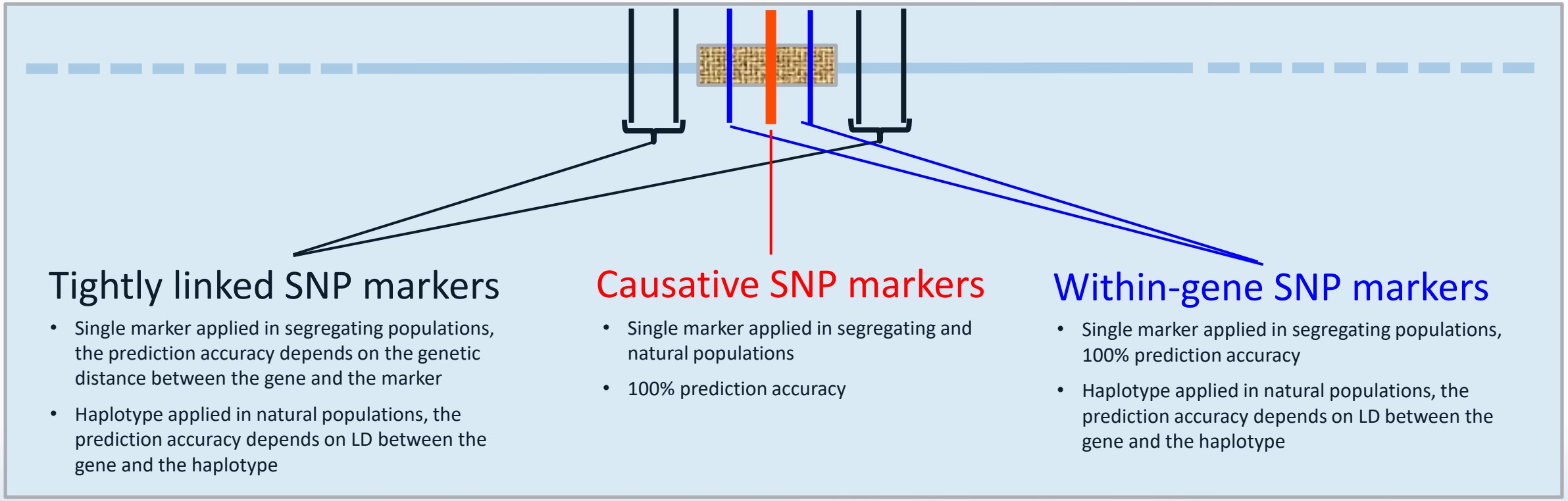
SNP genotyping production

Molecular breeding technologies

SNP discovery

Line 01: ……AGACGGCCTTACTTGCGAATCCAGGCAACCGTACGGCTA……
Line 02: ……AGACGGCCTTACTTGCGAATCCAGGCAACCGTACGGCTA……
Line 03: ……AGACGGCCTTACTTGCGAATCCAGGCAACCGTACGGCTA……
Line 04: ……AGACGGCCTTACTTGCGAATCCAGGCAACCGTACGGCTA……
Line 05: ……AGACGGCCTTACTTGCGAATCCAGGCAACCGTACGGCTA……
Line 06: ……AGACGGCCTTACTTGCGAATCCAGGCAACAGTACGGCTA……
Line 07: ……AGACGGCCTTACTTGCGAATCCAGGCAACAGTACGGCTA……
Line 08: ……AGACGGCCTTACTTGCGAATCCAGGCAACAGTACGGCTA……
Line 09: ……AGACGGCCTTACTTGCGAATCCAGGCAACAGTACGGCTA……
Line 10: ……AGACGGCCTTACTTGCGAATCCAGGCAACAGTACGGCTA……
Line 11: ……AGACGGCCTTACTTGCGAATCCAGGCAACAGTACGGCTA……

Three types of SNP markers associated with major gene/QTL



Tightly linked SNP markers

- Single marker applied in segregating populations, the prediction accuracy depends on the genetic distance between the gene and the marker
- Haplotype applied in natural populations, the prediction accuracy depends on LD between the gene and the haplotype

Causative SNP markers

- Single marker applied in segregating and natural populations
- 100% prediction accuracy

Within-gene SNP markers

- Single marker applied in segregating populations, 100% prediction accuracy
- Haplotype applied in natural populations, the prediction accuracy depends on LD between the gene and the haplotype

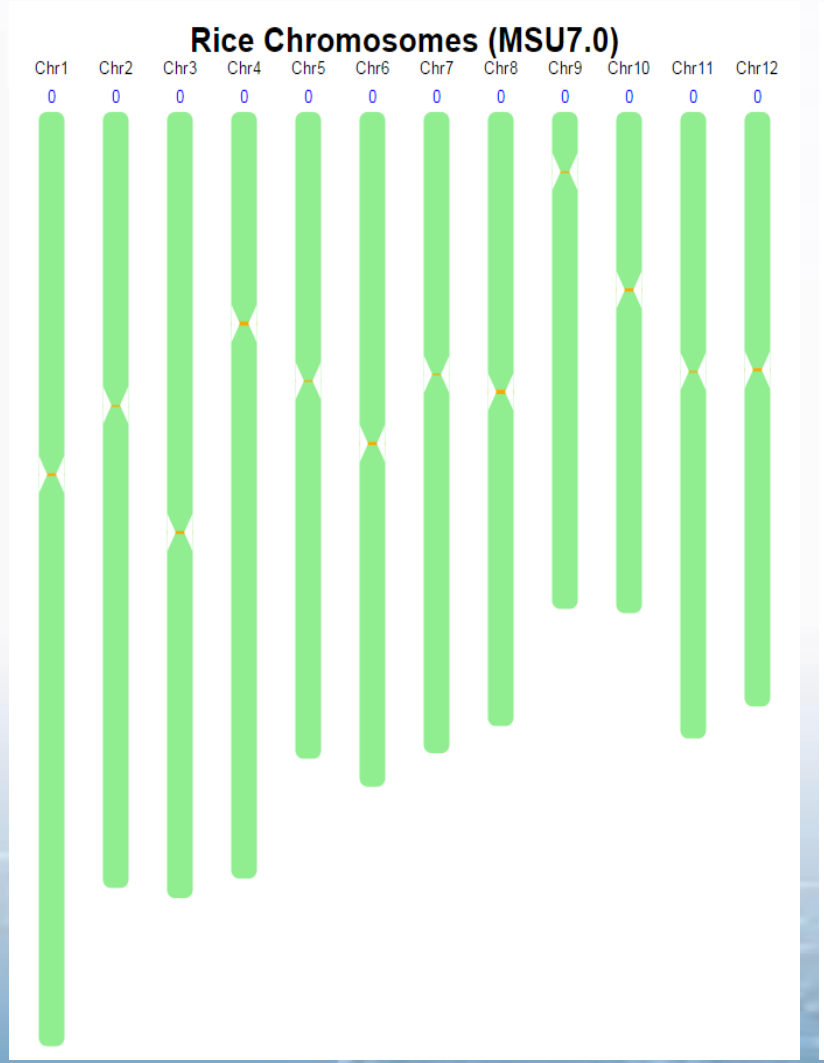
Avenues to discovering target gene SNP markers:

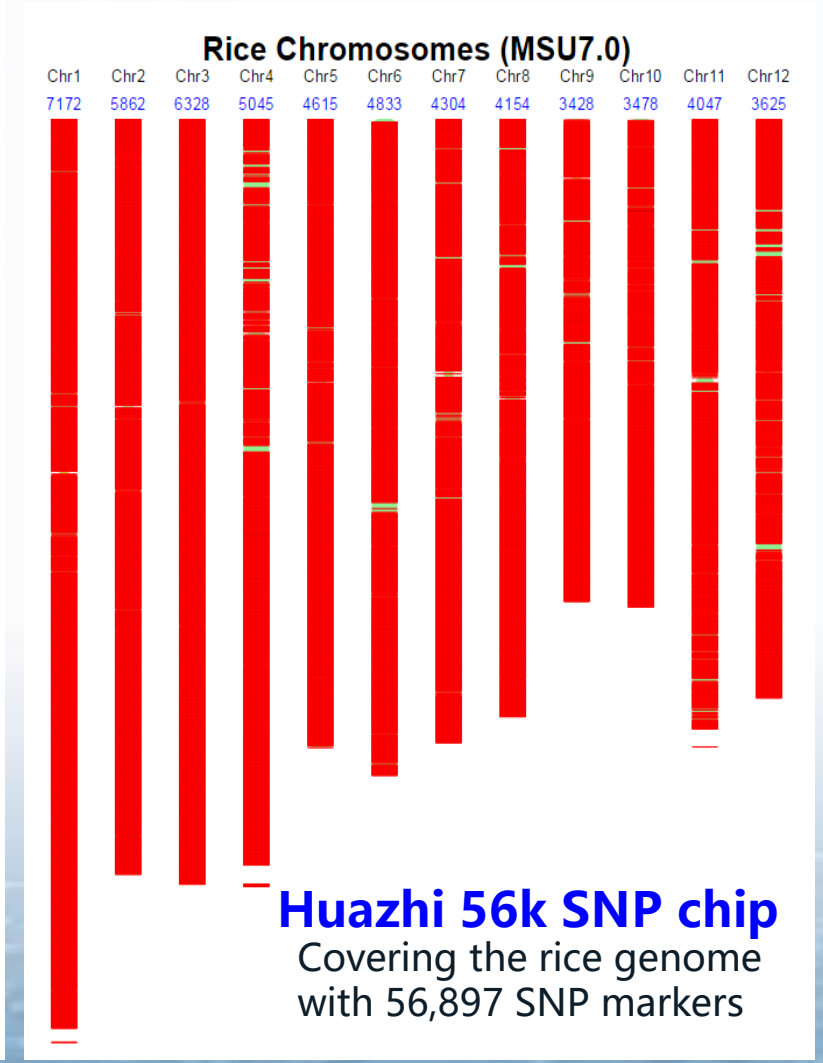
- DNA sequences of cloned genes
- *de novo* mapping
- association mapping

Genome-wide SNP marker development

Requirements:

- Locus-specific
- High PIC value
- High assay quality
- Even distributed across the entire genome
- Marker density matching breeding application type



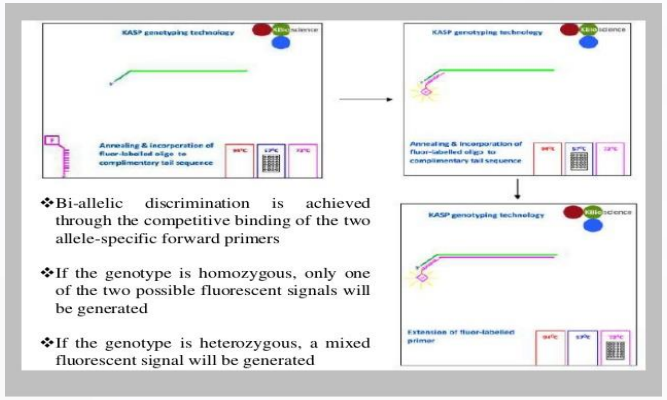


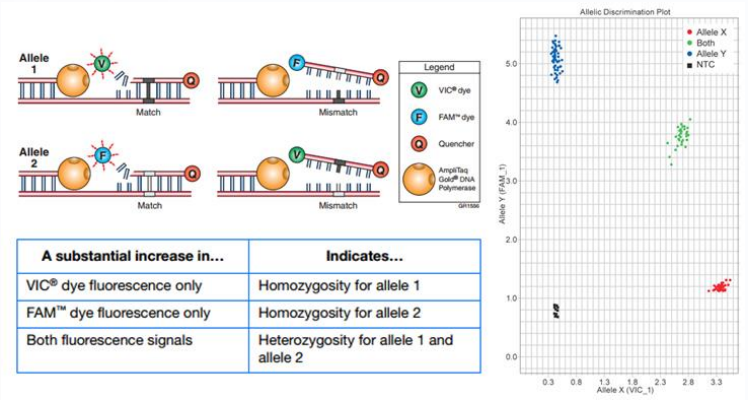
Huazhi 56k SNP chip

Covering the rice genome with 56,897 SNP markers

SNP genotyping technologies

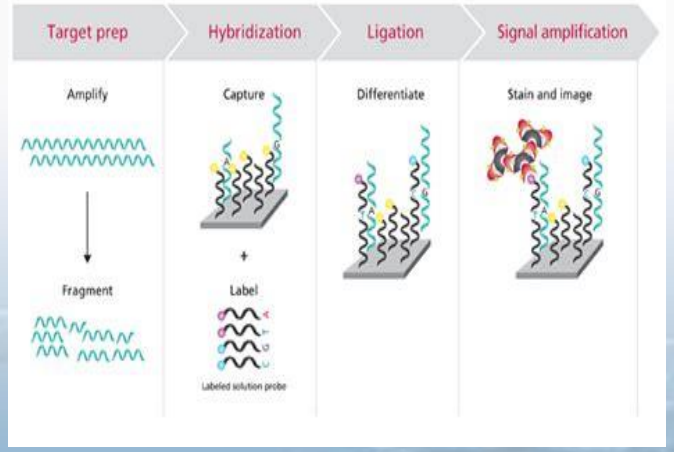
- **PCR-based**
  - KASP
  - End-point TaqMan
  - one sample, one marker at a time

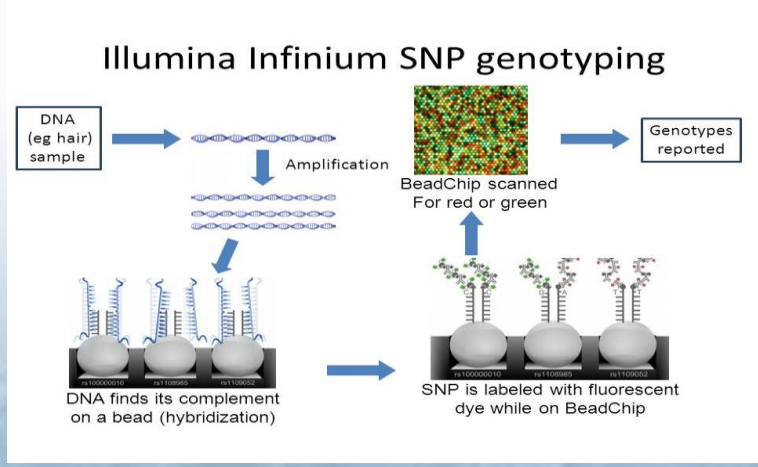




A substantial increase in...	Indicates...
VIC® dye fluorescence only	Homozygosity for allele 1
FAM™ dye fluorescence only	Homozygosity for allele 2
Both fluorescence signals	Heterozygosity for allele 1 and allele 2

- **DNA fragment hybridization-based parallel microarray**
  - Affymetrix Axiom SNP chip
  - Illumina Infimium SNP chip
  - One sample, many markers (100s-1,000,000) simultaneously





Assay types of SNP markers and breeding applications

KASP, TaqMan SNP markers

- **Major genes/QTL**
  - ✓ MAS
  - ✓ MARS
  - ✓ Haplotype-based discovery of novel alleles
- **Genome-wide**
  - ✓ MABC
  - ✓ Low density-marker based DNA fingerprinting
  - ✓ Linkage drag elimination or minimization
  - ✓ genetic diversity assessment (low density marker-based)
  - ✓ Reconstruction of parents of hybrids
  - ✓ F1 hybrid confirmation
  - ✓ Seed genetic purity assessment
  - ✓ Variety identity verification

SNP chip

- **High density**
  - ✓ Genome-wide selection (GWS)
  - ✓ High density variety DNA fingerprint
  - ✓ Detailed genome-wide genetic diversity assessment
  - ✓ Variety identity verification
- **Low density?**

Outline

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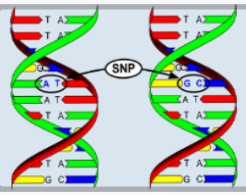
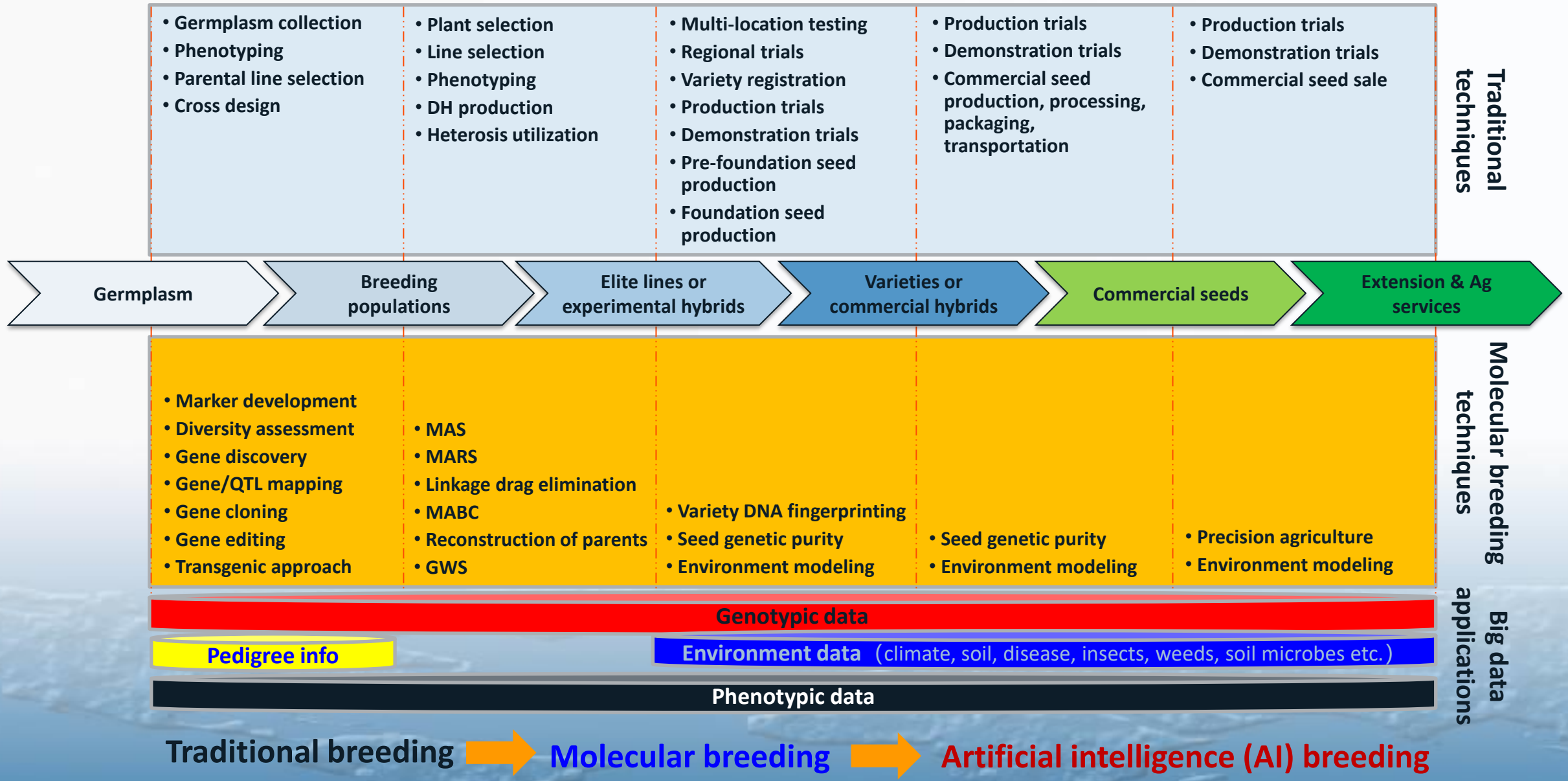


SNP marker development

Molecular breeding technologies

Trend of molecular breeding

Molecular breeding technologies deployed into variety development & commercialization pipeline



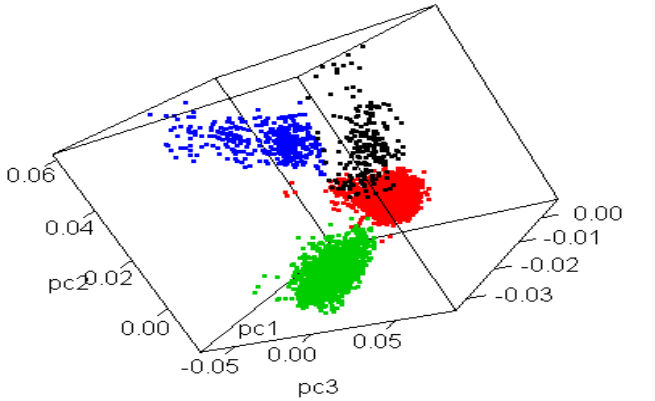
Traditional breeding → Molecular breeding → Artificial intelligence (AI) breeding

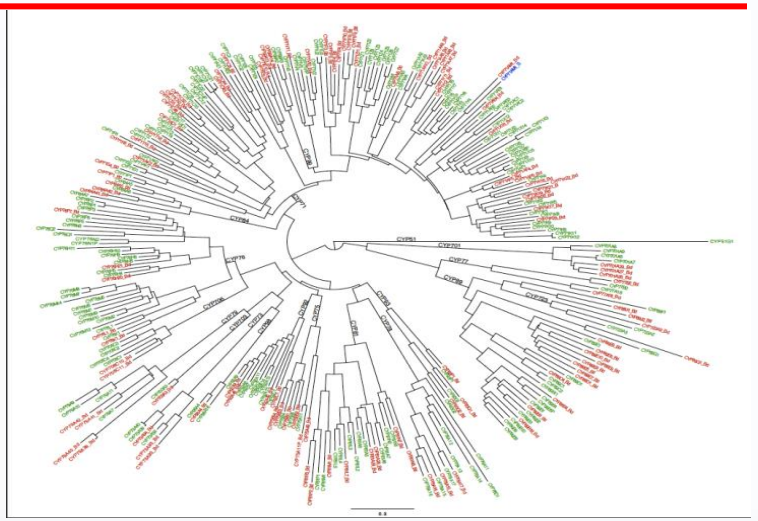
Genetic diversity assessment of parental lines

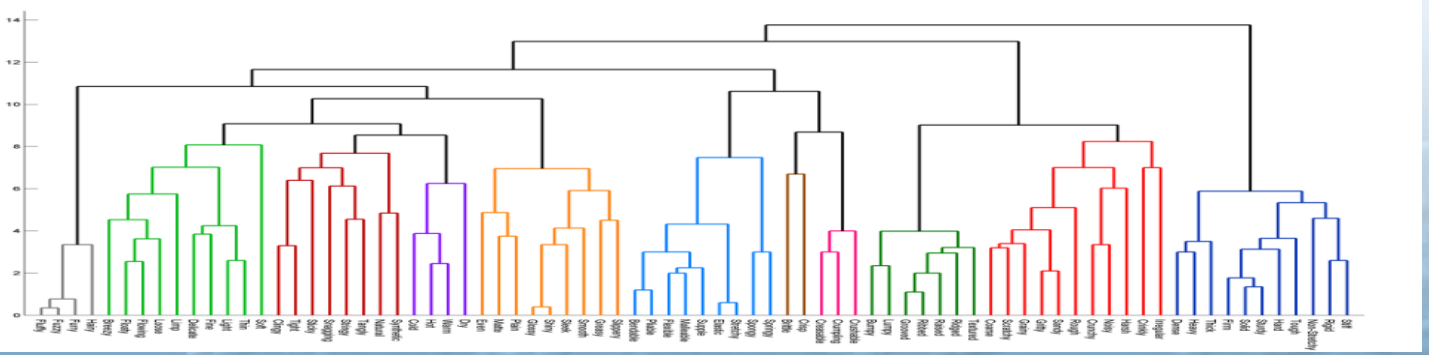
Traditional methods

- Phenotypes such as plant height, plant type, growth duration, adaptability, photo-sensitivity, biotic resistance, abiotic tolerance, yield, quality traits, etc.
- Originating sources
- relationship
- Pedigree info

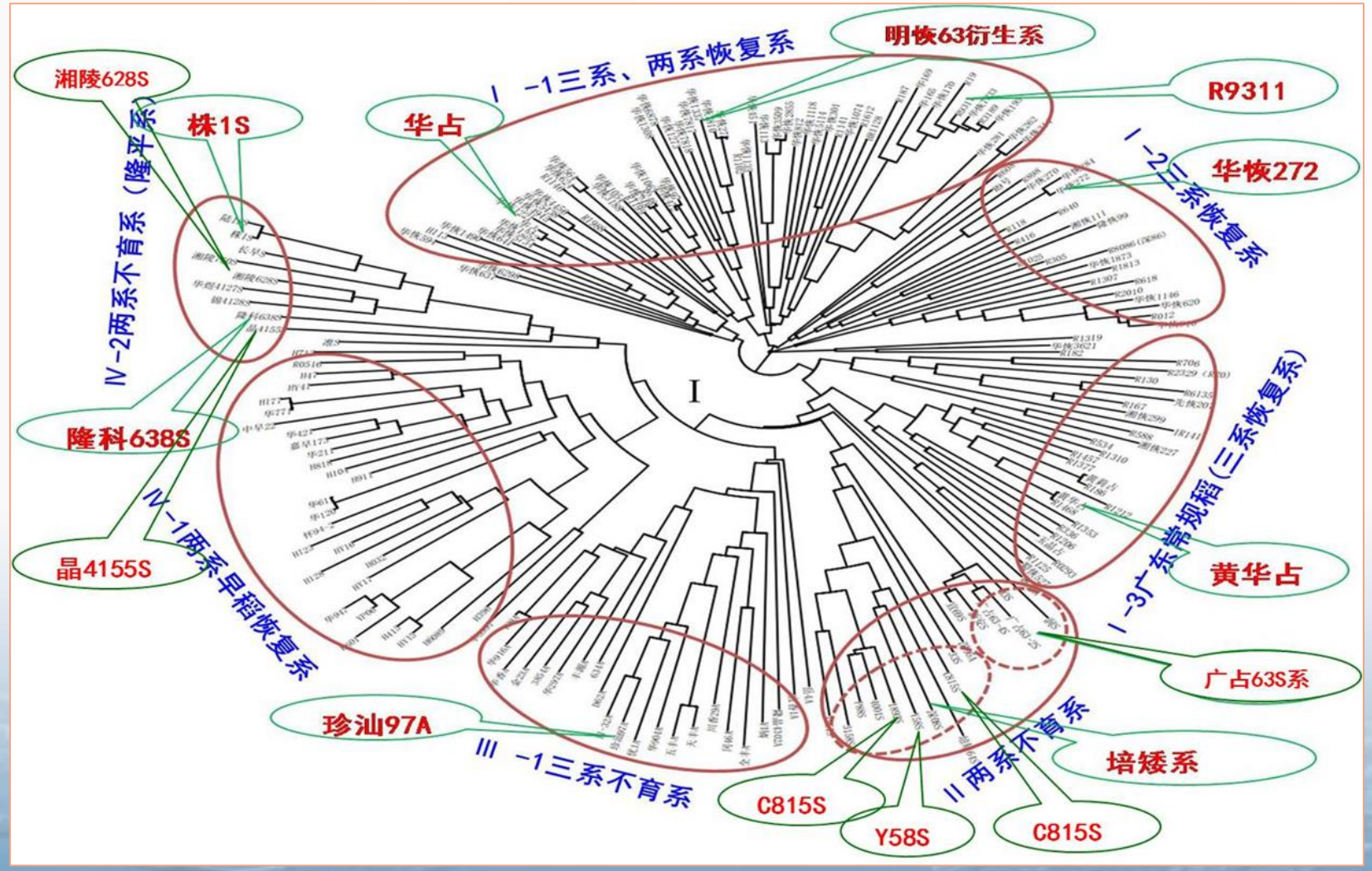
Based on SNP markers covering the entire genome







Clustering of a core set of 190 hybrid rice parental lines from LPHT



- Guide the design of crosses to construct breeding populations
- Predict the performance of potential hybrids
- Variety IP protection

Parental selection and design of crosses for breeding populations

Traditional

- Trait complementation
- Adaptability of target growing regions
- Pedigree info
- Originating sources

Outcome

✓ **Many crosses**

✓ **High genetic duplication of crosses**

✓ **Low predictability**

Molecular marker-assisted

- Trait complementation
- Adaptability of target growing regions
- Pedigree info
- Originating sources
- Major genes of target traits
- Genome-wide diversity、similarity and distance

Outcome

✓ **Fewer crosses and highly selective**

✓ **Low genetic duplication of crosses**

✓ **higher predictability**

F1 hybridity confirmation

Traditional

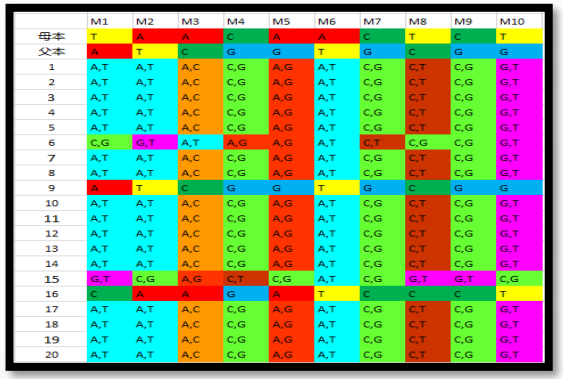
- F1 plant trait observation

Outcome

- ✓ **Low accuracy**
- ✓ **May require to grow to maturity**
- ✓ **May delay F1 crossing or backcrossing a generation**

Molecular markers

- Trait or non-trait markers



	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
母本	T	A	A	C	A	A	C	T	C	T
父本	A	T	C	G	G	T	G	C	G	G
1	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
2	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
3	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
4	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
5	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
6	C,G	G,T	A,T	A,G	A,G	A,T	C,T	C,G	C,G	G,T
7	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
8	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
9	A	T	C	G	G	T	G	C	G	G
10	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
11	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
12	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
13	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
14	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
15	G,T	C,G	A,G	C,T	C,G	A,T	C,G	G,T	G,T	C,G
16	C	A	A	G	A	T	C	C	C	T
17	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
18	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
19	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T
20	A,T	A,T	A,C	C,G	A,G	A,T	C,G	C,T	C,G	G,T

Outcome

- ✓ **High accuracy**
- ✓ **Fast (typically 5 business days)**
- ✓ **Low cost**

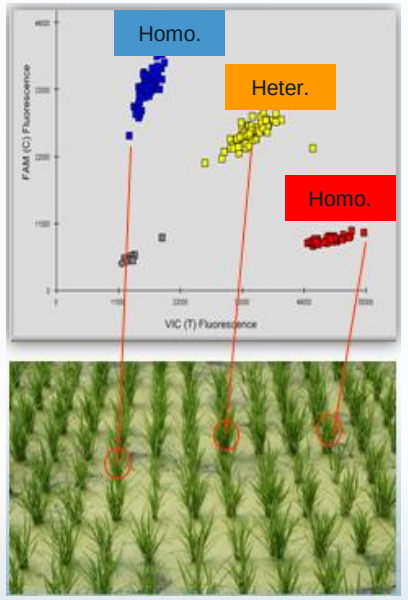
Selection of favorable genotype of major genes/QTL

Traditional phenotype selection

- Trait phenotype required
- Low accuracy in natural environment (high rate of false-positive such as disease resistance, insect-resistance)
- Costly in controlled environment and low throughput
- Cannot distinguish between homo. and heter. genotype of a dominant gene (progeny evaluation required)
- Typically cannot perform selection at more than one gene locus

Marker-assisted selection (MAS)

- No phenotype required
- Low cost
- High throughput
- fast
- High selection accuracy
- Early selection
- distinguish between homo. and heter. genotype of a dominant gene
- Selection of multi-gene loci simultaneously



MAS: low cost, fast, accurate – a rice example

A breeder needs to identify 500-600 F2 blast resistant plants homozygous at *Pi2* from a F2 population

IF traditional artificial inoculation employed

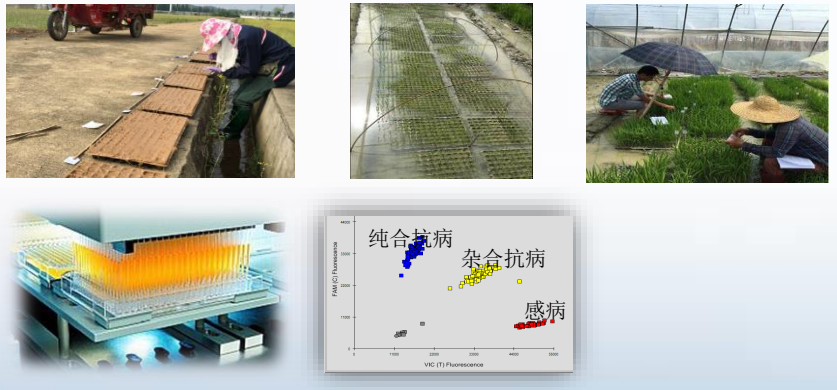
3,069 F2 plants：
F2 seed sowing → plant labeling → fungi culturing → inoculating → resistant/susceptible phenotype observation → transplanting into field → F3 seed harvest

2,213 F2:3 progeny inoculating to identify homozygous F2 plants：
F2:3 seed sowing → labeling → fungi culturing → inoculating → resistant/susceptible phenotype observation

Cost： ¥~355,000
Time： ~ 200 days
Accuracy： ~80%

MAS

F2 seed sowing → plant labeling → leaf tissue sampling → DNA extracting → SNP genotyping → identified 566 F2 resistant plants homozygous at Pi2 from 3,069 F2 plants



Cost： ¥~30,000
Time： 21 days
Accuracy： >99%

MAS: low cost, fast, accurate – sunflower examples

Downy Mildew

- Two different sources of resistance
- Prediction accuracy in segregating populations: >99%

Orobanche

- A major gene originating from wild sunflower
- Prediction accuracy in segregating populations: ~98%

Accumulation of the favorable alleles at multiple independent loci

Traditional recurrent selection

- Require phenotype of desirable plants to inter-mat
- Almost impossible to purposely accumulate the favorable alleles of more than 6 independent loci
- Very time-consuming (20 independent loci would need about 60 years)

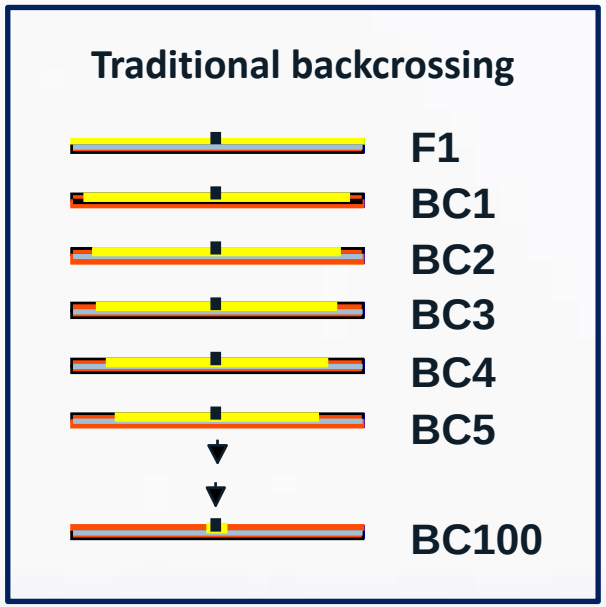
Marker-assisted recurrent selection (MARS)

Recurrent selection cycle	Frequency				
	Favorable allele	Desirable genotype (homo for favorable allele at all the loci)			
		No. of independent loci under selection			
		20	15	10	5
0 (F2)	0.51	1 in 500 billion	7 in 4 billion	3 in 2 million	1 in 1,000
1	0.62	1 in 200 million	3 in 5 million	7 in 100,000	8 in 1,000
2	0.81	1 in 5,000	9 in 5,000	3 in 2 million	3 in 25
3	0.96	1 in 5	3 in 10	9 in 20	6 in 10

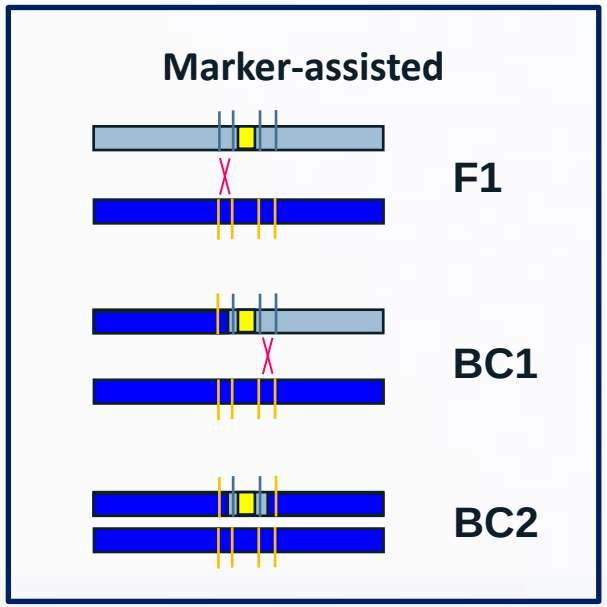
In every recurrent selection cycle, only needs to sample ~200 plants for genotyping of SNP markers associated with the genes, then ~10 plants are to be selected for inter-matting to produce segregating progeny for next cycle.

In the forward breeding， where it is necessary to accumulate the favorable alleles at multiple independent loci， MARS is the most powerful tool to achieve this.

Linkage drag elimination or minimization



50.5 years (2 gens/year)

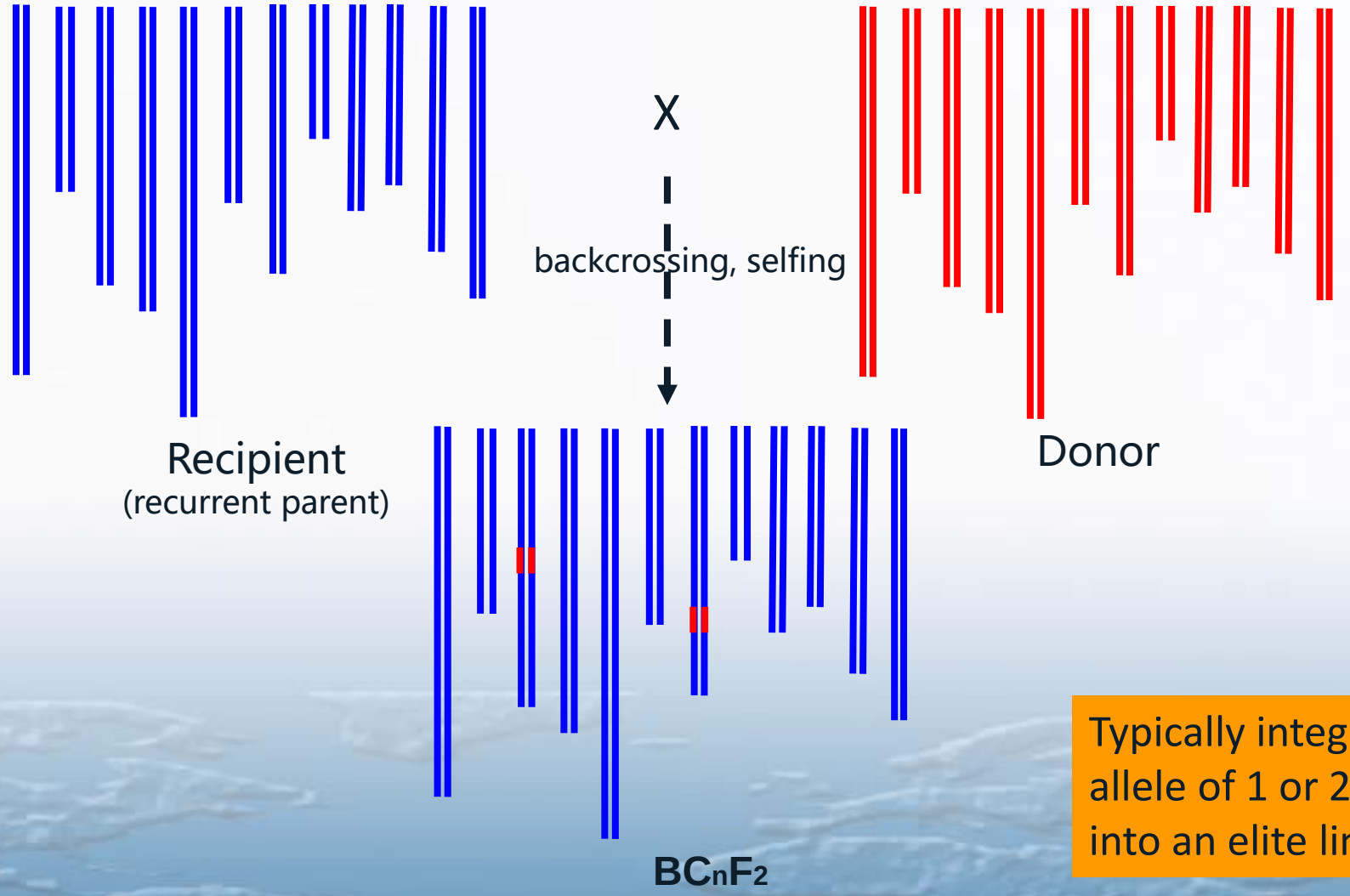


1.5 years (2 gens/year)





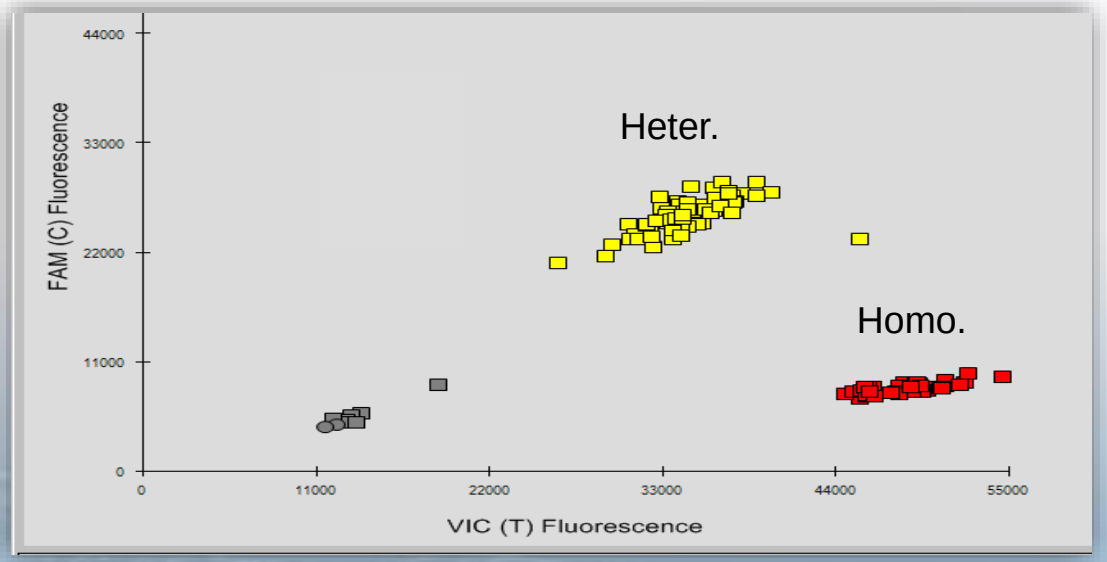
Backcrossing conversion



Typically integrate the favorable allele of 1 or 2 genes or transgenes into an elite line or variety

Marker-assisted backcrossing conversion (MABC)

Marker	DP	RP	Backcross progeny									
			1	2	3	4	5	6	7	8	9	10
1	AA	CC	AC	CC	CC	AC	CC	CC	CC	AC	CC	AC
2	GG	TT	TT	TT	GT	GT	GT	TT	TT	GT	TT	TT
3	CC	TT	TT	CT	TT	CT	CT	CT	TT	TT	CT	CT
4	TT	GG	GT	GG	GT	GG	GG	GT	GG	GT	GG	GT
5	AA	GG	AG	AG	GG	GG	GG	AG	GG	GG	AG	GG
6	TT	AA	AA	AA	AA	AT	AT	AA	AA	AT	AA	AA
7	GG	AA	AG	AA	AA	AG	AG	AA	AA	AA	AG	AA
8	DD	II	II	DI	II	II	DI	DI	II	DI	II	II



Foreground selection

Background selection: use markers covering the entire genome to identify the backcross progeny most similar to the recurrent parent.

Traditional

A recurrent x B donor

F1 (50% recurrent)

BC1 (75% recurrent)

BC2 (87% recurrent)

BC3 (94% recurrent)

BC4 (97% recurrent)

BC5 (98% recurrent)

BC6 (99% recurrent)

Marker-assisted

A recurrent x B donor

F1 (50% recurrent)

BC1 (88-92% recurrent)

BC2 (95-97% recurrent)

BC3 (98-99% recurrent)

Benefit: improved variety gets into seed market two years earlier

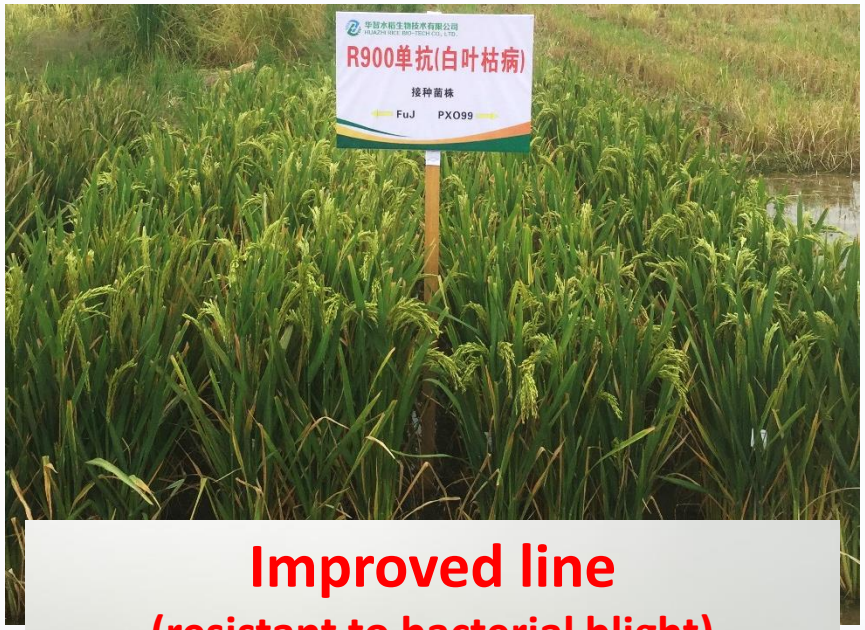
Bacterial blight resistance integration into an elite line through MABC

16 months： April, 2016 – August, 2017

Bacterial blight resistance integration into R900 through MABC

Original line

(susceptible to bacterial blight)



Improved line

(resistant to bacterial blight)

MABC to speed up transgene integration: corn examples

At least one BC3F1 plant whose recurrent parent genome recovery is >98.5% in all 20 inbreds for insect-resistance and herbicide-tolerance transgene conversions

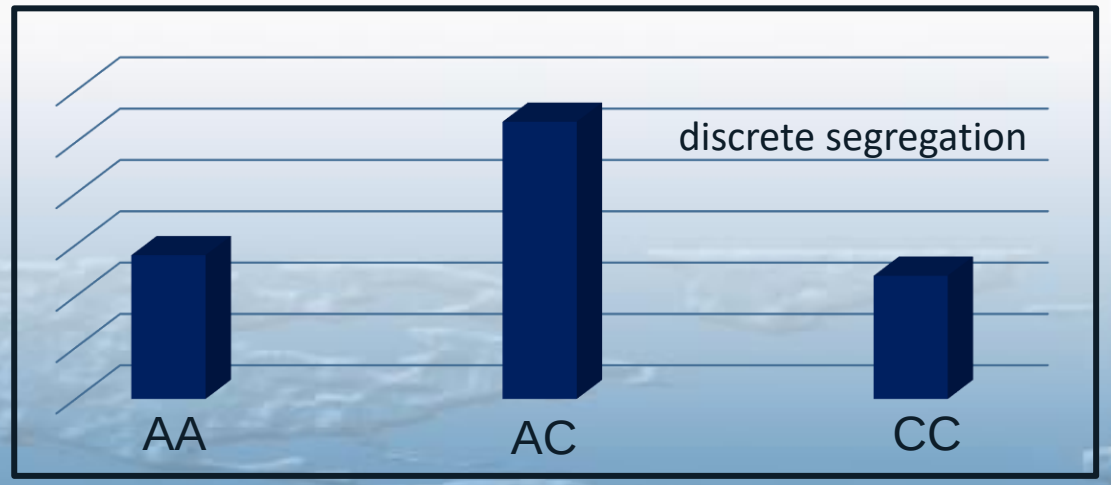
MAS, MARS only applicable to selection of major genes/QTL

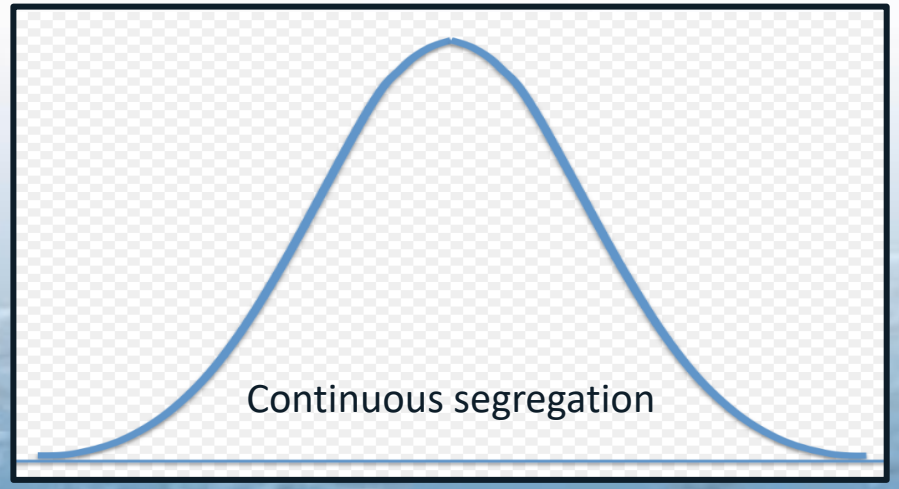
Suitable for selection of qualitative or simple quantitative traits such as race-specific disease resistance, biotype-specific insect resistance

- ✓ Genotype-independent
- ✓ Environment has no or little effect on
- ✓ Controlled by one or few major genes or QTL

Not suitable for selection of complex traits such as yield, abiotic stress tolerance, polygenic biotic stress resistance

- ✓ Genotype-dependent
- ✓ Affected largely by the environment
- ✓ Polygenic control

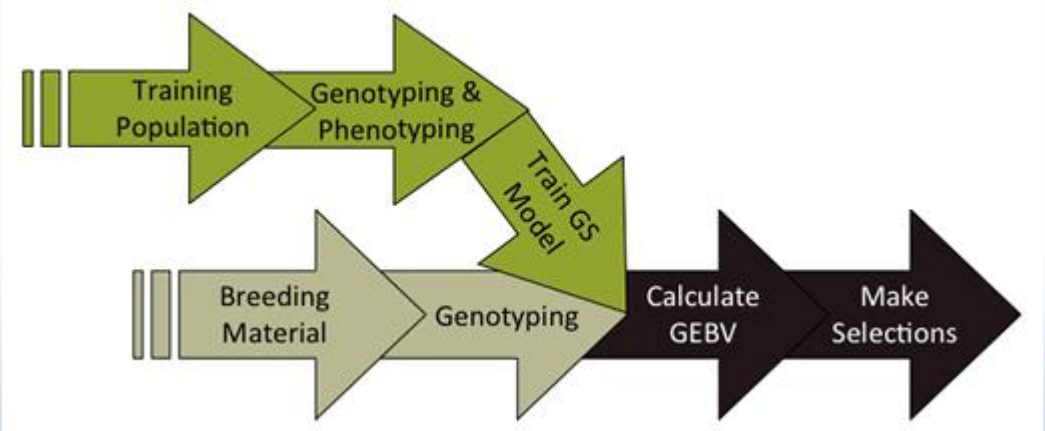




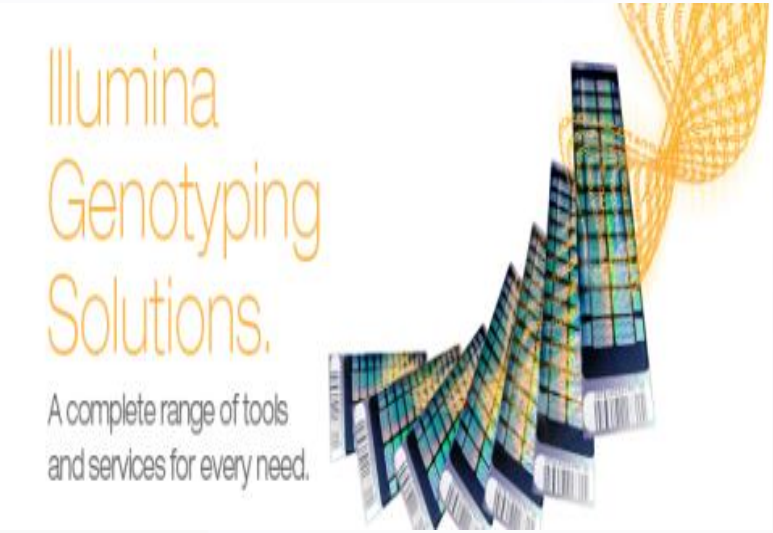
Genome-wide selection (GWS): concept

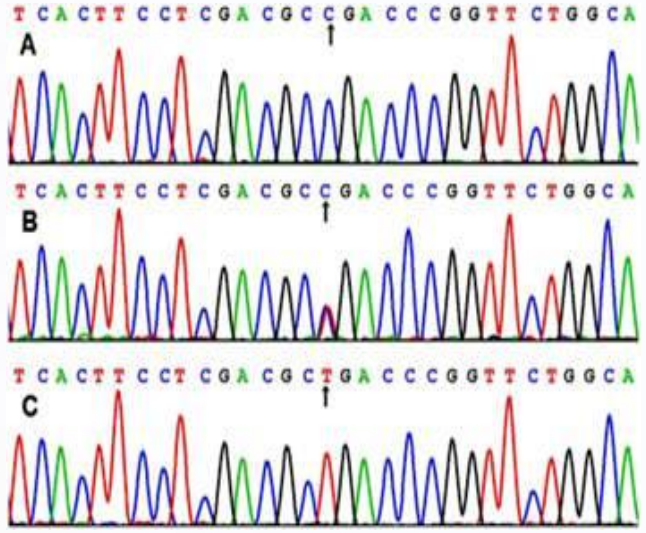
Meuwissen, T. H., Hayes, B. J., & Goddard, M. E. (2001). Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. *Genetics*, *157* (4), 1819-1829.

Individual or Family	Genotype	Phenotype	Genomic Estimated Breeding Value
1	x	x	x
2	x	x	x
3	x	x	x
.	x	x	x
.	x	x	x
.	x	x	x
k	x	x	x
k + 1	x		x
k + 2	x		x
k + 3	x		x
.	x		x
.	x		x
.	x		x
N	x		x



SNP genotyping cost lower then phenotyping cost made GWS possible

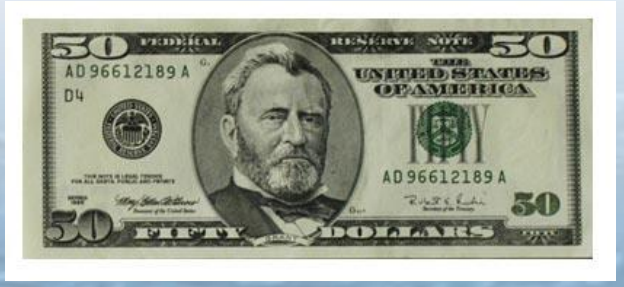




One line field tested at 5 locations with 1 plot each

$200

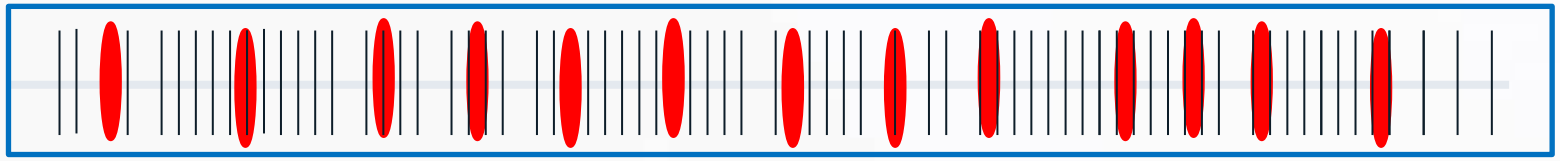
One line genotyped at 50, 000 SNP markers



$50

GWS: rationale and advantages

- Designed for phenotypic value prediction of polygenic traits such as yield, abiotic stresses
- All QTL are in LD when the density of markers covering the entire genome is high enough



- GWS is the core technology of molecular breeding
- Only multi-national seed industry giants such as Bayer-Monsanto and Dow-DuPont have integrated GWS into traditional breeding process
- Advantages of GWS
  - Higher genetic gain: ~two times of traditional breeding's
  - Reducing cost: reduce number of lines or hybrids to be conducted for field trials
  - Speeding up breeding cycles: reduce one or two field testing seasons
  - Faster recycling of parental lines: advanced breeding lines as parental lines for new breeding population

GWS-guided creation of heterotic hybrids: flowchart

Model building
（SNP marker and trait data known）

- Select female and male parents（3,000 – 5,000)
- Purify parental lines genetically
- Conduct SNP genotyping
- Perform genetic and clustering analyses
- Design hybrid combinations for model training
- Produce F1 hybrid seeds
- Design field experiment
- Conduct field trials
- Normalize trait data
- Deduce the SNP genotypes of F1 hybrids
- Perform model fitting and cross-validation (hybrid, female, and male models)

Model validation
（SNP marker and trait data known）

- Design hybrid combinations for model validation
- Produce F1 hybrid seeds
- Design field experiment
- Conduct field trials
- Normalize trait data
- Deduce the SNP genotypes of F1 hybrids
- Assess the accuracy of model prediction
- Re-build and refine models

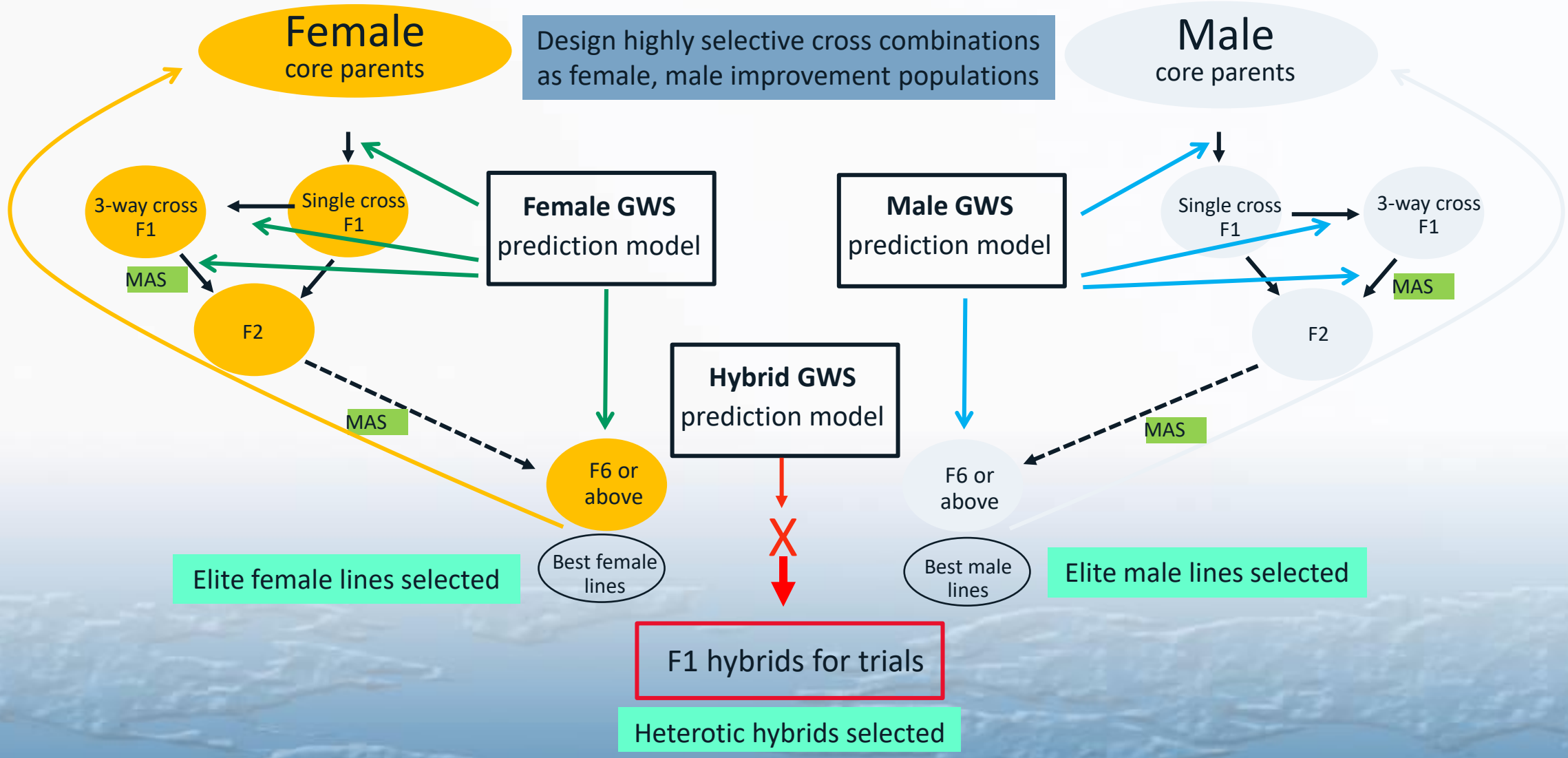
Model application
（SNP marker data known）

- Hybrid model to predict the performance of hybrids
- Female model to select elite female lines from female improvement populations
- Male model to select elite male lines from male improvement populations
- Female model to simulate cross combinations and design highly selective combinations as female improvement populations
- Male model to simulate cross combinations and design highly selective combinations as male improvement populations

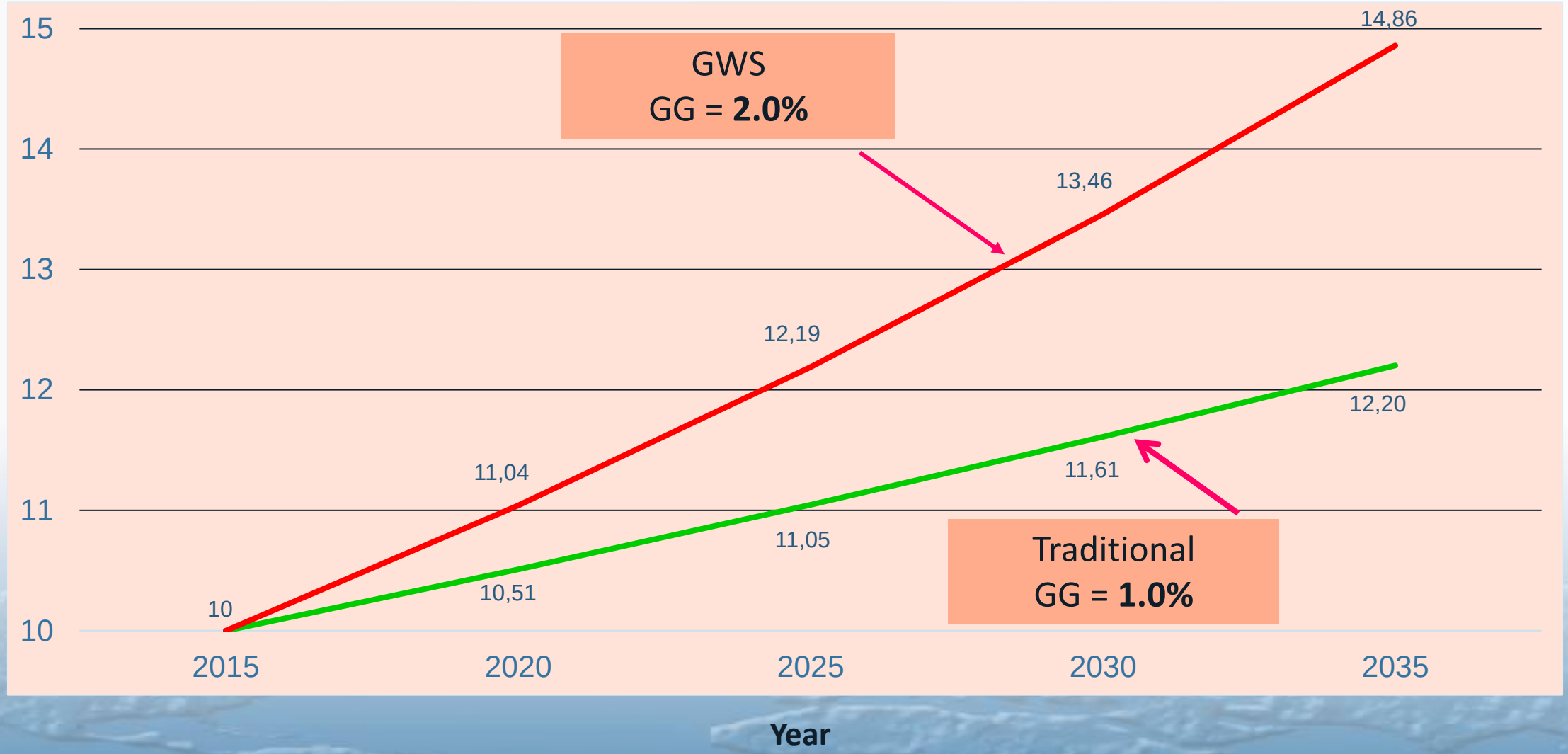
3 years → 2 years →

$$y = a + b_1x_1 + b_2x_2 + b_3x_3 + \ldots\ldots + b_nx_n$$ *Where, X = SNP genotype*

GWS prediction model application



GWS increases genetic gains



Seed genetic purity/plant genetic mixture assessment

Traditional

- Field observation of plant uniformity

Outcome

- ✓ Low accuracy
- ✓ May require to grow to maturity
- ✓ costly

SNP markers

SNP	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10	M11	M12	M13	M14	M15	M16	M17	M18	M19	M20	M21	M22	M23	M24
ref	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
1	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
2	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
3	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
4	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
5	T	T	T	C	A	A	T	A	T	A	C	C	A	T	T	A	T	A	A	C	G	A	T	C
6	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
7	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
8	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
9	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
10	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
11	G	A	A	C	G	T	C	T	C	T	C	C	G	C	A	T	T	A	A	C	T	A	C	C
12	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
13	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
14	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
15	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
16	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
17	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
18	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
19	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C
20	T	A	A	C	A	A	C	T	C	T	T	G	G	C	A	T	C	C	G	G	G	G	C	C

Outcome

- ✓ Highly accurate
- ✓ Fast (about a week after seed or leaf tissue sampling)
- ✓ Low cost

Variety identity verification and proprietary germplasm protection

Traditional

- Observation in the field

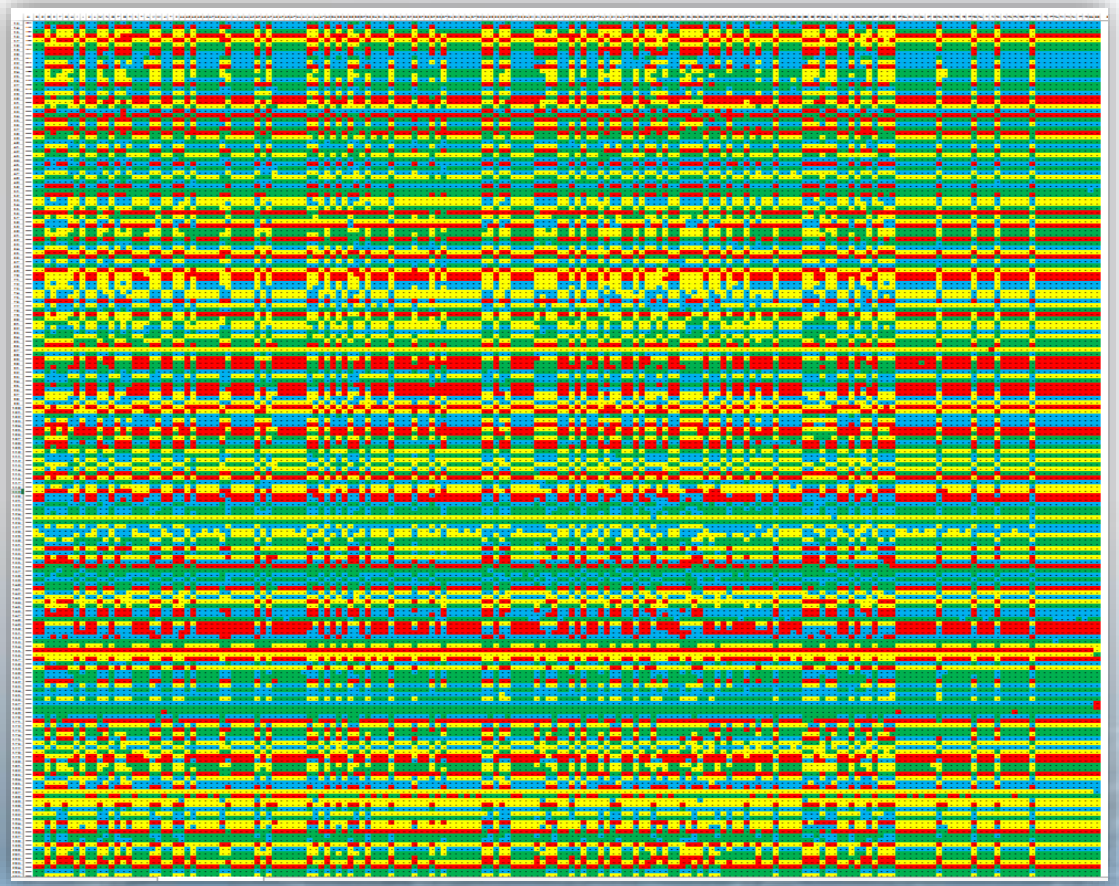
SSR standard

- 48 pairs of SSR

Outcome

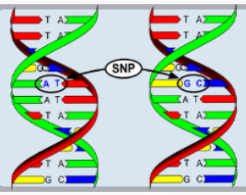
✓ Indistinguishable in many cases

DNA fingerprint based on genome-wide SNP markers



Outline

Molecular breeding and seed industry development — Monsanto as an example



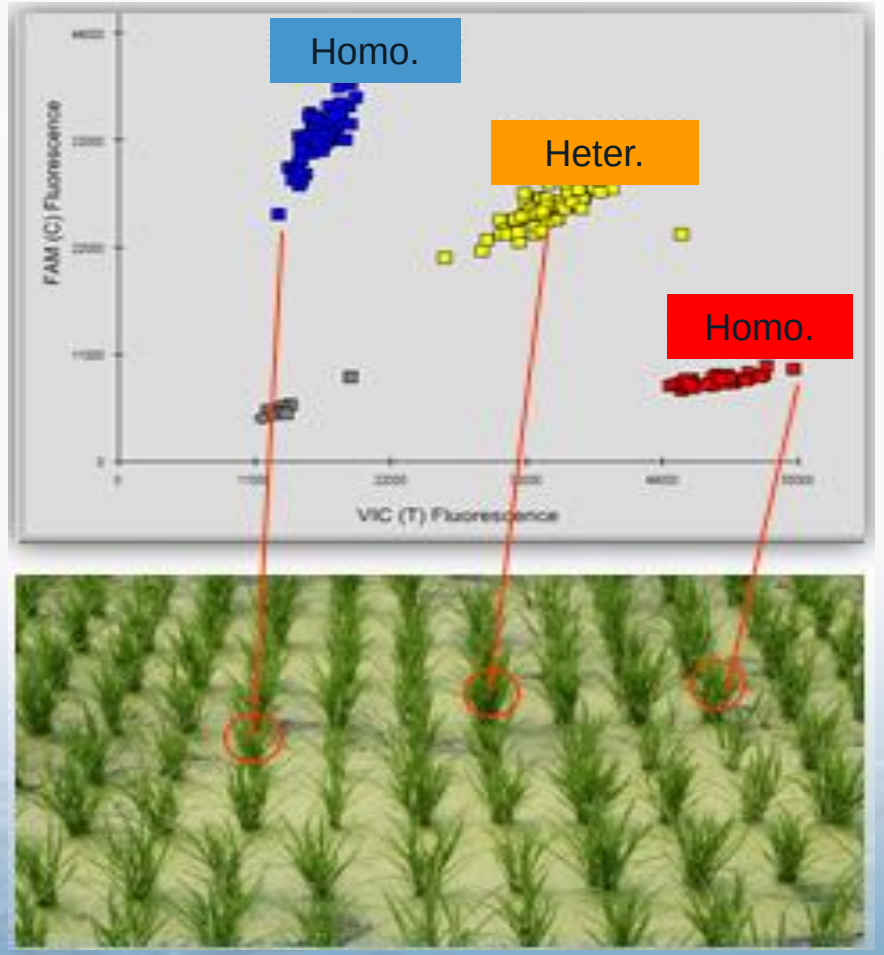
SNP marker development

Molecular breeding technologies

Trend of molecular breeding

MAS, MABC are becoming routine

MAS：accurate, fast, low cost



MABC： accurate, fast, high success

Traditional

A recurrent x B donor

F1 (50% recurrent)

BC1 (75% recurrent)

BC2 (87% recurrent)

BC3 (94% recurrent)

BC4 (97% recurrent)

BC5 (98% recurrent)

BC6 (99% recurrent)

Molecular markers

A recurrent x B donor

F1 (50% recurrent)

BC1 (88-92% recurrent)

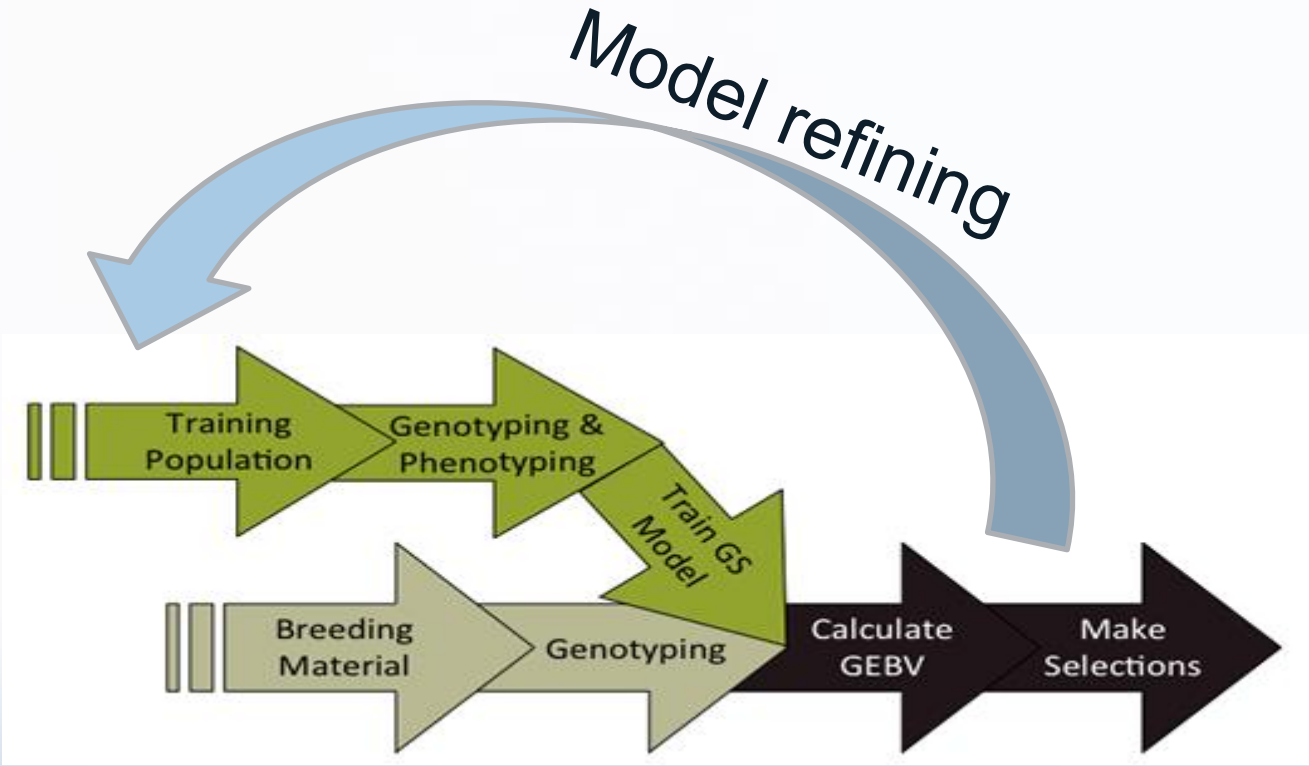
BC2 (95-97% recurrent)

BC3 (98-99% recurrent)

MAS and MABC have been applied to breeding programs in a large scale at multi-national seed companies for decades. But, they just got started in other seed industry, are becoming routine.

GWS is becoming the theme of molecular breeding

Individual or Family	Genotype	Phenotype	Genomic Estimated Breeding Value
1	x	x	x
2	x	x	x
3	x	x	x
.	x	x	x
.	x	x	x
.	x	x	x
k	x	x	x
k + 1	x		x
k + 2	x		x
k + 3	x		x
.	x		x
.	x		x
.	x		x
N	x		x



GWS is the core technology of molecular breeding. Only multi-national seed industry giants such as Bayer-Monsanto and Dow-DuPont have integrated GWS into traditional breeding process. Higher genetic gains, reducing cost, speeding up breeding cycles, faster recycling of parental lines.

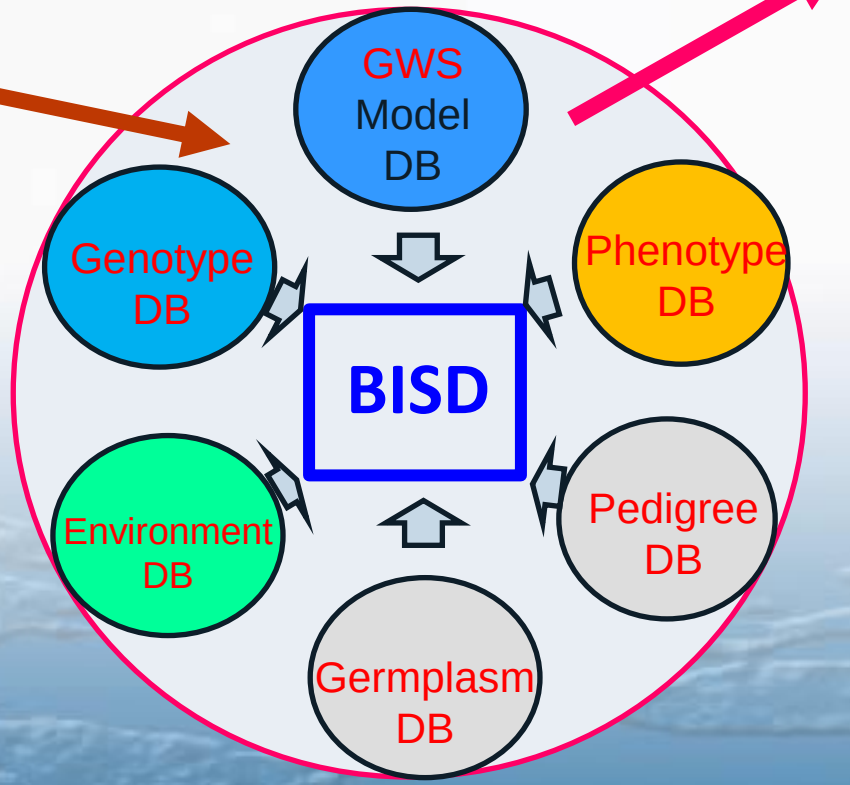
BISD will open the door to artificial intelligence (AI) breeding

BISD = Breeding by *In Silicon* Design®

***In Silico* breeding aims at increasing genetic gains through computer simulations, while reducing the needs for field and lab work tremendously.**

New variety parameters

- Target planting areas
- Yield
- Quality traits
- maturity
- Biotic resistance
- Abiotic stress tolerance
- others



Seq. #	Cross combination	MAS loci	GWS model	Success rate
C01	(P1034/P2059)//(P3315/P1908)	Pi2、Pita、Xa23、Xa21、Bph14、Bph27	D	85%
C02	(P4034/P2109)//P3765	Pigm、Pi1、Xa23、Xa21、Bph14、Waxyb	F	83%
C03	(P1023/P4108)//P3215	Pi9、Xa23、Xa7、Bph14、Bdh2	G	79%
C04	P1556/P4732	Pi2、Xa23、Xa21、Bph3、xa5	C	78%

Evolution of molecular breeding

MAS、MABC、MARS

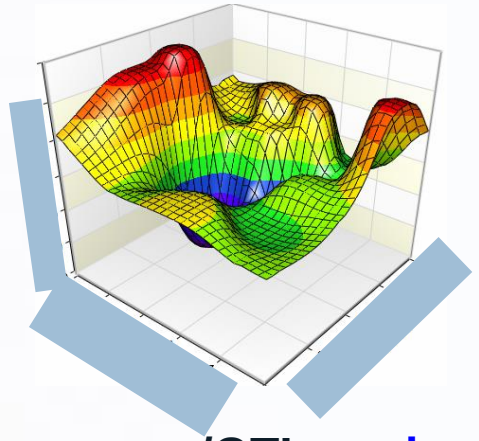
- Major genes/QTL
- Qualitative traits, simple quantitative traits
- Selection

MAS 、MABC、MARS + GWS

- Major genes/QTL + minor genes/QTL
- Qualitative traits, simple quantitative traits + complex traits
- Selection

Multi-national seed industry giants

BISD

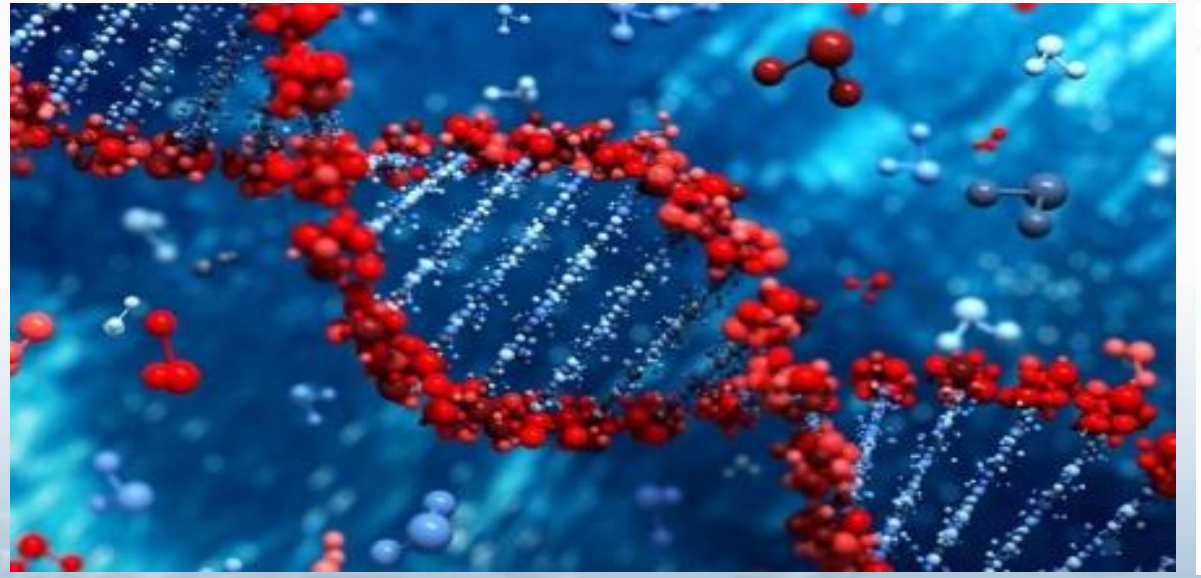


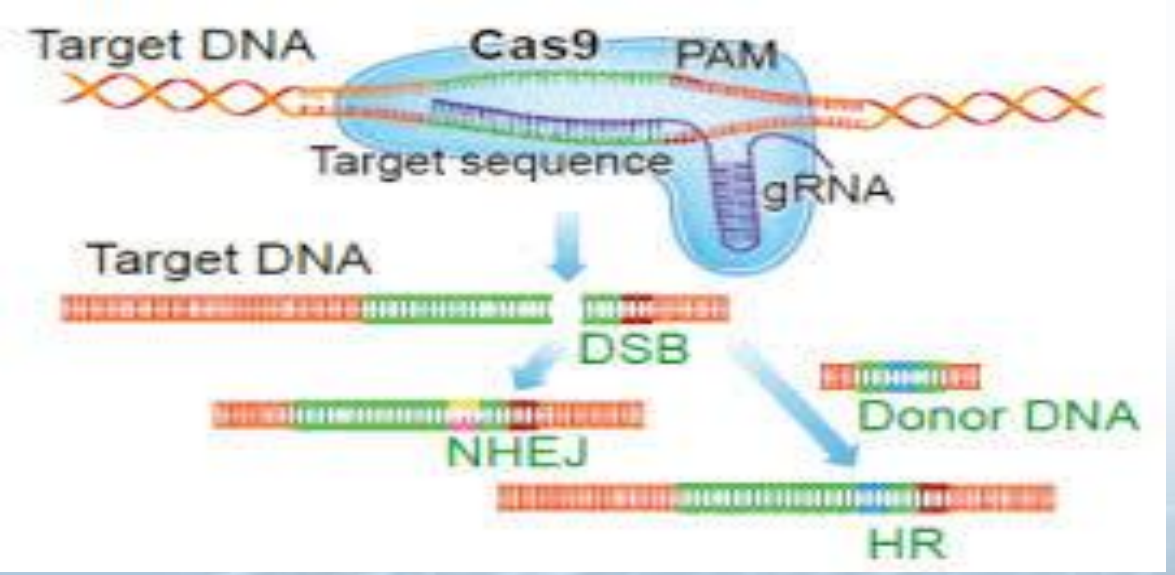
- Major genes/QTL + minor genes/QTL
- Qualitative traits, simple quantitative traits + complex traits under different environments
- Design + selection

??

Gene editing will become the mainstream in creating novel genetic variation

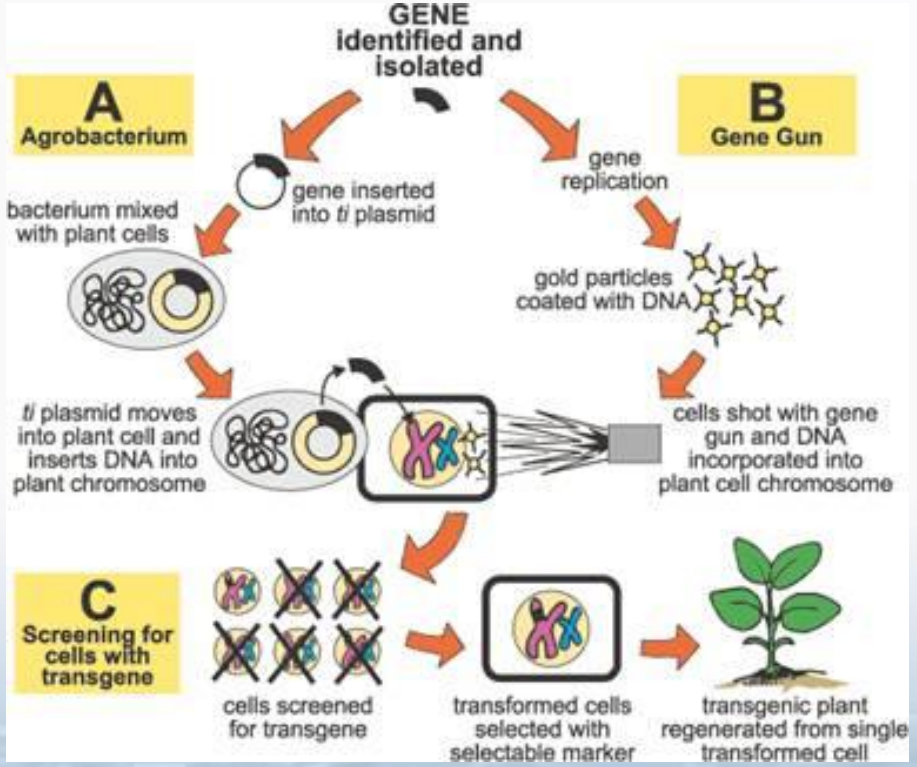
- creating novel superior alleles at known genes/QTL
- changing a minor gene into a major gene



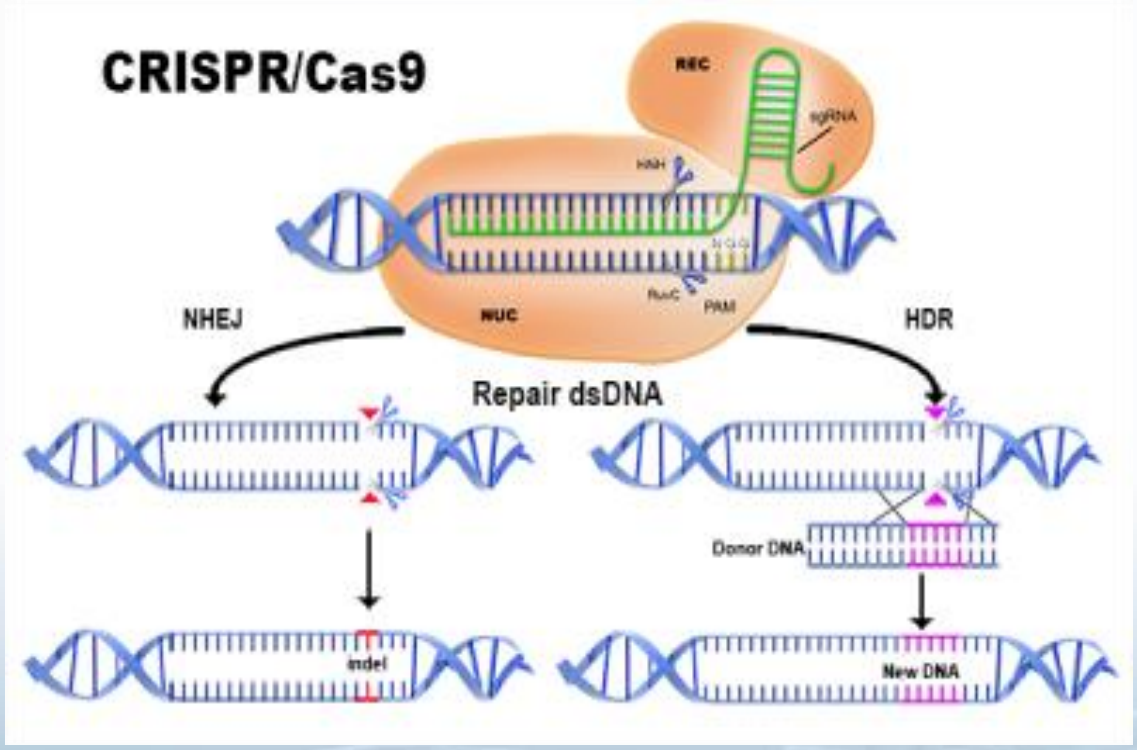


Gene editing will replace foreign gene transfer approach

Traditional gene transfer approach: random insertion of foreign gene

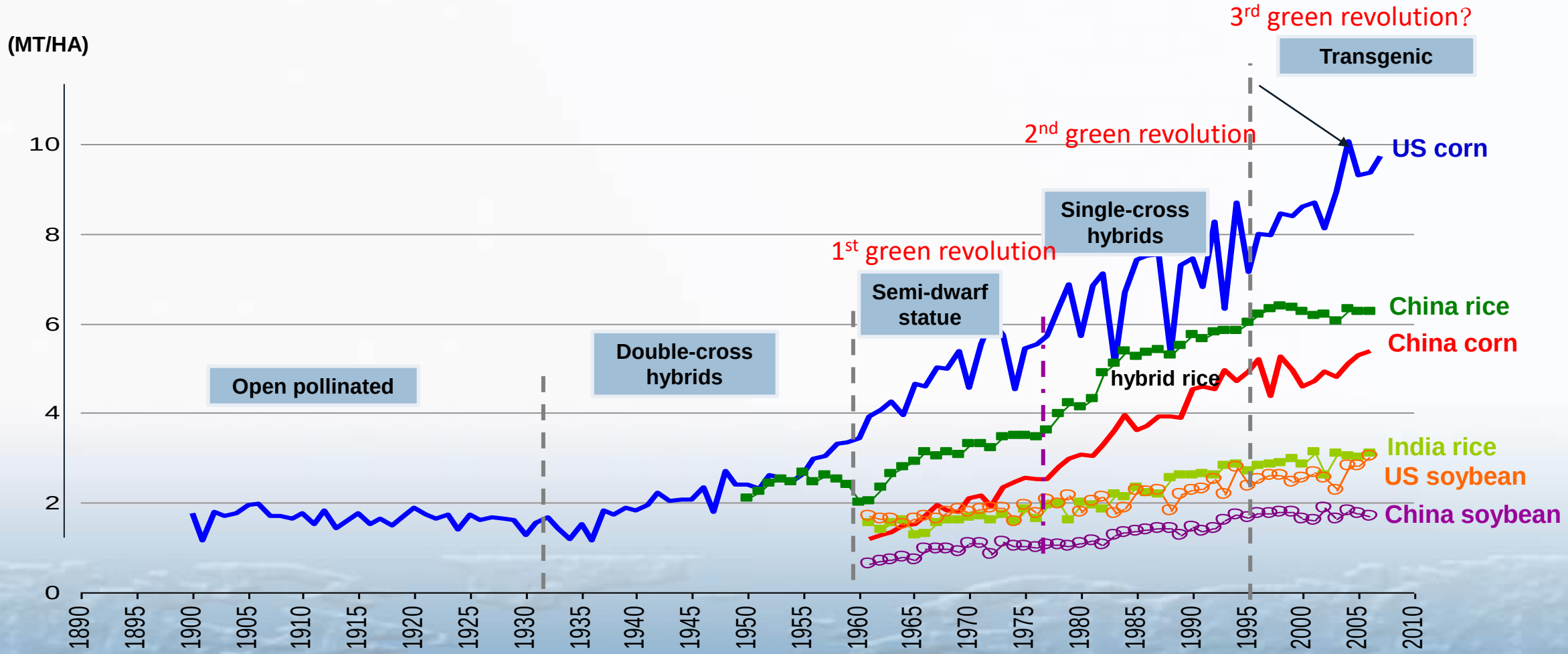


Gene editing approach: site pre-defined insertion of foreign gene



Gene editing will replace foreign gene transfer approach for moving genes between sexual incompatible species

Major breakthroughs in the history of crop genetic improvement



Source : USDA, IRRI and FAO

The major breakthroughs attributed to

- Innovation in breeding methodologies
  - open pollinated to double-cross hybrids in corn in 1930s
  - double-cross hybrids to single-cross hybrids in corn in 1960s
- Discovery/creation of novel genetic variation
  - semi-dwarf status genes rice and wheat in 1950s
  - rice CMS in 1970
  - rice photo-sensitive male sterility in 1973
  - rice therm-sensitive male sterility in 1980s
  - Insect-resistance, herbicide-tolerance transgenes in 1990s

Molecular breeding will bring the next breakthrough in crop genetic improvement

Innovation in breeding methodologies

Discover/create novel trait-improving genetic variation


SUPERB wallpapers
"Molecular Breeding, Seeds of the Future"
— Jinhua Xiao, 1995

Thanks !

Website：www.wiserice.com.cn

WeChat：huazhi-rice

Huazhi, leading commercial crop molecular breeding in China!