

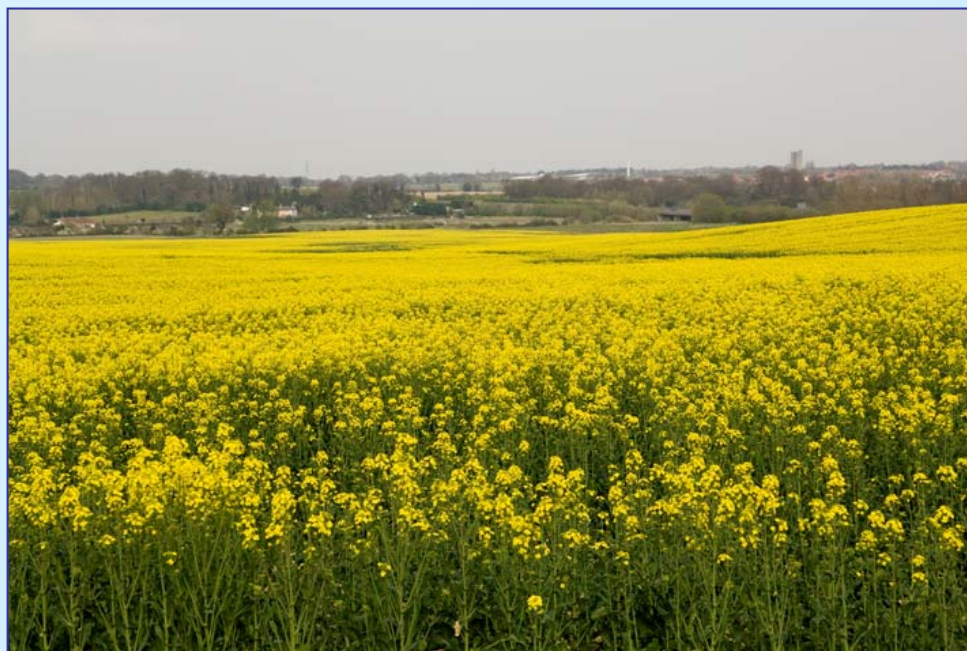


**Update:**

## **Brassica Genome Sequencing**

**Ian Bancroft**

**21<sup>st</sup> May 2008**



## Agreed methodology for the *B. rapa* Genome Sequencing Project

Sequencing Chinese cabbage var. Chiifu using a BAC-by-BAC approach focussed on gene space, with allocation by chromosome

~600 seed BACs sequenced in Korea and genetically mapped on CKDH population, with mapping of Chiifu alleles in BACs confirmed

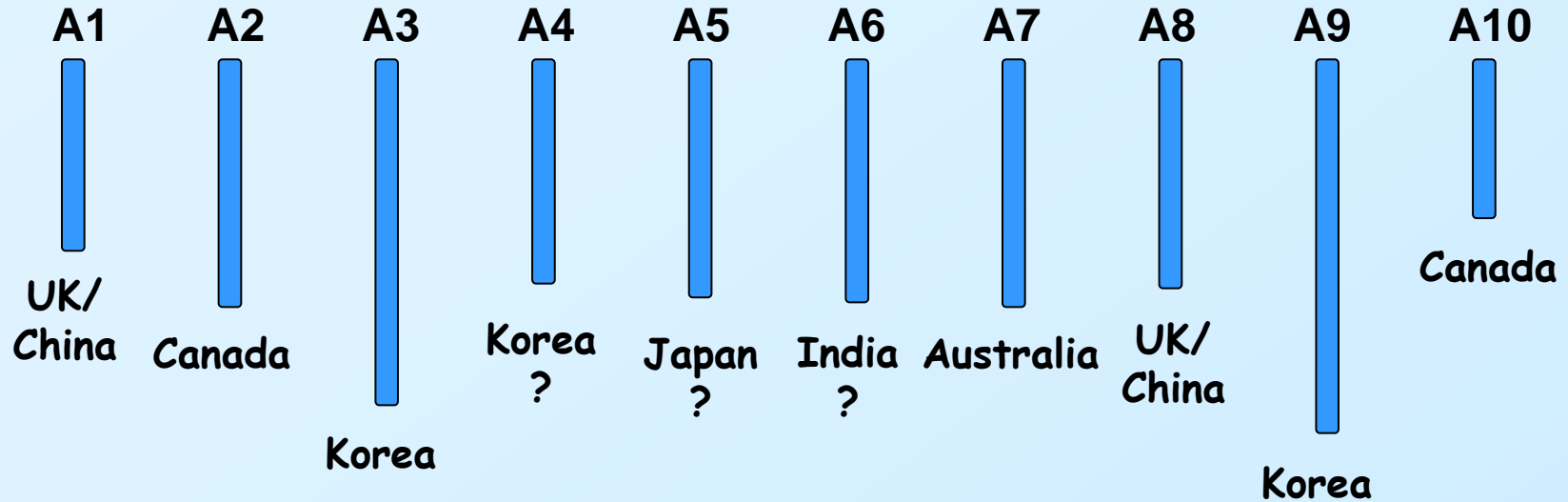
110,000 BAC clones end-sequenced by international consortium

Walking from seed BACs via end-sequences

BACs finished to Phase 2 standard (single ordered and oriented sequence contig, but some gaps and ambiguous bases permitted)

All trace files to be deposited in public databases to enable “finishing” of specific BACs

## *B. rapa* Genome Sequencing Project



Participation in full BAC sequencing (May 2008):

7 Chromosomes funded for sequencing of gene space

3 Chromosomes funding actively being sought

# BBSRC-funded project

Sequencing conducted in China, funded by BBSRC

Collaboration between JIC, WHRI, RRes, BGI, WAU

Aim to:

Sequence 700 BAC clones, corresponding to the gene space of two medium-sized chromosomes, A1 and A8

End-sequence *B. napus* JBnB BAC library (73,728 clones)

Annotate BAC sequences

Develop comparative displays to link through to genetic maps and QTL

# BBSRC-funded project

Started July 2007

Progress at May 2008:

99 BACs sequenced to Phase 2 standard

25 putatively on A1

26 putatively on A8

3 re-mapped to other linkage groups

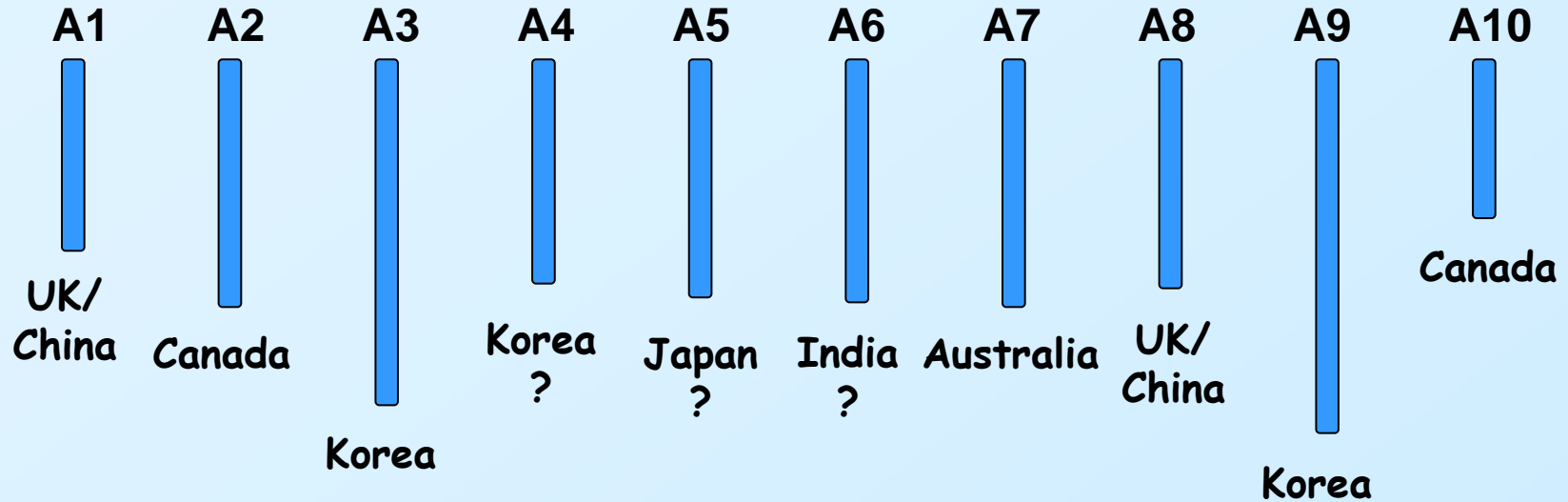
45 new seed BACs (to complement existing)

12,276,763 bp in all

Plus 9 potential seed BACs completed to Phase 1 only

20,954 *B. napus* BAC ends received (53% success rate)

## *B. rapa* Genome Sequencing Project



Data released into public domain (May 2008):

2005-2008 Korea: 522 seed BACs

0 chromosome BACs

2006-2008 Australia: 0 seed BACs

1 chromosome BAC

2007-2008 BBSRC: 54 seed BACs

54 chromosome BACs

# BBSRC-funded project

BAC registry (<http://www.brassica.info/resource/sequencing/status.php#>)

Transferred to RRes December 2007

Updated monthly

BAC annotation (<http://brassica.bbsrc.ac.uk>)

Predicted genes (FGENESH)

Assembly gaps

BLAT alignment to Arabidopsis genes

BLAT alignment to JIC/JCVI/Cogenics microarray unigenes

BLAST alignment to *B. rapa* BAC end sequences

BLAST alignment to *Brassica* IGF probes

BLAST alignment to sequenced genetic markers

SSR motif identification and primer design

Restriction sites

# BBSRC-funded project

## Confirmation of anchoring of seed BACs

### FISH mapping (Pires lab)

10 confirmed on A1/8

2 on other chromosomes

### Linkage mapping (Guy Barker, Graham Teakle)

14 confirmed on A1/8

6 on other linkage groups



# Acknowledgements

Bioinformatics, initial annotation

Nizar Drou, Martin Trick

Clone selection, validation, sequence QA

Fiona Fraser, Eleni Soumpourou, Ian Bancroft

Genetic mapping

Guy Barker, Graham Teakle

BAC registry

Graham King