

# The role of genomics in crop improvement

**Mike Bevan**  
**UPOV, Geneva**



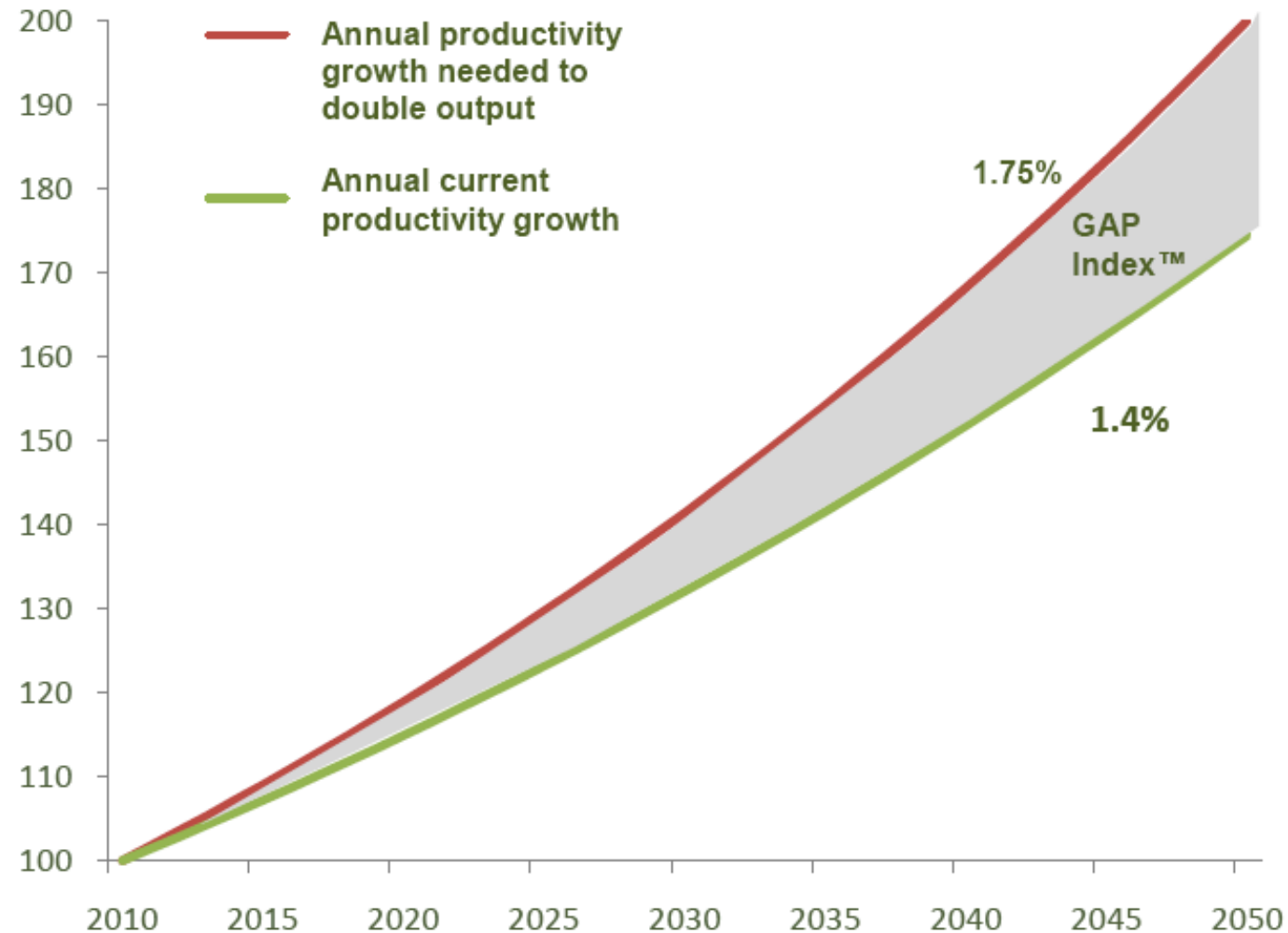


- 
- Supplying sufficient food in the 21 century
  - What is sustainable agriculture?
  - The key role of plant science and genomics

# The Global Harvest Initiative

# 2010 GAP Report™

## Measuring Global Agricultural Productivity



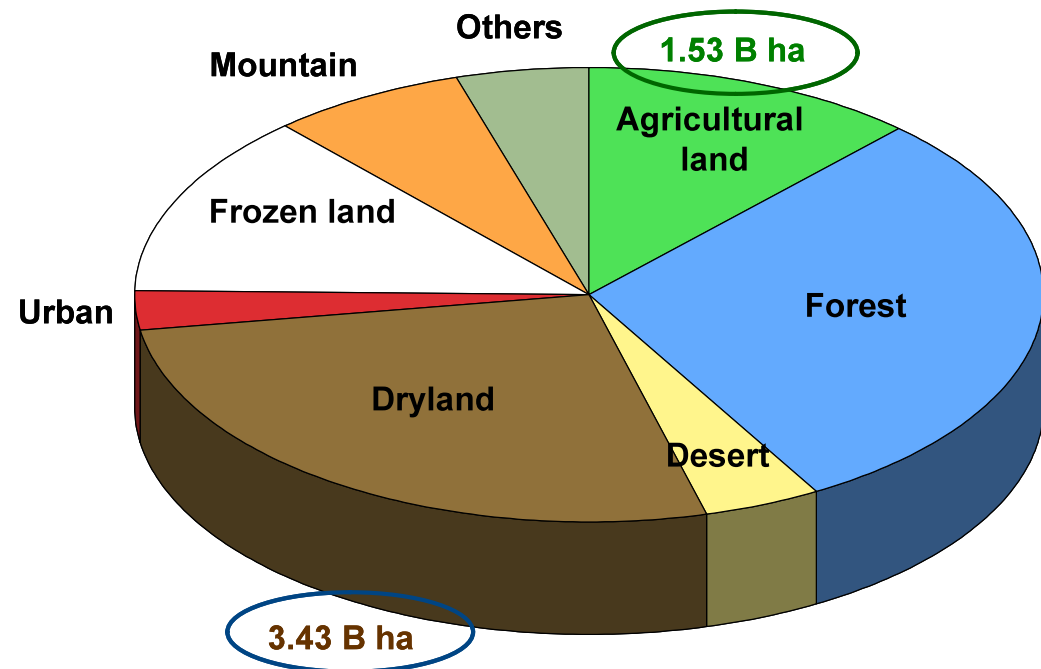
Source: Farm Foundation, NFP calculations (2010) based on USDA ERS data.



# Land is a limiting resource for plant productivity



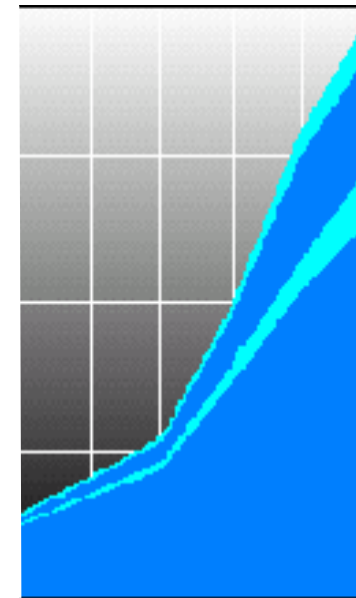
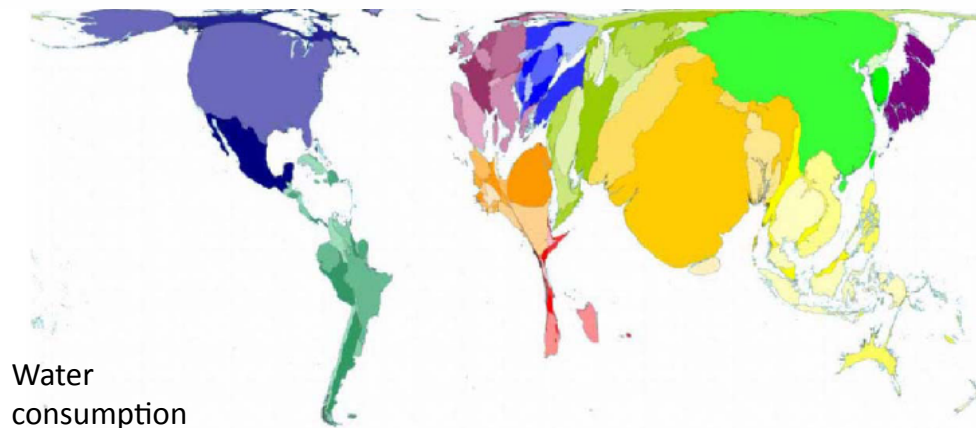
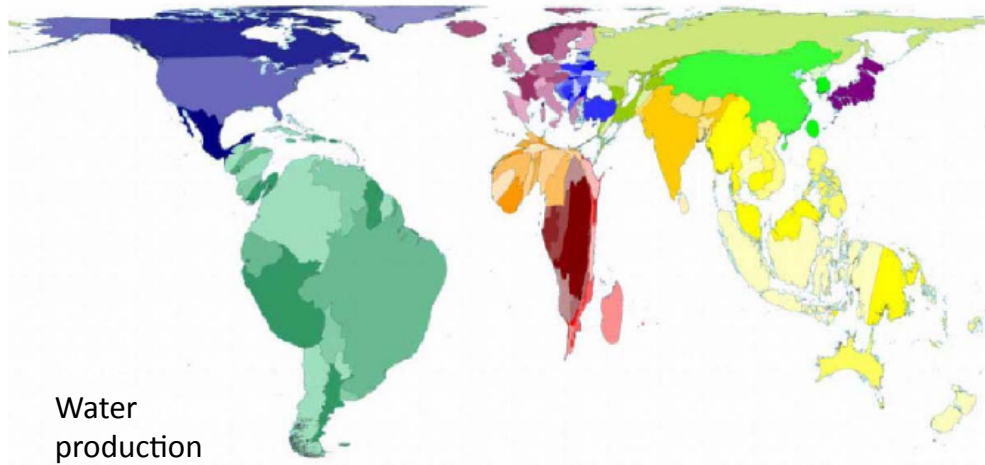
*Total land on earth:  
12.8 billion hectares*



decline  
from 0.38 hectares in 1970 to  
0.15 hectares per person in 2050

# Water is a limiting resource for plant productivity

*Worldwide, 70% of all water is used for agriculture*



L/day/person used

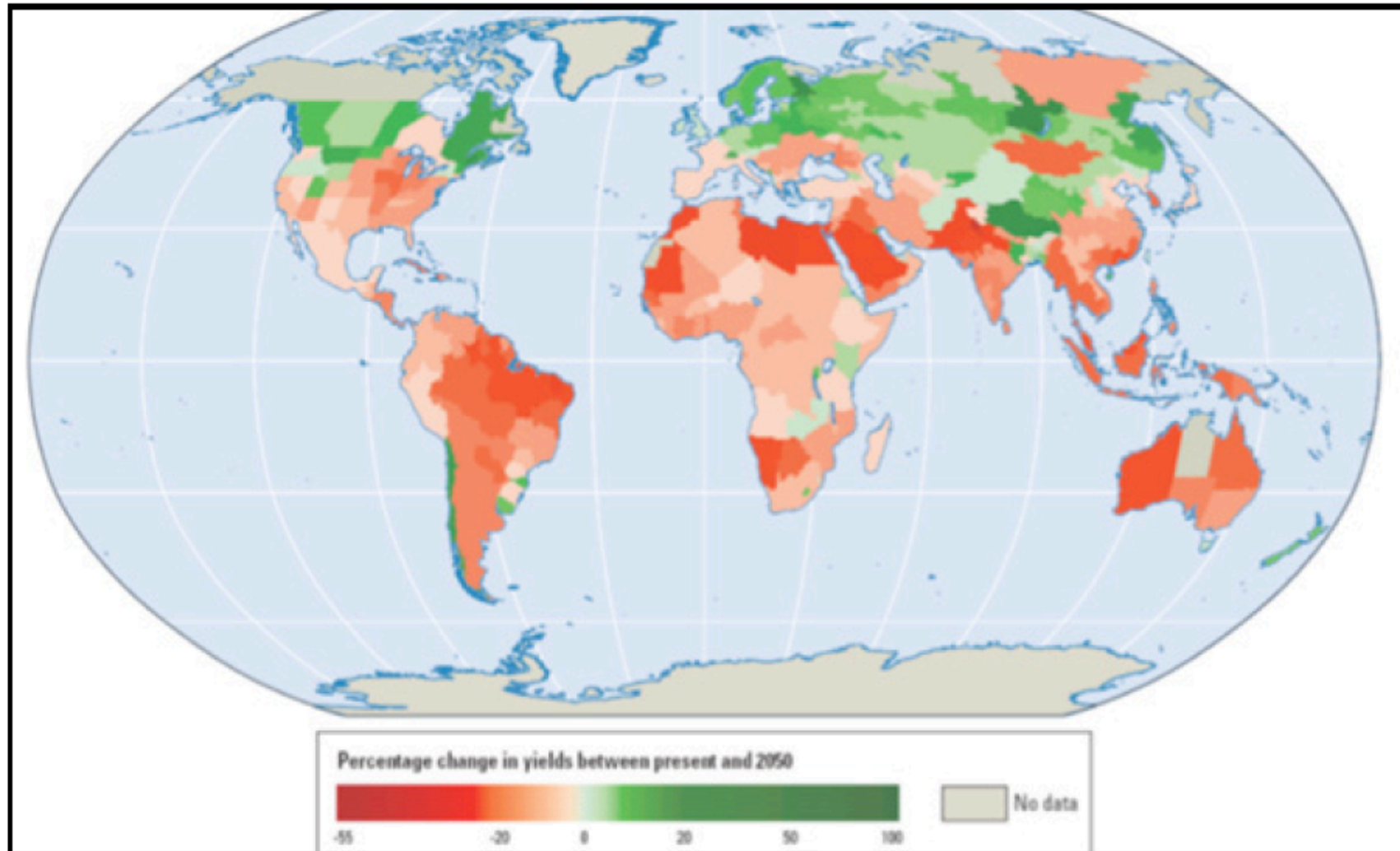
- AU 1,440
- EU 210
- USA 617
- Africa 48

- World water consumption doubled over the last 50 years
- Still 1.3 billion people do not get enough drinking water, by 2050 this number could double

Source: United Nations Environment Program 2005

# Predicted impact of global climate change on agricultural productivity

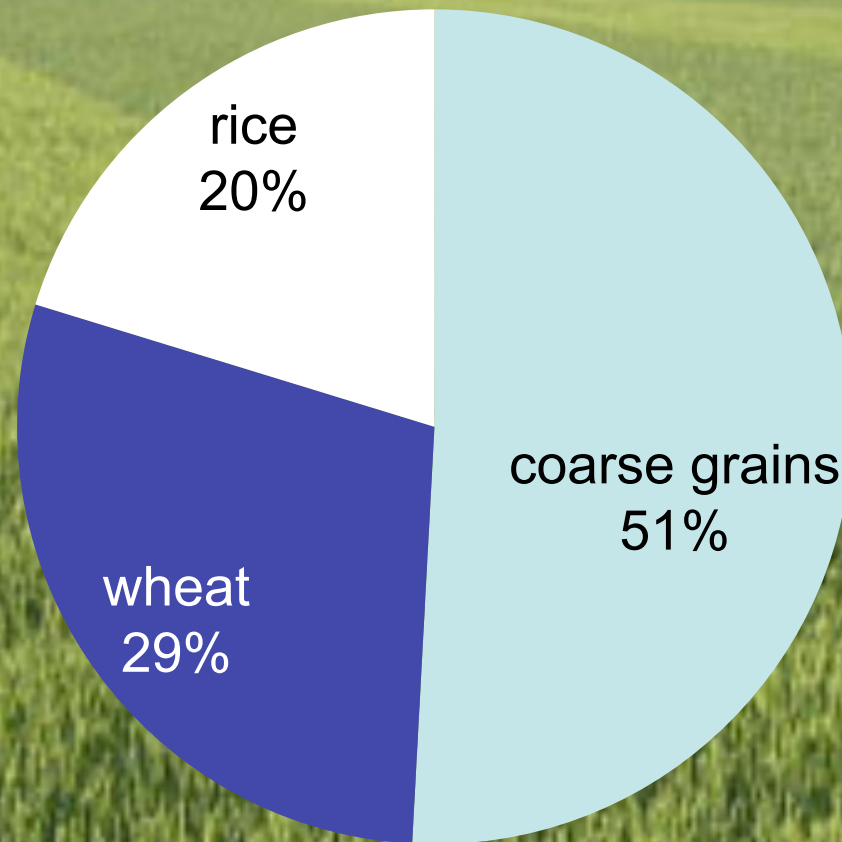
Figure 5.1. Impact of climate change on potential agricultural yields by 2050



Source: World Bank 2009b

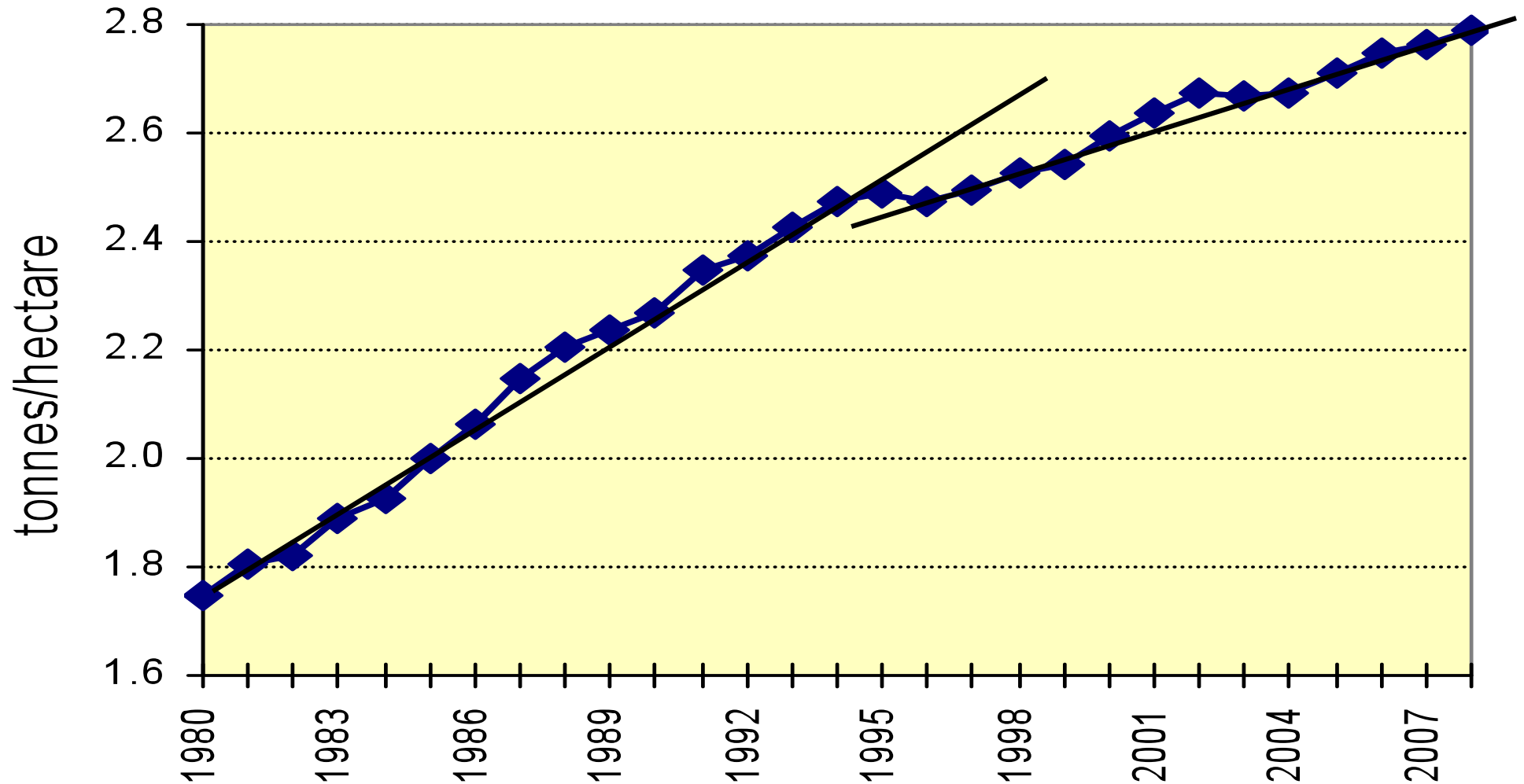


# Grasses provide the bulk of human nutrition



# WORLD WHEAT YIELD TRENDS

(5 Year Moving Average - tonnes/ha)



Source: Chudleigh, 2008

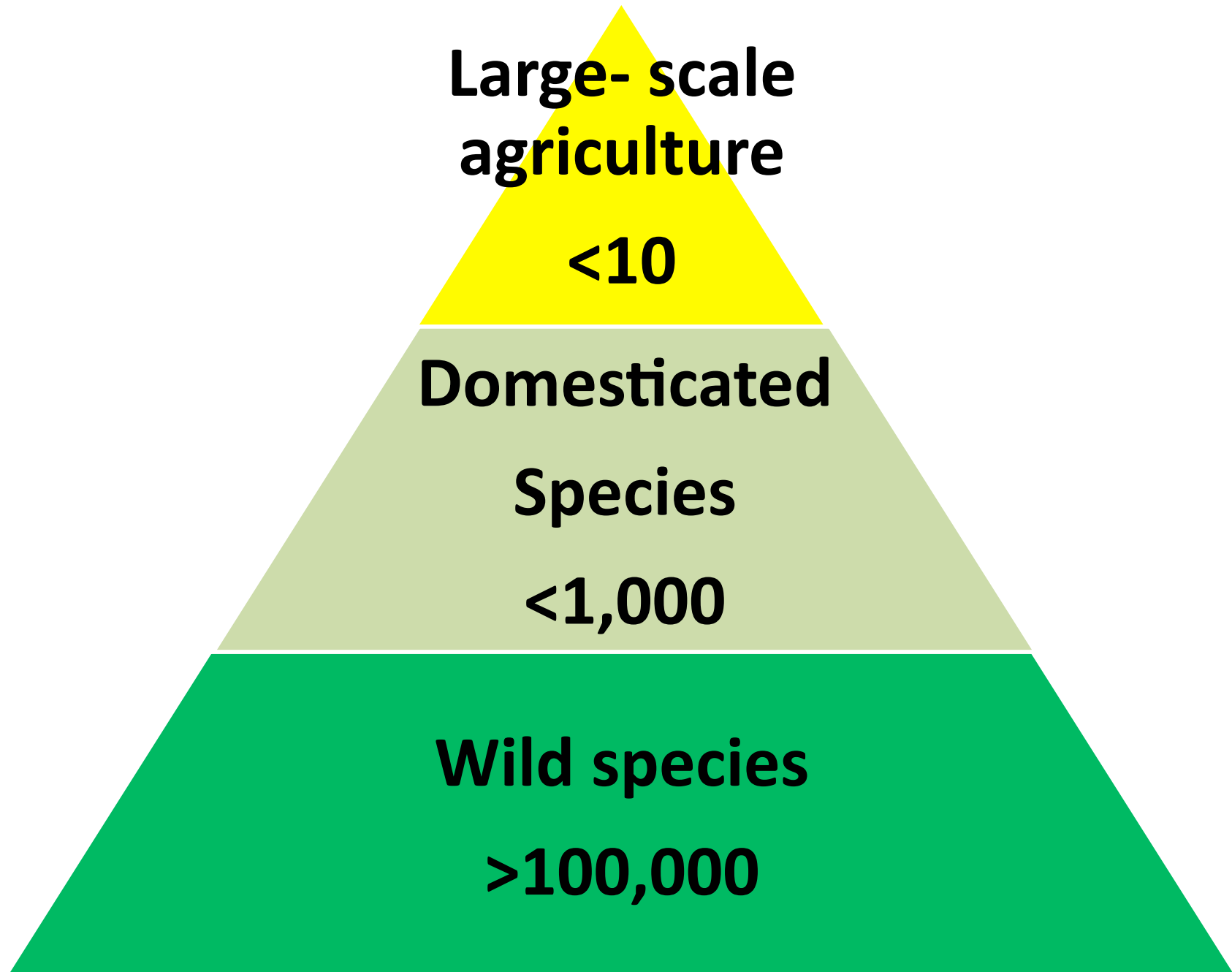


# Understand to exploit

- More from less: 2x by 2050 (“Sustainable intensification”)

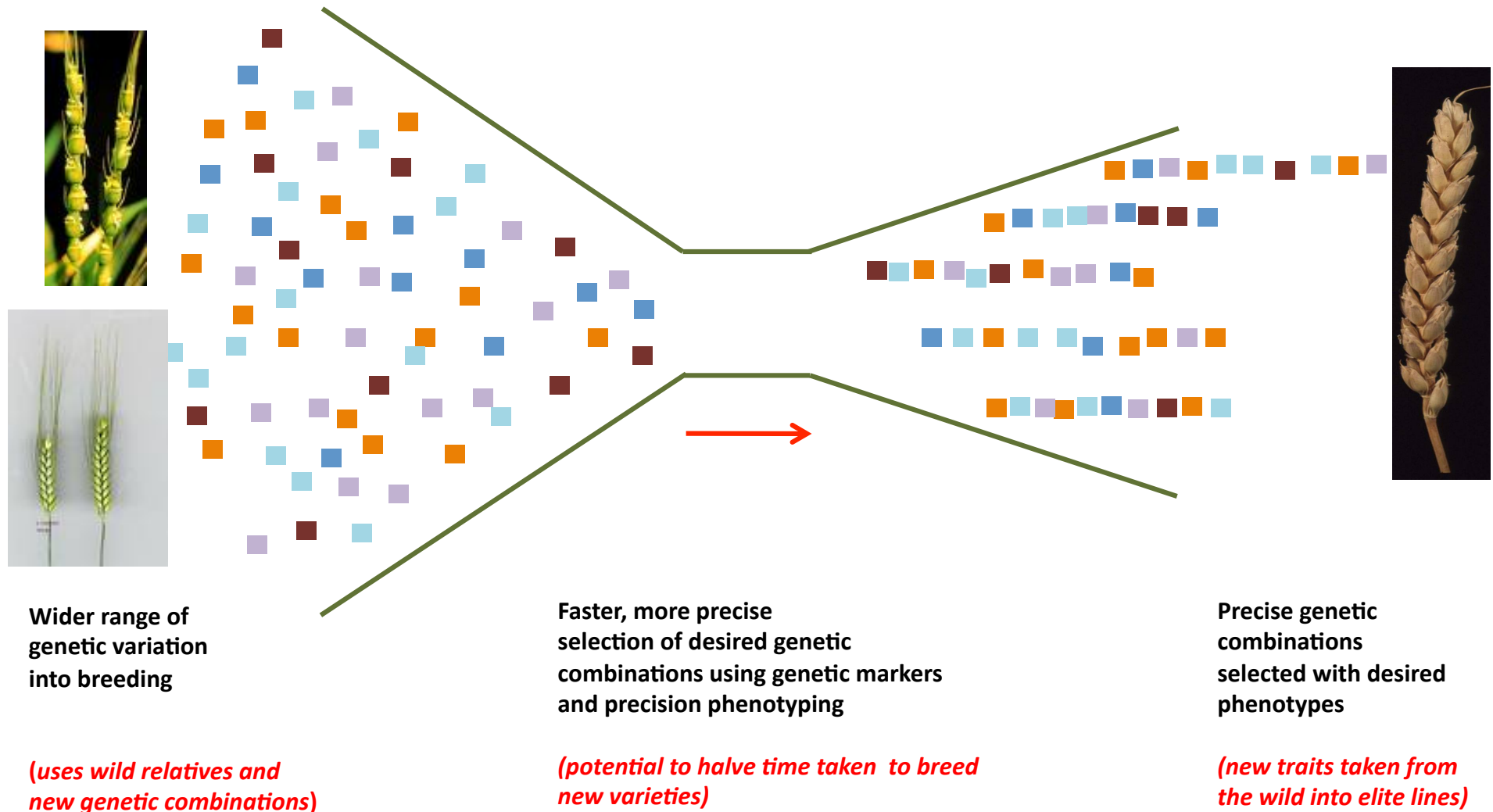


**Most of our food comes from a few domesticated species**





# Genomics can accelerate plant breeding using more diverse germplasm

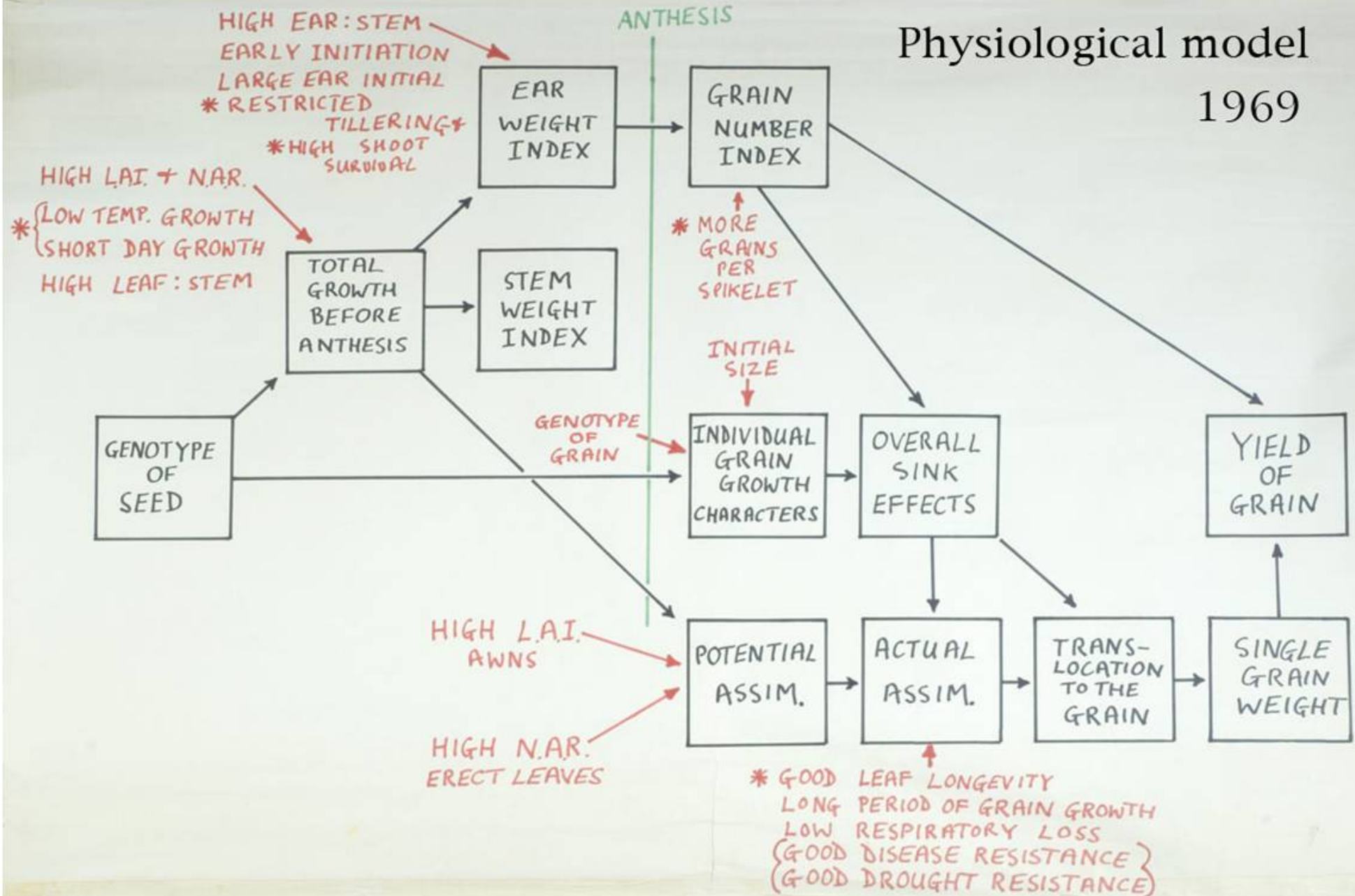


# Advanced crop breeding systems

- Genome sequencing of multiple lines
- High throughput genotyping
- Greater understanding of gene function using model systems such as Arabidopsis and Brachypodium
- Efficient gene transfer systems
- Exploiting new sources of genetic variation
- More efficient breeding pipeline from the lab to the field



# Physiological model 1969

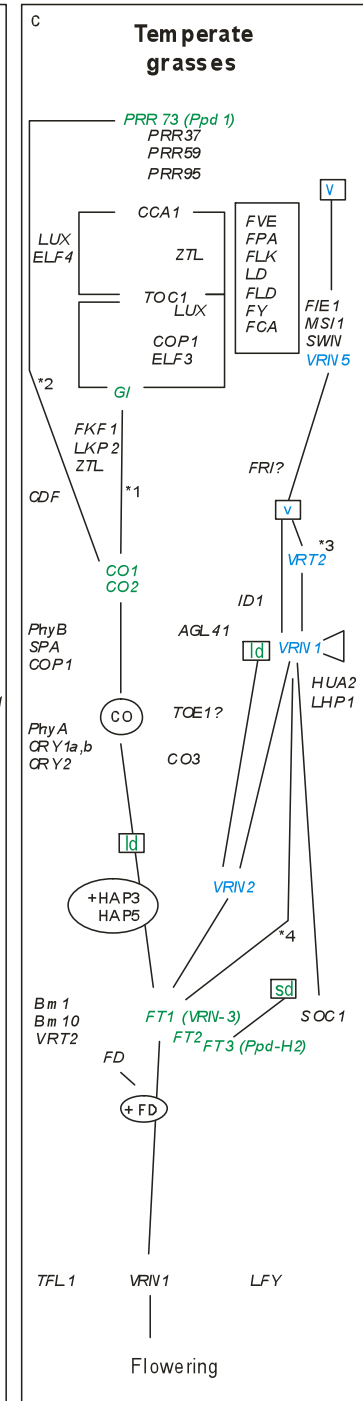
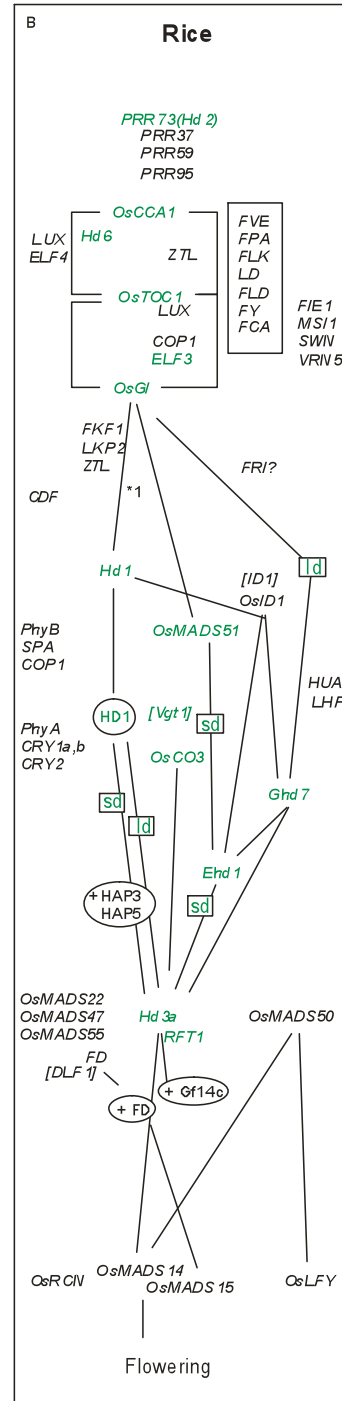




The diagram illustrates a genetic regulatory network with the following components and interactions:

- Inputs:** LUX and ELF4 (green) activate CCA1 and LHY (green).
- Intermediate Nodes:**
  - CCA1 and LHY activate PRR7 and PRR9 (green).
  - PRR7 and PRR9 activate PRR5 and PRR3 (green).
  - PRR5 and PRR3 activate ZTL (green).
- Regulation:**
  - ZTL inhibits TOC1 and LUX (green).
  - TOC1 and LUX activate COP1 and ELF3 (green).
  - COP1 and ELF3 inhibit GI (green).
  - GI inhibits LUX and ELF4 (green).

The diagram uses black lines for activation and T-bars for inhibition. A green oval labeled "+GI" is next to the ZTL node.

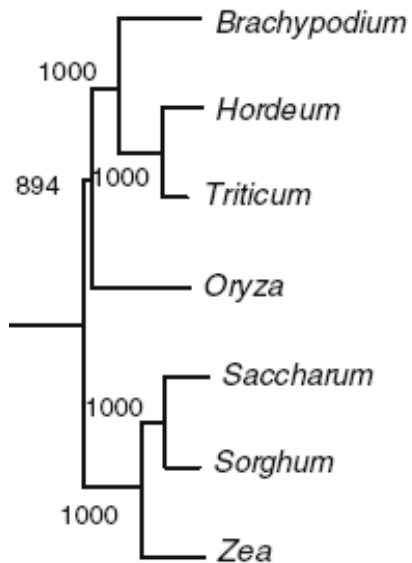


# Economically significant grass sub-families

## Ehrhartoideae

### Oryza

*Oryza sativa* (rice)



## Panicoideae

### Paniceae

*Panicum* (switchgrass)

### Andropogoneae

*Sorghum*

*Saccharum* (sugarcane)

*Zea* (maize)

*Miscanthus*

## Pooideae

### Aveneae

*Avena* (oat)

### Brachypodieae

*Brachypodium*

### Triticeae

*Hordeum* (barley)

*Secale* (rye)

*Triticum* (wheat)

### Poeae

*Lolium*

*Festuca*

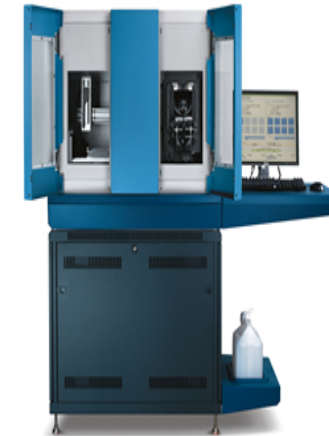
# Genome analysis technology is changing



454 XLR



Illumina Hi Seq

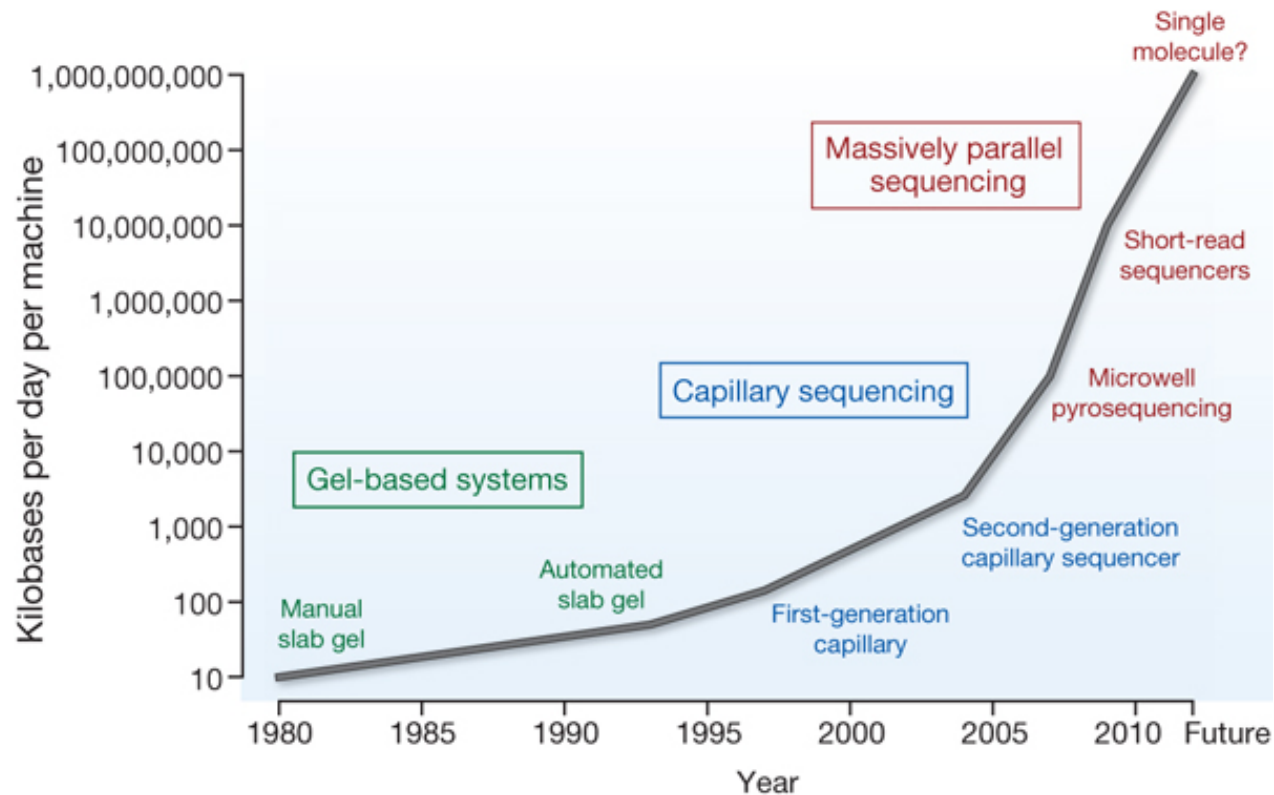


SOLiD/ABI

|               |             |               |               |
|---------------|-------------|---------------|---------------|
| bases/read    | 500         | 35            | 50            |
| Read length   | >750        | 120           | 50            |
| Bases per run | 500,000,000 | 2,000,000,000 | 5,000,000,000 |
| cost/run      | £4000       | £3000         | £6000         |
| Cost/kb       | £0.016      | £0.003        | £0.00012      |
| Accuracy      | Very Good   | Excellent     | Very Good     |



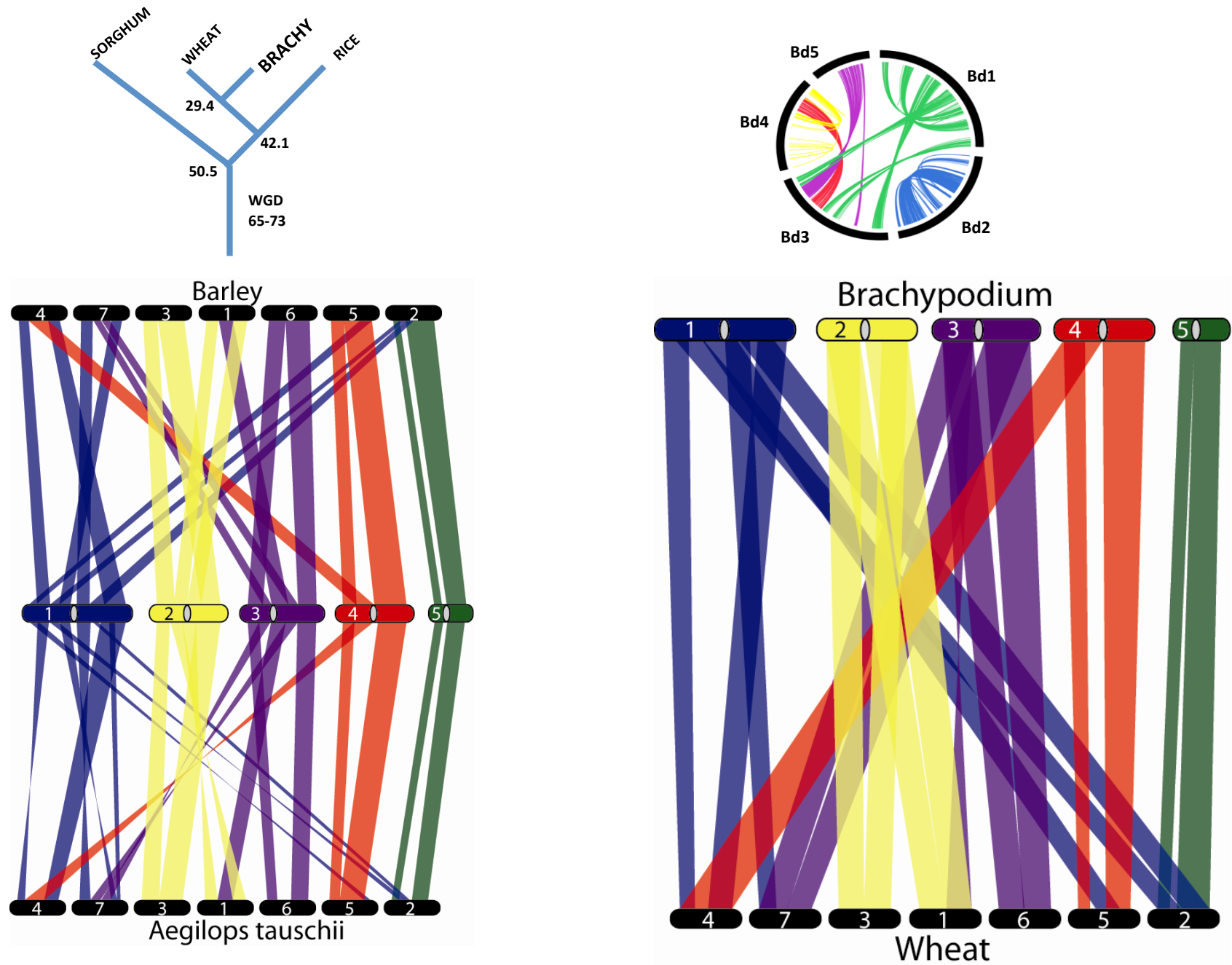
# Improvements in the rate of DNA sequencing over the past 30 years and into the future.



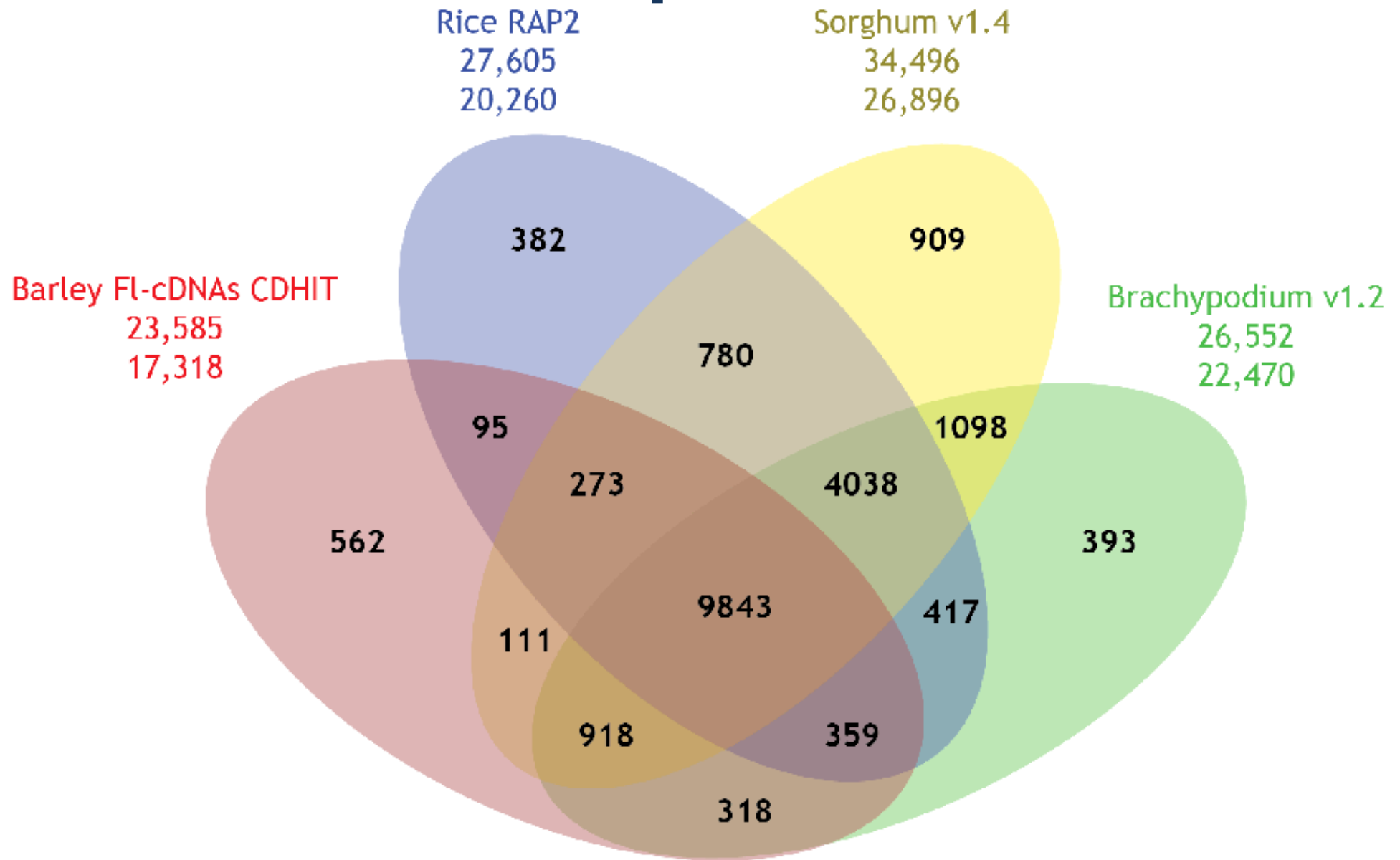
MR Stratton *et al. Nature* **458**, 719-724 (2009) doi:10.1038/nature07943

nature

# Whole genome synteny analysis

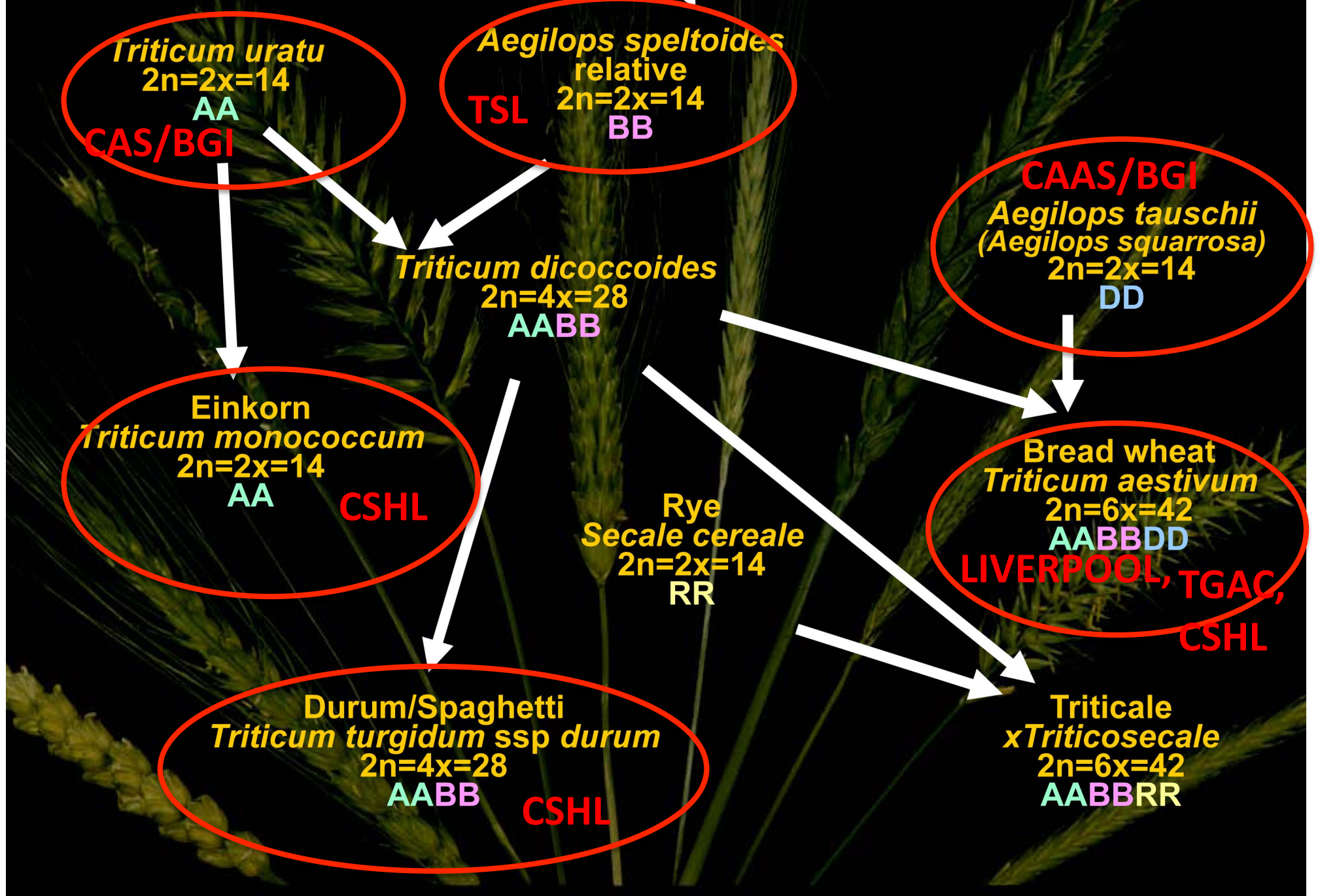


# Defining an orthologous gene set for comparison

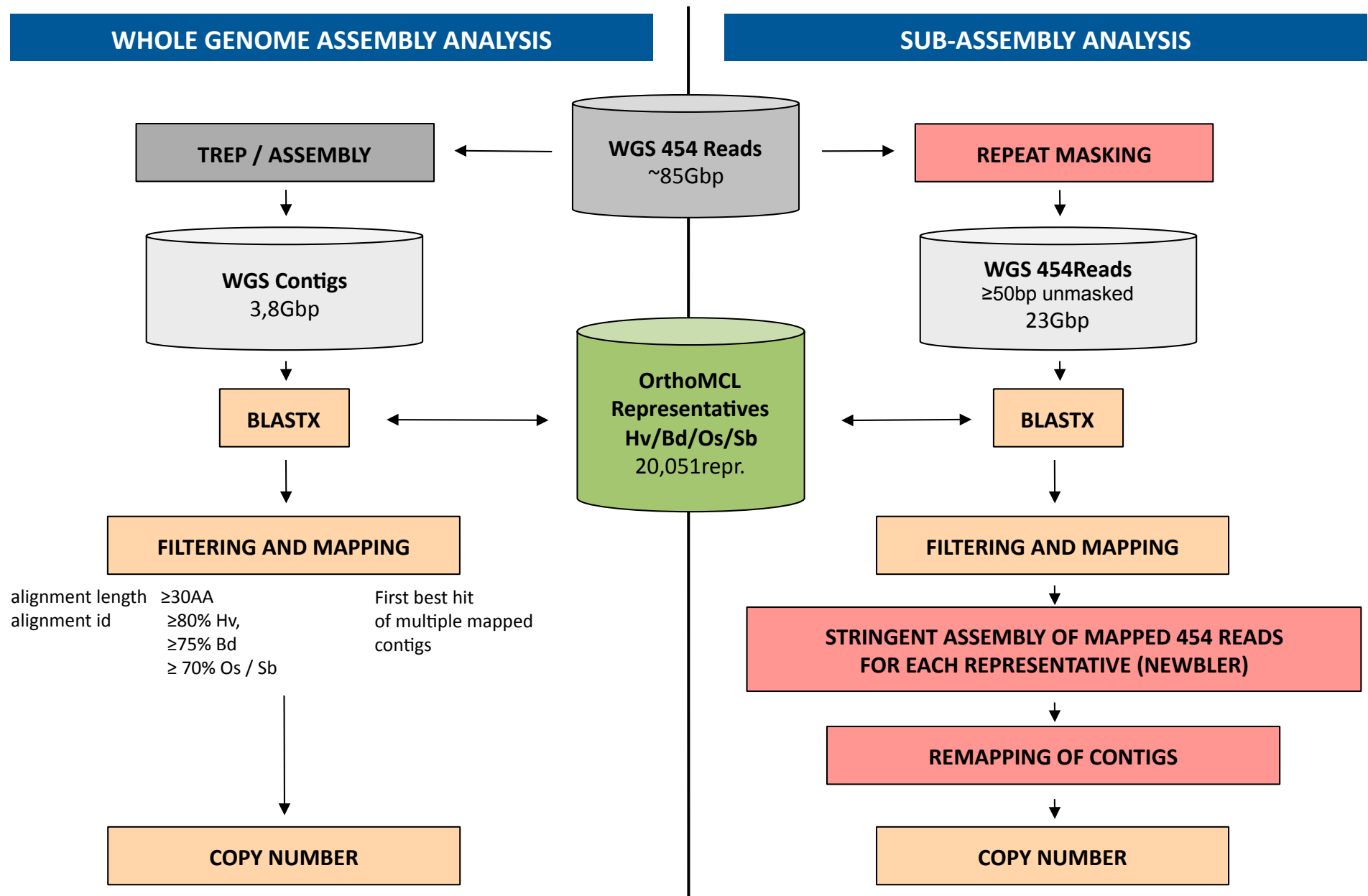




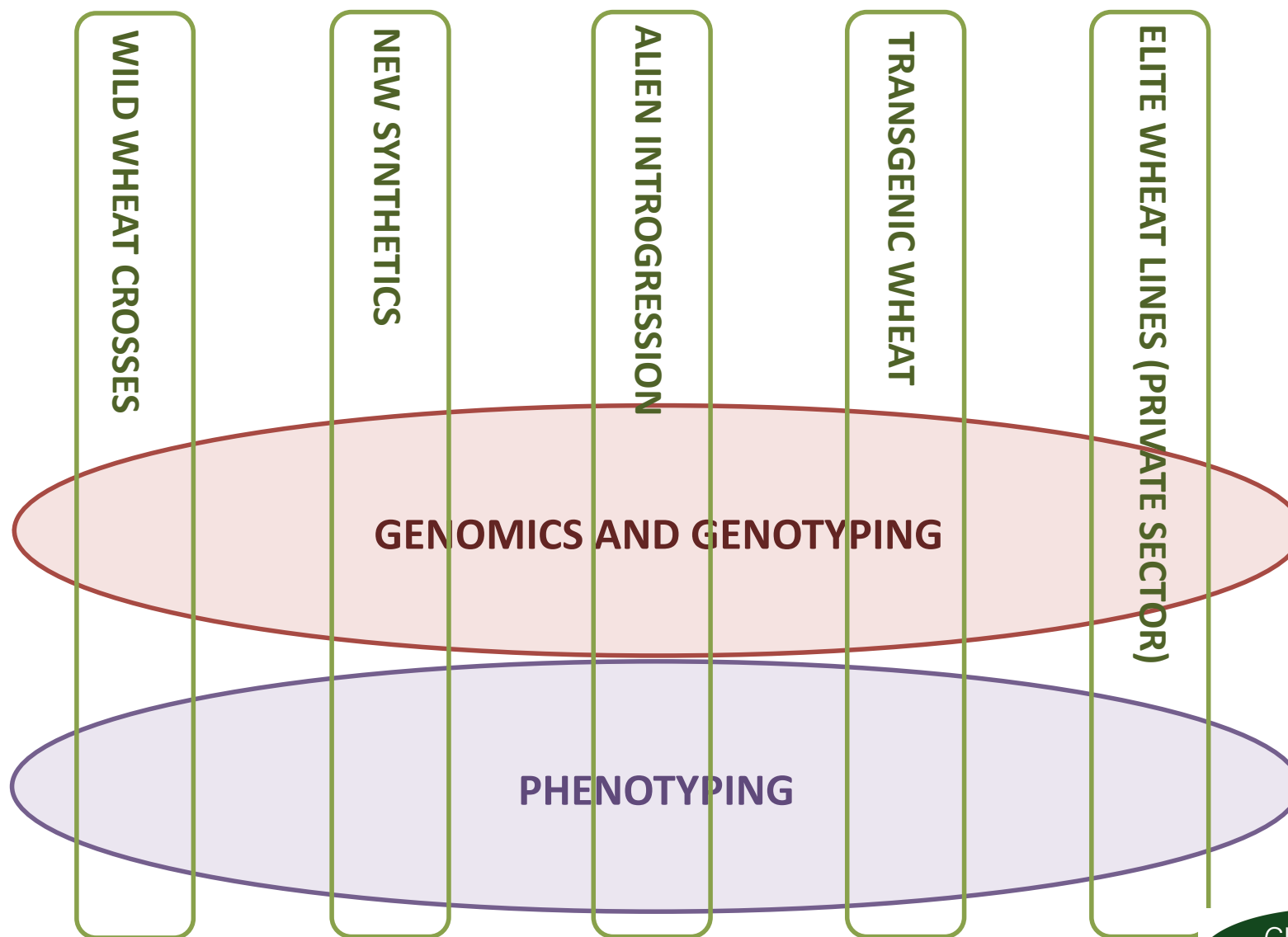
# WHOLE GENOME SEQUENCING ACTIVITIES



# Analysis pipelines for genome sequence



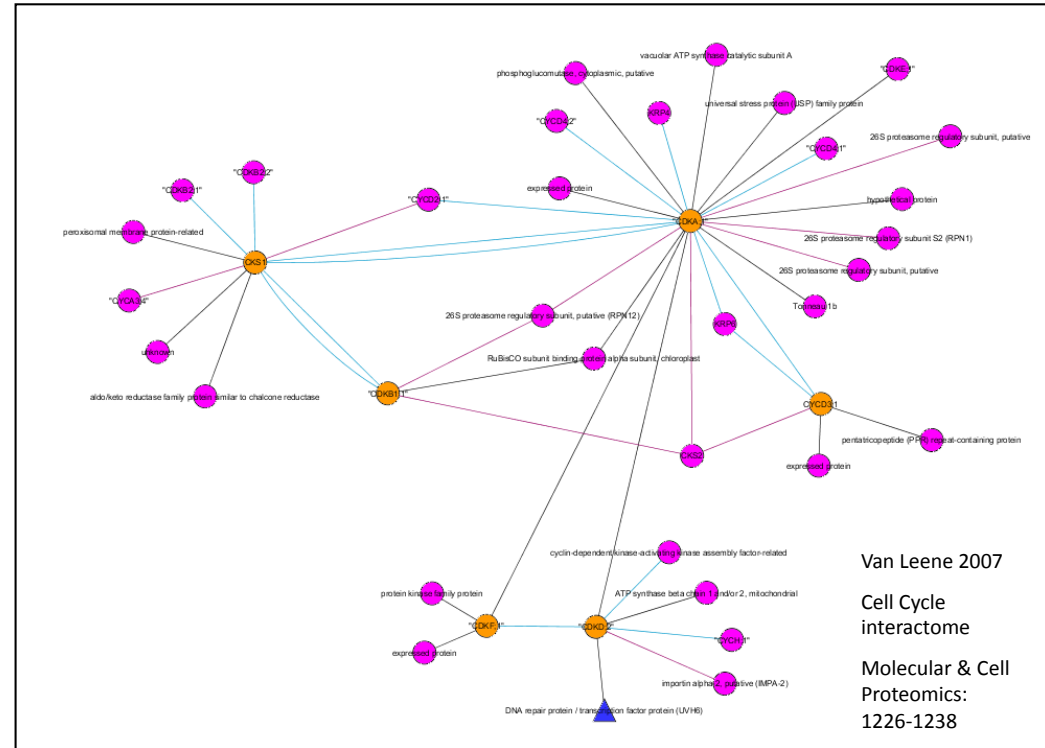
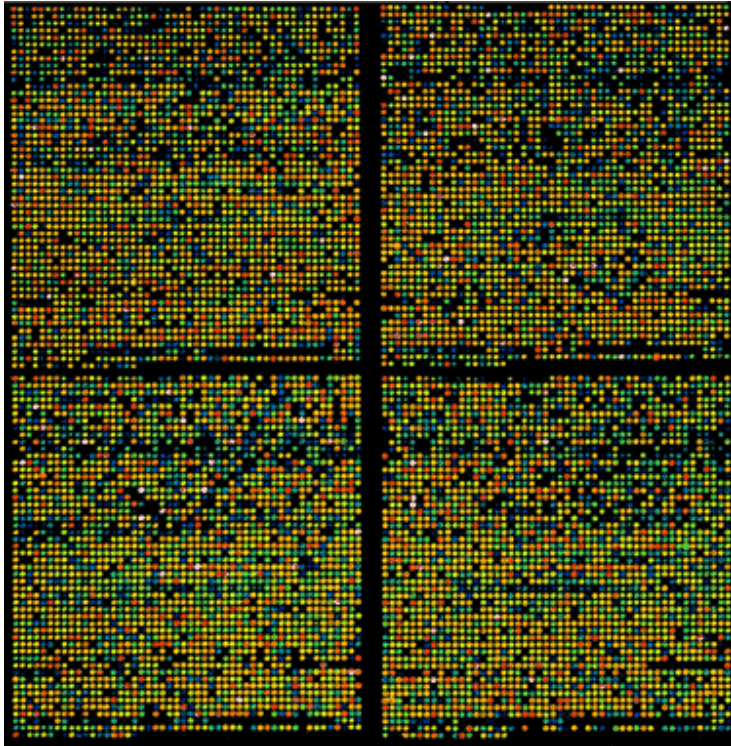
# AN INTEGRATED WHEAT GERmplasm IMPROVEMENT PROGRAMME



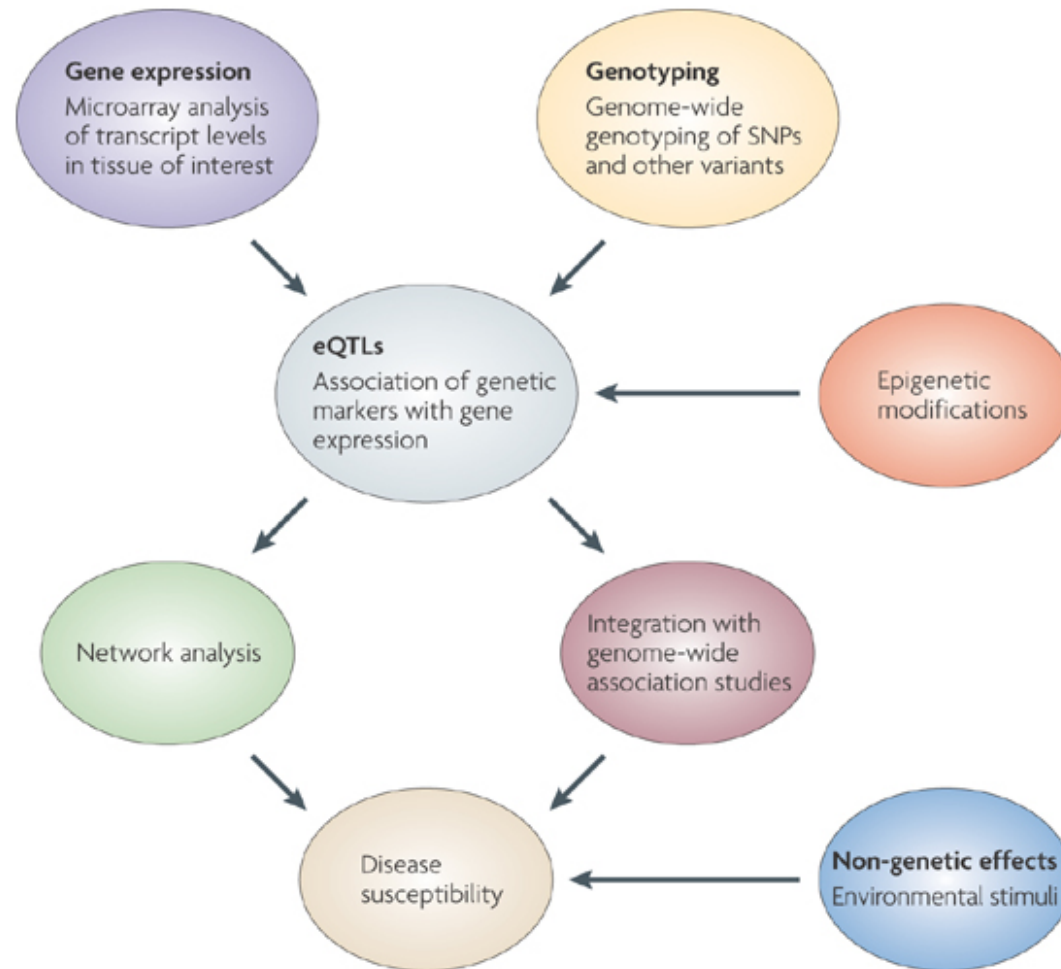
**Graham Moore, JIC**



# GENE NETWORK ANALYSIS



# Systems genetics analysis of complex traits



# The Future – 2011-2015. A WAVE OF NEW & IMPROVED BIOTECH CROPS

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- **Many new crop/trait** options will be ready before 2015
- **Drought tolerance**—principal trait—maize in US 2012/13
- **Biotech rice** – major crop, up to 1 billion beneficiaries
- **Quality traits** – Golden Rice in 2013, omega-3, others
- More biotech crops developed by countries from the South in public inst. – **more South-South cooperation**
- Biotech applications for “**Speeding the breeding**” – MAS and biotech crops, to provide a faster response to more severe and rapid changes in climate change
- **Asia will grow more in 2nd decade** than first decade

# ISAAA Prediction for 2<sup>nd</sup> Decade, 2006-2015



|                                            | 2006                 | 2010                 | 2015                  |
|--------------------------------------------|----------------------|----------------------|-----------------------|
| <u># of Biotech Countries</u>              | 22                   | 29                   | ~ 40                  |
| <u># of Farmers Planting Biotech Crops</u> | 10 Million           | 15.4 Million         | ~ 20 Million          |
| <u>Global Biotech Area m. hectares</u>     | 100 Million Hectares | 148 Million Hectares | ~200 Million Hectares |

Source: Clive James, 2011



# Acknowledgements

- Neil McKenzie, Cristobal Uauy, Andreas Magusin (JIC)
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