



# **Facilitating access and generation of genetic materials with breeding value and high resolution for genetic analysis**

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# Two issues

- **Access (availability)**
- **Production**

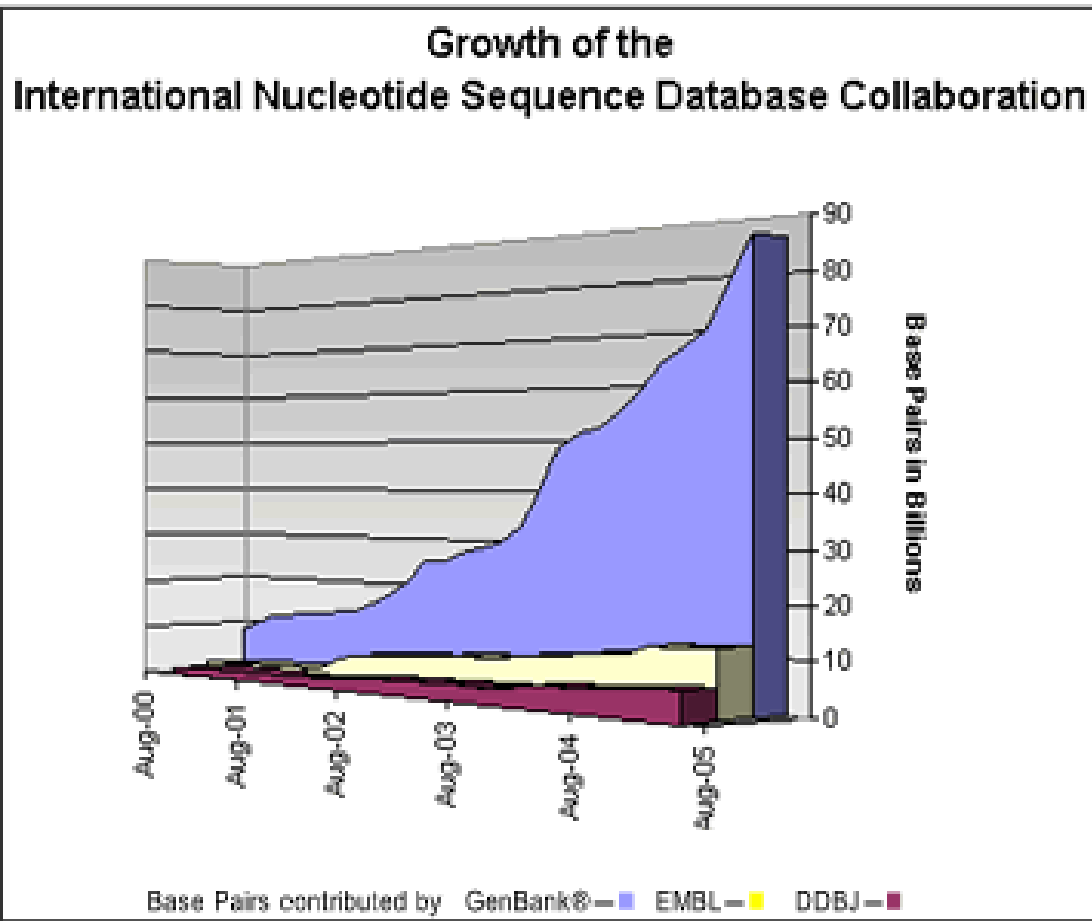


# Why we are discussing?

- *Research environment* is changing
- Sequencing and genotyping becoming cheaper
- Genomes/gene space of about half CG crops expected to be available in next 5-10 years
- Genome initiatives (e.g. Gates Foundation)
- Appropriate genetic material may be an issue, if not bottleneck!
- Should the community develop/start to develop new genetic populations!

*Need for populations having more than 2 (typically) alleles per locus for better genetic analysis and breeding value!*

# Sequencing costs going down!



## Cost/1000 bp

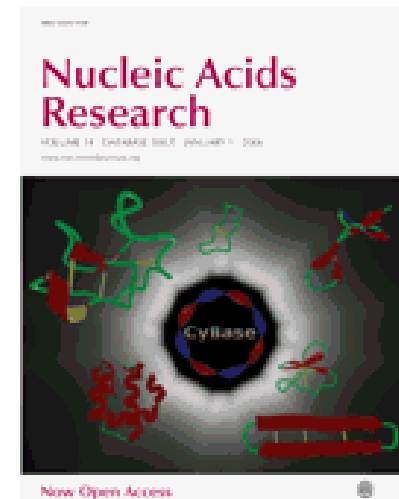
1990 ~ \$10.00

2000 ~ \$3.00

2005 ~ \$1.00

2006 ~ \$0.10

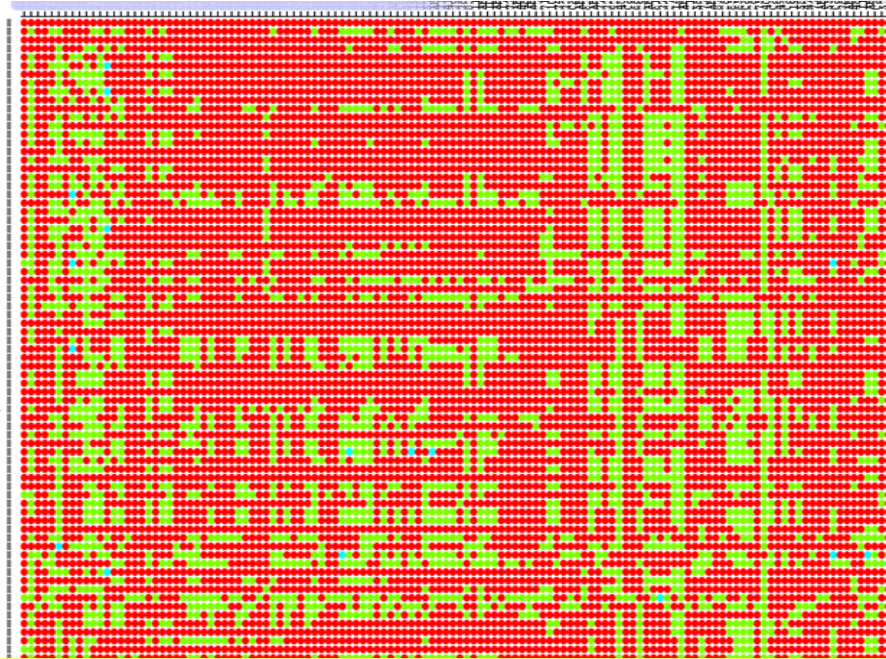
2007 ~ \$0.03



New technologies: 454 (Roche), Solexa (Illumina), ABI Solid

# Low cost marker genotyping

- Spectrum of markers available
- SSRs- markers of choice  
(trait mapping)
- SNP genotyping- gaining momentum
- Illumina OPA assay/ DArTs  
(costs <0.10 cent / data point)
- Whole genome breeding possible



*Marker density is not going to be a problem!*

*Genotyping data can be generated in short time!*

*Appropriate genetic populations can not be produced "quickly!"*

# Recapping the discussions!



- Reference collections
  - represent the global diversity
- Multiparent design/ Multiparent Advanced Generation Intercross (MAGIC) populations
  - cheap to set up and their value as mapping resources increases with each generation
  - can be used to combine coarse mapping with low marker densities on lines derived from an early generation,
  - or fine mapping using lines derived from a more advanced generation of crossing and a higher marker density.

# Specialized genetic populations!

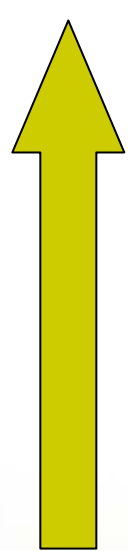


- Near isogenic lines (NILs)
  - good resource for functional genomics/ gene validation
- (advance) Back cross populations (AB-QTL)
  - for discovery and introgression of superior alleles (trait) from wild species (rice, barley, tomato, soybean)
- Chromosome segment substitution lines (CSSLs)
  - for conducting QTL mapping with higher mapping precision
- Introgression libraries (genome wide)
  - to study the genes effecting complex phenotype (tomato)

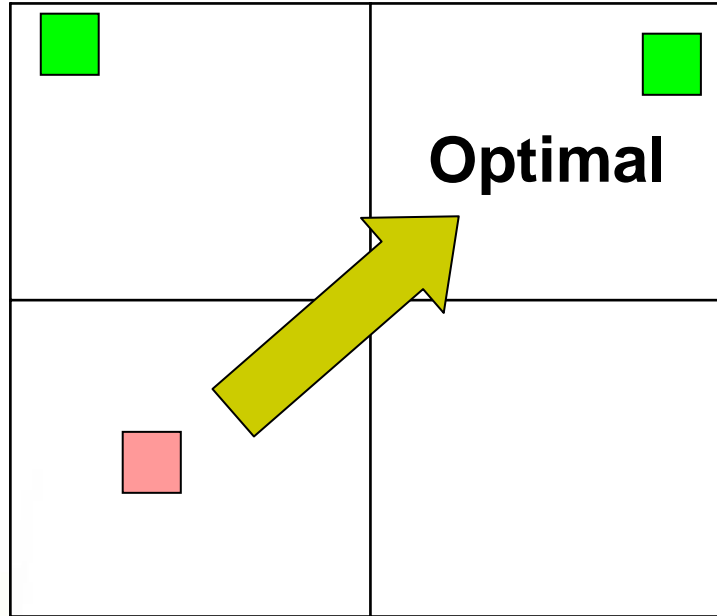
# 2 x 2 table



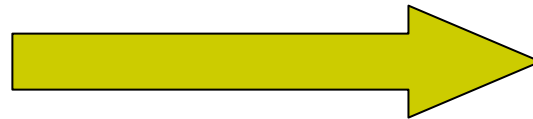
Crop groups or specific crops



Genetic analysis resolution



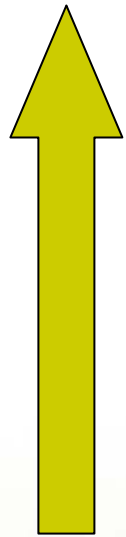
Breeding value for certain traits



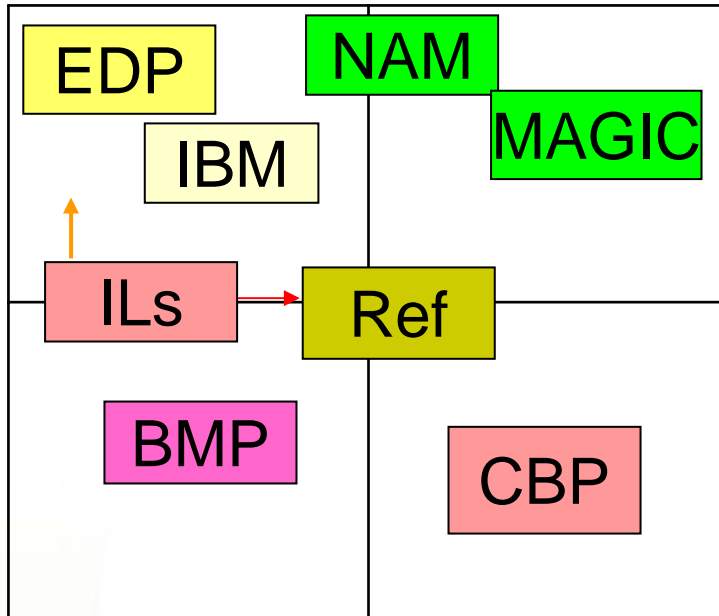
Classic case:  
Good x Bad

*Specialized genetic populations do not need to be optimal for both breeding and genetic analysis; may be good only for one purpose*

# Example: Maize



Genetic analysis resolution



Breeding value for certain traits



CBP= conventional Breeding population

BMP= Biparental mapping population

IBM= B73 x Mo67

ILs= Introgression lines

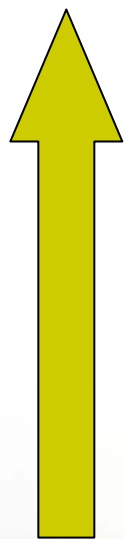
Ref= reference collection

EDP= Ed Buckler's Diversity Panel

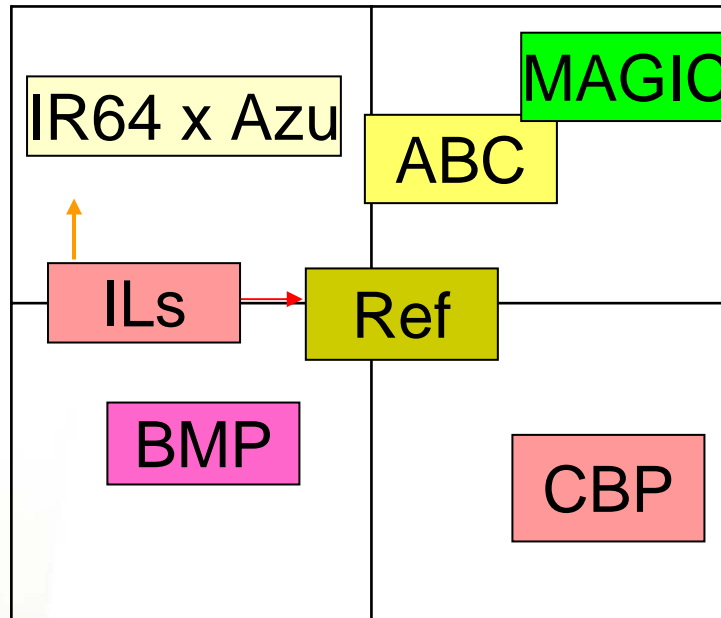
NAM= Nested Association Mapping

MAGIC= Multiparent advanced generation intercross

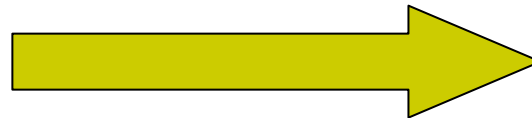
# Example: Rice



Genetic analysis resolution



Breeding value for certain traits



**CBP= conventional Breeding population**

**BMP= Biparental mapping population**

**IR 64 x Azucena**

**ILs= Introgression lines**

**Ref= reference collection**

**ABC= advanced backcross population**

**MAGIC= Multiparent advanced gen intercross**

# Values of genetic populations!



Population	Time required	Discovery value - Gene/QTL identification	Breeding value
RIL (Bad x Good)	++	+++	+
RIL (Good x Good)	++	+	++
Het Inbred Family (HIF)	+	+++	+ to +++ (1)
NILs	+++	++++	+ to +++ (1)
Adv backcross	+	+++	+++
ILs	++++	+++	+++
Reference	+	+++	+
CSSLs	++++	+++	+++
MAGIC	+++	++++	+ to +++ (1)

(1) Depending on choice of parents

*Midnight brainstorming:*

*Roberto Tuberosa, Alain Ghesquiere, Hei Leung, Rajeev Varshney*

# ***Which options for GCP populations development?***



- ❖ **Maize and millet (*M Warburton* and *V Vadez*), Cycad 5**
- ❖ **Sorghum (*T Hash* and *C Billot*), Cycad 6**
- ❖ **Wheat and Barley (*P Langridge* and *A Blum*), Cycad 1**
- ❖ **Rice (*H Leung* and *A Guesquiere*), Cycad 2**
- ❖ **Roots / tubers (*M Fregene* and *E Okogbenin*), Cycad 7**
- ❖ **Legumes (*S Muranaka* and *D Hoisington*), Cycad 3**

# Lead-in questions



## 1. Take stocks:

- What (and where) are the existing rich, and publicly accessible population top?
- Where do they fit in the 2 x 4 table?
- How to facilitate usage?

## 2. Desirable scenarios

- What it takes to move more materials into the “high value”

## 3. Feasibility

- What can be produced in 2-3 years if investment is made

Thank you

***Have a nice session!***