



Update:

Progress in *Brassica* Genome Sequencing

Ian Bancroft

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Brassica rapa Genome Sequencing Project

1014 BAC clones sequenced (345 from BBSRC project)

- Sequences in public databases
- Annotation and sequences available from *Brassica* Genome Gateway (<http://brassica.bbsrc.ac.uk/>)
- BrassEnsembl display available from [brassica.info](http://www.brassica.info) (<http://www.brassica.info>)

Chris Love will describe

Brassica rapa Genome Sequencing Project

In 2009, incorporated Chinese *B. rapa* sequencing initiative

- Whole genome shotgun (Illumina) + BAC end sequences
- Represents 284 Mb gene space in 40,509 scaffolds (half of the genome is represented in scaffolds >339kb)
- 90% of genome sequences anchored to linkage maps
- Identified 41,174 protein-coding genes
- Manuscript nearing completion; data release early July?



Xiaowu Wang, Jian Wu, Hanwen Huang, Rifei Sun, Xixiang Li, Bo Liu, Silong Sun

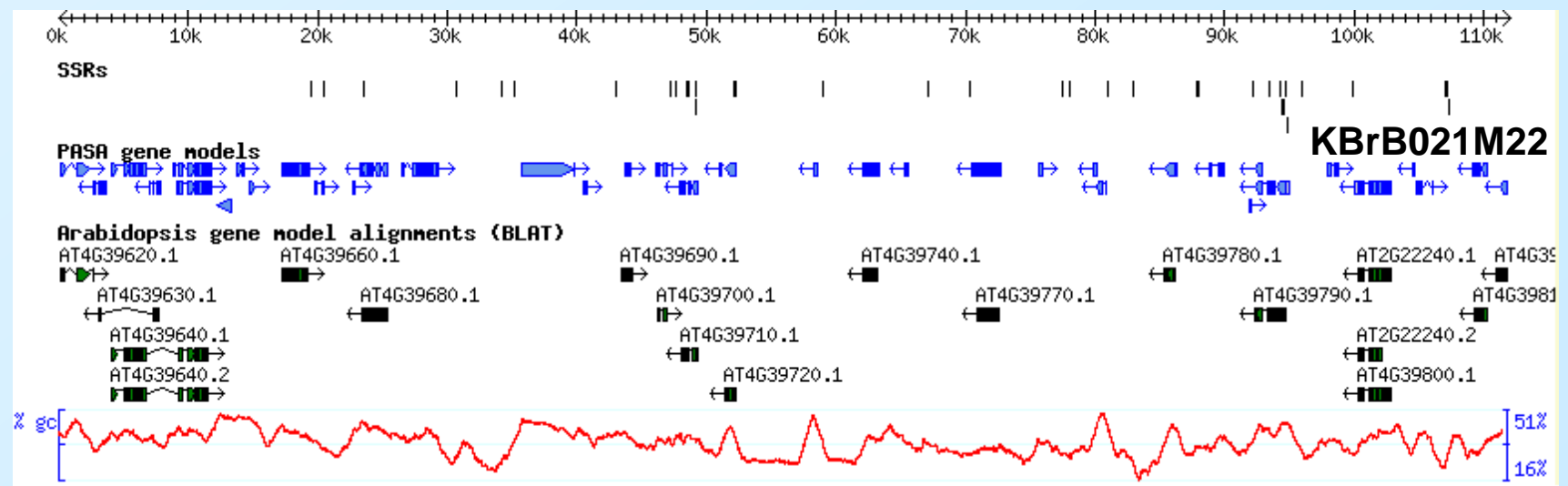
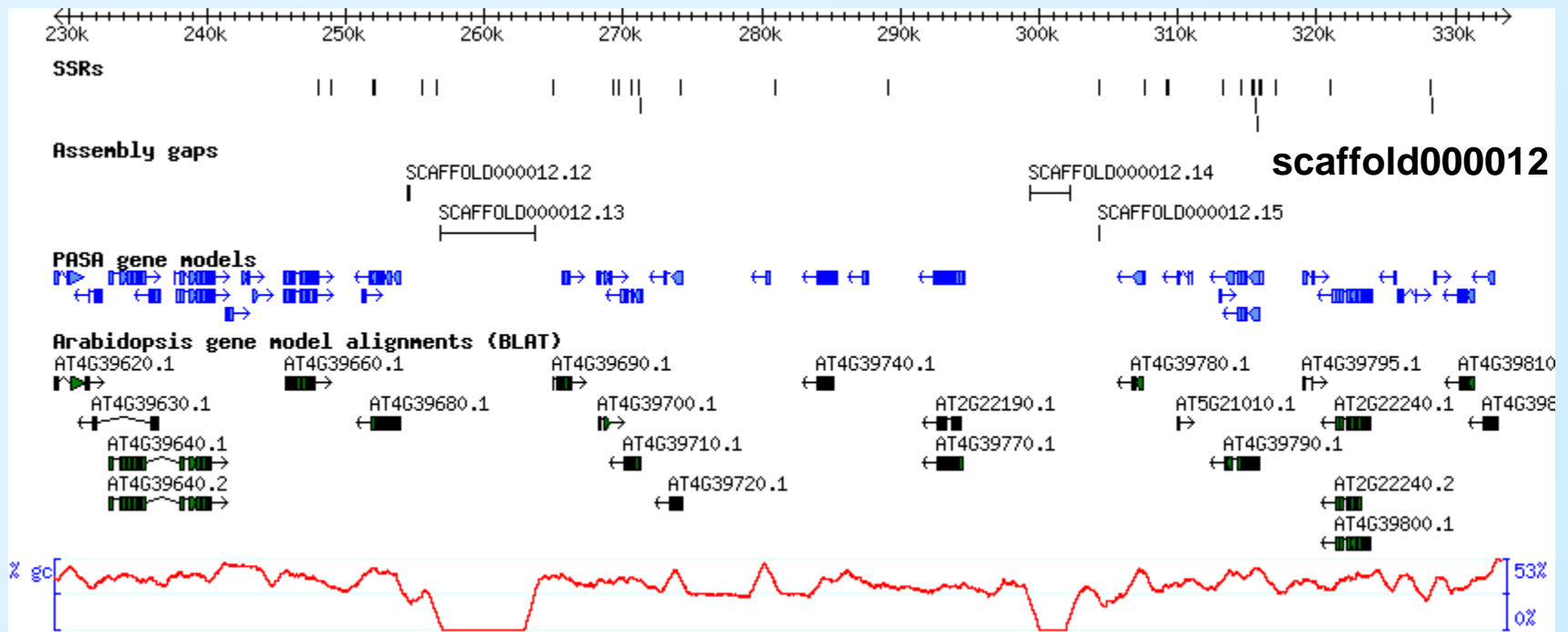


Hanzhong Wang, Shengyi Liu
Wei Hua

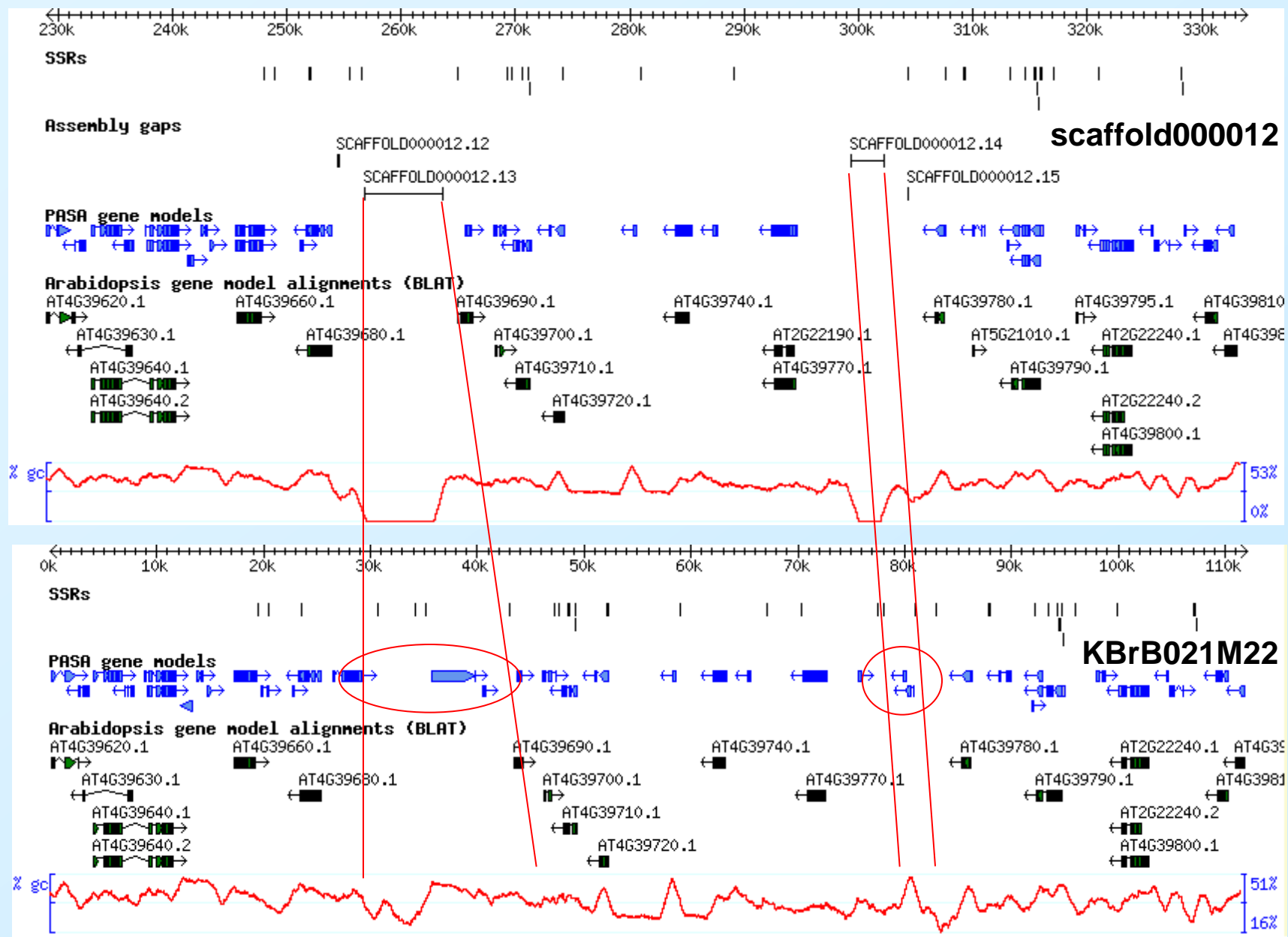


Ruiqiang Li, Junyi Wang, Peixiang Ni,
Desheng Mu, Bo Li, Yinqi Bai

Annotations of Illumina scaffolds and BACs are very similar



Many assembly gaps; generally affect transposon-related gene models



Outputs of the BBSRC *Brassica* Sequencing Project

Original activity:

89,444 *B. napus* BAC end sequences submitted to EMBL

Further activities:

Contributed to genome sequencing of *B. oleracea* TO1000 (Barker/Warwick)

Contributed to genome sequencing of *B. napus* Tapidor and Ningyou 7

Genome re-sequencing: *B. rapa* R-o-18

Leaf transcriptome re-sequencing for SNP discovery:

- 52 lines other *B. napus* cultivars, mostly from OREGIN DFFS

Leaf transcriptome re-sequencing for high density linkage map construction:

- 47 lines of TNDH mapping population

Further *Brassica* "reference" sequencing projects presently underway

Listed on [brassica.info](http://www.brassica.info) (<http://www.brassica.info/resource/sequencing.php>)

Species	Genotype	Crop type	Aims	Strategy	Consortium	Contact
<i>B. oleracea</i>	TO1000	Rapid cyclers	ref. 'C'	Illumina + 454	Canada +USA +France + UK	Isobel Parkin
<i>B. oleracea</i>	O212	Cabbage	ref. 'C'	Illumina + 454	CAAS, Wuhan, China	Shengyi Liu
<i>B. napus</i>	Tapidor DH	Winter oilseed	ref. 'AC'	Illumina + 454	HAU, China + UK	Jinling Meng
<i>B. napus</i>	Ningyou7	Spring oilseed	ref. 'AC'	Illumina + 454	HAU, China + UK	Jinling Meng
<i>B. napus</i>	DH12075	Spring oilseed	ref. 'AC'	Illumina + 454	Can-Seq	Isobel Parkin
<i>B. napus</i>	Darmor DH	Winter oilseed	ref. 'AC'	Illumina, 454, Sanger	INRA, France	Boulos Chaloub
<i>B. napus</i>	Zhongshuang 11	Spring oilseed	ref. 'AC'	Illumina + 454	CAAS, Wuhan, China	Shengyi Liu
<i>B. rapa</i>	B3	Rapid cycling, sc	?	Illumina + 454	JGI	-

Brassica "re-sequencing" projects presently underway

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Species	Genotype	Crop type	Aims	Strategy	Consortium	Contact
<i>B. oleracea</i>	?	Cabbage	re-seq. x5	Illumina	CAAS, Wuhan, China	Shengyi Liu
<i>B. oleracea</i>	Early Big	Broccoli	re-seq	Illumina	USA	Dick McCombie
<i>B. oleracea</i>	var. gongylodes (wild) ATC 94684	Kohlrabi	re-seq	Illumina	University of Queensland, Australia	Dave Edwards
<i>B. napus</i>	123 lines	various	leaf transcriptome	Illumina	UK, various	Ian Bancroft
<i>B. nigra</i>	wild (PI 597829) ATC 95249	Black mustard	re-seq	Illumina	University of Queensland, Australia	Dave Edwards
<i>B. rapa</i>	Chiifu-401	Chinese cabbage	re-seq	Illumina	University of Queensland, Australia	Dave Edwards
<i>B. rapa</i>	Kenshin-402	Chinese cabbage	re-seq	Illumina + 454	University of Queensland, Australia	Dave Edwards
<i>B. rapa</i>	R-o-18	Yellow sarson	re-seq. x12	Illumina	Rothamsted	Graham King

B. napus transcriptome sequencing projects presently underway

123 *B. napus* lines for nucleotide and expression polymorphism (JIC/TGAC)

SNPs identified between parents of OREGIN mapping populations (based on 2Gb mRNA-derived sequences; minimum 8-fold coverage of polymorphism)		
Population	Traits	SNPs identified
Temple x TN172	Good early vigour	40,075
Temple x Lesira	hairy leaves, seedling slug resistance	44,782
Temple x POSH MC169	pod shatter resistance	47,660

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Bioinformatics, BAC annotation

Nizar Drou, Martin Trick

Clone selection, validation, sequence QA, mRNA-seq libraries

Fiona Fraser, Eleni Soumpourou, Leah Clissold, Ian Bancroft

Genetic mapping & TO1000 sequencing

Guy Barker, Graham Teakle

BAC registry/BrassEnsembl

Jun Wang, Chris Love, Pierre Carion, Graham King

Collaborating institutions

HAU, BIG, TGAC

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