Report on chromosome 7A project

R Appels

The BAC libraries for the chromosome arms, 7AS and 7AL were produced in the Dolezel lab (Czech Replublic, http://olomouc.ueb.cas.cz) during the first half of 2011. The 7AS library (Hind III cloning site) had an average insert size of 134 kb and the 7AL library (Hind III cloning site) had an average insert size of 124 kb.

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The BAC fingerprinting of the 7AS and 7AL libraries was completed in September 2011 in UC Davis (Mingcheng Luo), and the output is summarized in the following Table:

BAC library	No. clones targeted	No. clones with fingerprints	clone failed	success rate %	No. clones realized (excluding controls)	No. clones in assembly	FPC rate %
7AS	47,232	46,091	1,141	97.58	45,123	42,244	93.62
7AL	53,376	52,320	1,056	98.02	51,221	47,776	93.27
Total	**100,608**	**98,411**	**2,197**	**n/a**	**96,344**	**90,020**	**n/a**

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The LTC and FPC software packages are currently being utilized (Gabriel Keeble and Matthew Bellgard) to provide an optimal assembly, based on the DNA fingerprint data (5 restriction endonucleases used), of the physical map and define minimum tiling paths (MTPs) for the entire chromosome 7A. Contigs as large as 7Mb have been identified.

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FPC Project wheat_7AS
9.4 Date: 14:27 Thu 24 Nov 2011 User: gkeeble

Clones Total 42244

Class	Contig	Single	Percentage of bands Avg	<60	<80	<100	<120	<140	<160	>=160
BAC	32794	9450	87.0	6.1	30.4	39.5	18.6	4.5	0.8	0.2

No markers

No sequenced clones

Contigs 1879 Dead contigs 0 Singles 9450
Q-Contigs 293 Unknown 0 Qs<=15% 293 Qs>15% 0

Range	INF	999	799	599	399	199	99	49	24	9
	---1000---	--800--	--600--	--400--	--200--	--100---	---50---	---25---	---10----	---3--	=2
Contig	0	0	1	0	16	66	122	129	162	471	912
>15% Qs	0	0	0	0	0	0	0	0	0	0	0
Chr	0	0	0	0	0	0	0	0	0	0	0

If Average Band Size 1500

	Bands	Coverage
Total Contigs	396475	594712 kb
Longest Ctg12	4844	7266 kb

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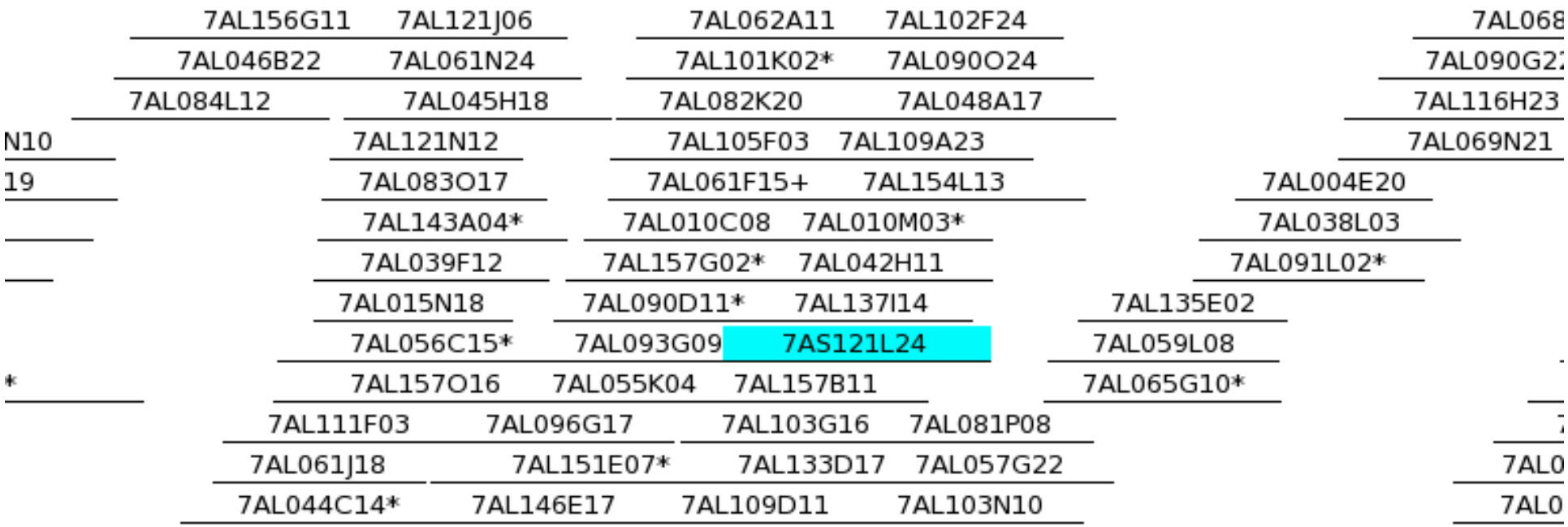
Largest contig is 7.266 Mb

Combining 7AS and 7AL fingerprints in a single assembly



Assemblies agree with the assemblies produced when the 7AS and 7AL are kept separate and only an occasional mix is seen.

This a convincing indication that the processing is effectively dealing with the problems generated by repetitive DNA sequences

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The Australian Genome Research Facility (AGRF) is carrying out the sequencing

Extractions of all 11,500 BAC clones will be completed by the end of June.

Pooling of clones for sequencing will be based on MTP (732 pools). Will include the TempliPhi amplification to reduce sequencing of E coli DNA in BAC preparations.