



Update:

Brassica Genome Sequencing

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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

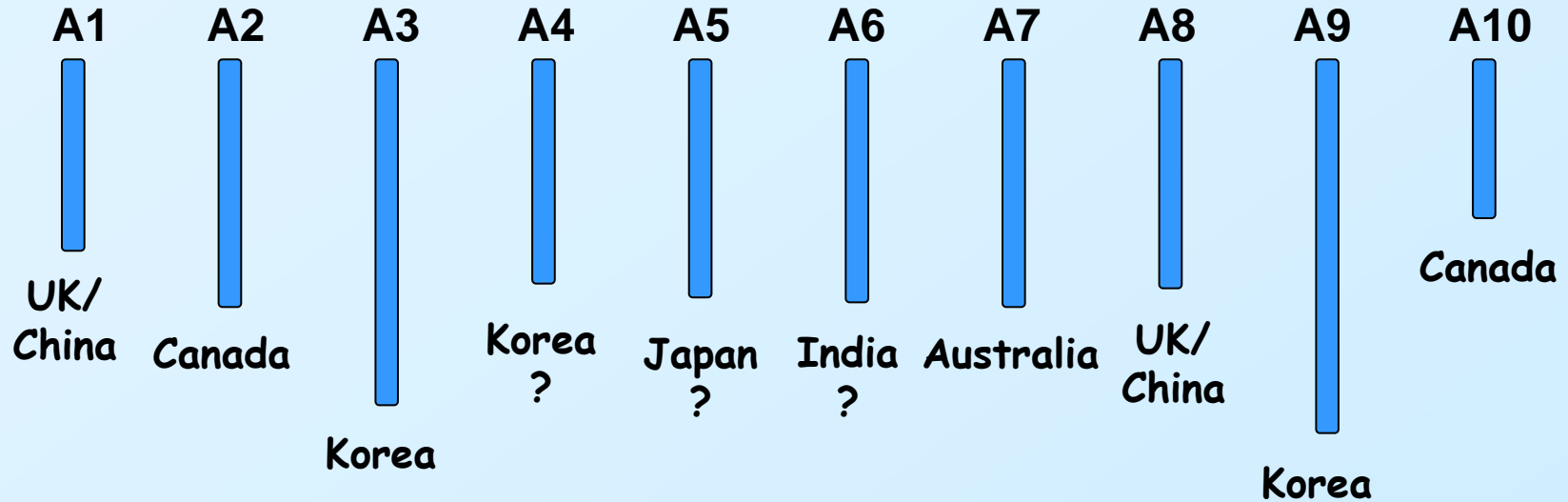
110,000 BAC clones end-sequenced by international consortium

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

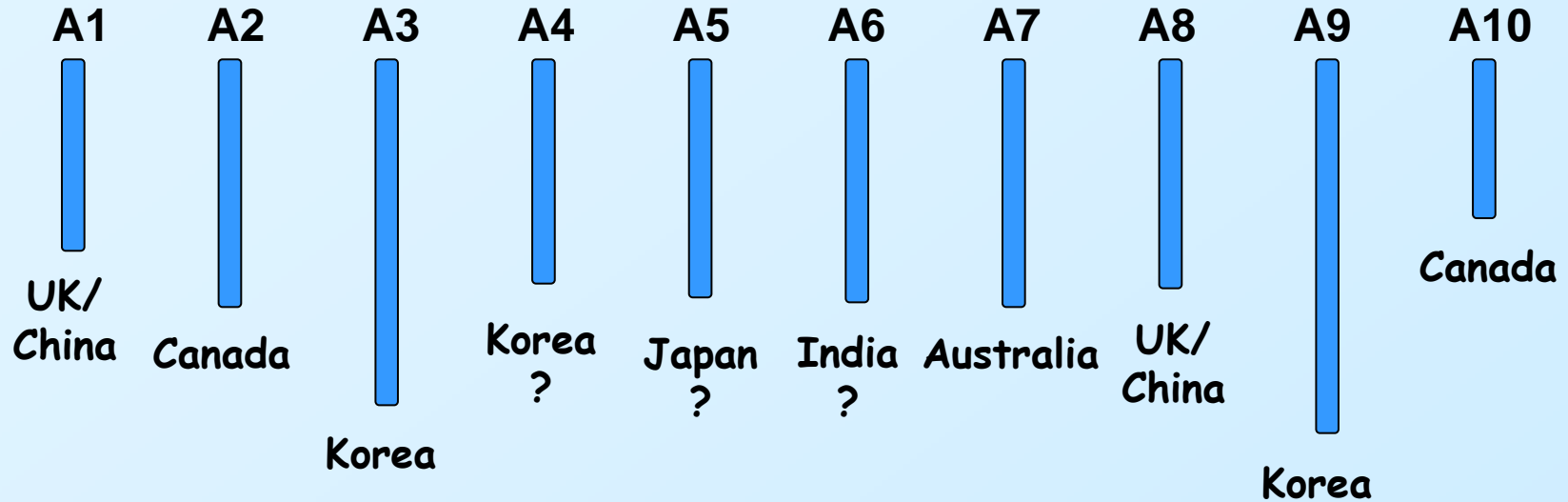
45 new seed BACs (to complement existing)

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