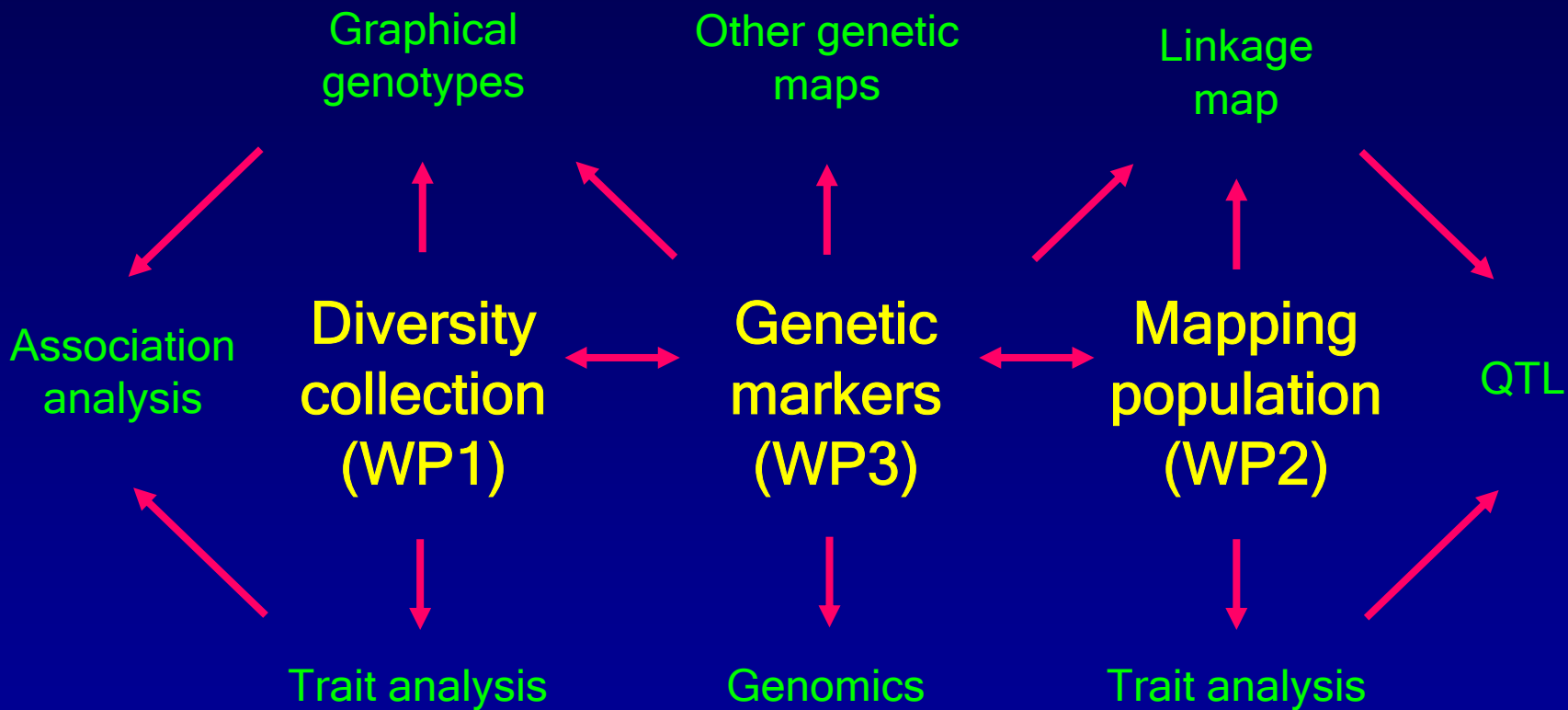


# OREGIN Plant Genetic Resources



Graham Teakle

Warwick HRI OREGIN project co-ordinator



# Diversity Collections

Genebanks - 1000s of accessions

Core collections - 100s of accessions

Diversity Fixed Foundation Sets (DFFS)

# DFFS

A structured set of genetically fixed lines representing a snapshot of diversity across the relevant genepool

- Immortal lines
- Homozygous alleles in marker assays
- Replicated trait testing
- Standard reference sets for diversity analysis

# Diversity Fixed Foundation Sets

Genetic resource accessions (1000s)



Representative subsets (2x 94 = 188)



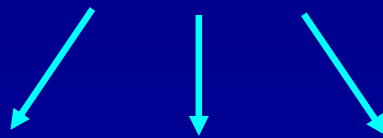
Founder plants



Archive:  
DNA  
seed



Fix (DH, single seed descent)



Multiply seed, DNA and distribute



Archive:  
DNA  
seed

\*\*\* PUBLIC DOMAIN \*\*\*

# DFFSs being generated



<i>B. napus</i>	188 lines	Defra/OREGIN Graham Teakle, Graham King, Dave Astley, Dave Pink
<i>B. oleracea</i>	376 lines	Defra/core breeding Graham King, Dave Astley, Dave Pink, Graham Teakle
<i>Brassica</i> C-genome species	94 lines	Defra/core breeding Dave Pink

# OREGIN DFFS - 188 lines



Base on EU GenRes core collection of 211 lines



Substitute with *B. napus* mapping parents



Substitute with other key vars



Substitute with fixed lines as they are donated



Substitute as advised by reviewers



Substitute with outliers from related species

Cytometric testing to confirm identity as *B. napus*

# BnDFFS composition



Winter OSR	<i>oleifera biennis</i>	one third
Spring OSR	<i>oleifera annua</i>	one third
Non-oilseed types:		one third
• Swede	<i>napobrassica</i>	
• Forage/fodder/leafy kale	<i>napus biennis/annua</i>	
• Siberian kale/Hanover salad	<i>pabularia</i>	
• Synthetics/Hakuran kale		
• Do the proportions of this breakdown seem balanced?		
• Is the representation from different ecogeographical regions balanced?		
• Donation of fixed lines?		

# MTAs



It is planned that the DFFS will be distributed under a simple MTA

The two key elements are:

- Public domain
- Limit liability to Warwick HRI

The full details will be posted when available

# TN Mapping Population - IMSORB

Jinling Meng, China

Ian Bancroft, JIC



## Tapidor

- Winter
- OO
- France
- TAC/BAC libraries

X



## Ningyou-7

- Semi-winter
- ++
- China

201 DH lines

\*\*\* PUBLIC DOMAIN \*\*\*

Map by Nov 2004

- 100 communal RFLPs (mostly from Tom Osborn)
- 100 SSR markers (BBSRC)
- Upto 500 SNPs

QTL data accumulating

# Summary of marker analysis

## Mostly SSRs in the first instance

- Genetically mapped/distributed over the genome/linked to genes of interest
- Sequence tagged
- Public domain
- Quality tested

## Diversity analysis

- Diversity estimates
- Graphical genotypes
- Association analysis .....

## Map in TN population

- Alignment of TN map with other maps (e.g. DY)

## Quality control