

Report on chromosome 7A project

R Appels

The BAC libraries for the chromosome arms, 7AS and 7AL were produced in the Dolezel lab (Czech Republic, <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

	7AL156G11	7AL121J06	7AL062A11	7AL102F24	7AL068
	7AL046B22	7AL061N24	7AL101K02*	7AL090O24	7AL090G2:
	7AL084L12	7AL045H18	7AL082K20	7AL048A17	7AL116H23
N10		7AL121N12	7AL105F03	7AL109A23	7AL069N21
19		7AL083O17	7AL061F15+	7AL154L13	7AL004E20
		7AL143A04*	7AL010C08	7AL010M03*	7AL038L03
		7AL039F12	7AL157G02*	7AL042H11	7AL091L02*
		7AL015N18	7AL090D11*	7AL137I14	7AL135E02
		7AL056C15*	7AL093G09	7AS121L24	7AL059L08
*		7AL157O16	7AL055K04	7AL157B11	7AL065G10*
	7AL111F03	7AL096G17	7AL103G16	7AL081P08	
	7AL061J18	7AL151E07*	7AL133D17	7AL057G22	7AL0
	7AL044C14*	7AL146E17	7AL109D11	7AL103N10	7AL0

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.



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