

# Developing a C genome diversity set

Dave Pink, Paul Hand, Sandy  
McClement, Liz Bailey and  
Helen Mayne

# Brassica 'C' genome wild species

98 accessions covering 14 species

- *B. alboglabra* (1)
- *B. atlantica* (2)
- *B. balearica* (1)
- *B. bourgaei* (1)
- *B. cretica* (8)
- *B. hilarionis* (3)
- *B. incana* (11)
- *B. insularis* (4)
- *B. macrocarpa* (16)
- *B. maurorum* (1)
- *B. montana* (4)
- *B. oleracea* (28)
- *B. rupestris* (5)
- *B. villosa* (13)

# Strategy

Sow 2 plants/accession

When a plant flowers!

Extract DNA  
sample

Archive  
sub  
sample

GenomiPhi

Screen with panel  
of mapped SSRs

Cross to AGSLDH150

MC F1s

Select SC, 'rapid'  
flowering DH lines

Screen with panel of  
SSRs

Select 3-4 DH lines to  
maximise wild sp alleles

Produce seed

Self to produce S1  
seed

# Progress to date

- 94 accessions - 2 misclassified, 2-plants died
- 6 accessions - plants still not flowered after 4 yrs!
- DNA extracted from all plants (genomiPhied when crossed to *oleracea* successfully)
- SSR screening initiated
- 84 accessions -selfed to produce S1 seed
- 79 accessions - crossed to *B. oleracea* - min 50 seeds
- Embryos produced from 28 F1 lines

