Radiation Hybrid Mapping: Towards a Complete Physical Map of the Wheat Genome

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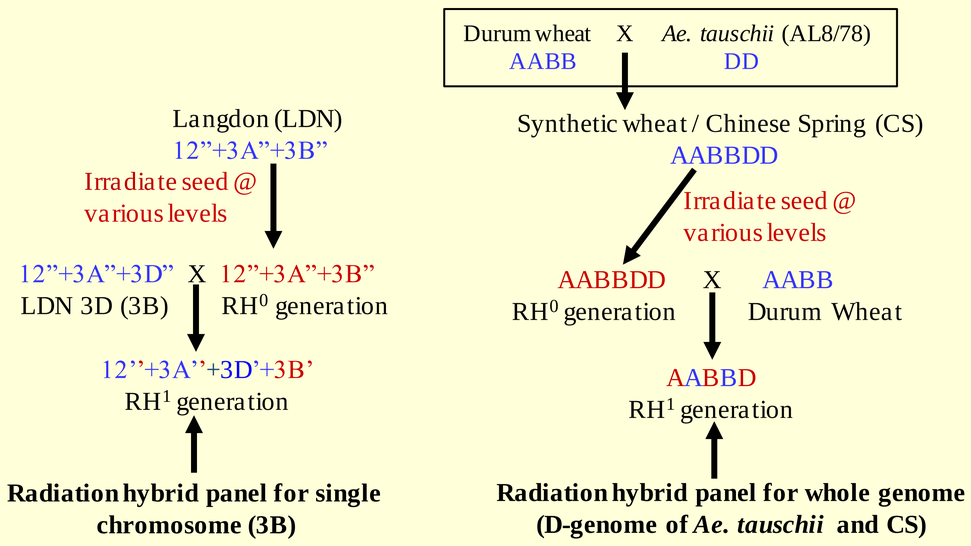
Abstract

Our experience with the radiation hybrid mapping shows that an average map resolution of ~ 200 kb can be achieved. This demonstrates the high potential of this technique for anchoring the BAC contigs to physical maps. To aid in the development of a complete physical map of wheat, we have developed RH panels for various individual chromosomes, in collaboration with the members of IWGSC, as well for the entire A, B and D genomes. A project data base (http://avena.pw.usda.gov/RHmapping/) provides up-to-date data information on tools, data and resources generated from our work.

Radiation Hybrid (RH) Mapping

- RH mapping uses radiation to induce chromosomal breaks
- Marker order and physical distance can be determined by co-retention of markers after irradiation
- Much higher resolution than genetic mapping can be achieved using fewer lines
- Independent of recombination events
- No need for polymorphic markers

Figure 1: Scheme for Development of RH Panel in Wheat

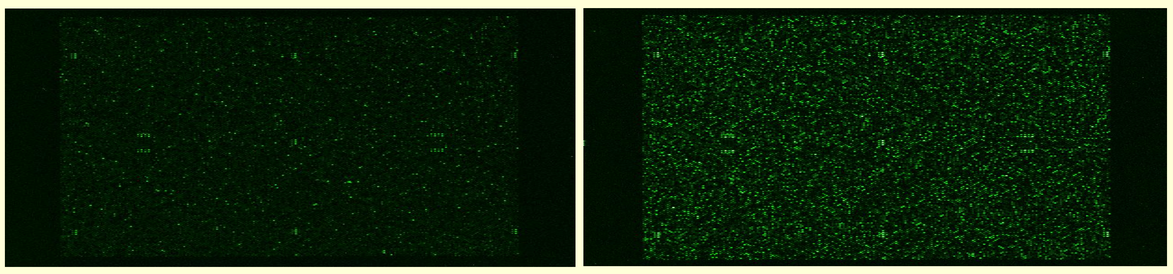


Whole D-genome RH mapping panel

- A set of 35 SSR markers across the entire D-genome was mapped in 1380 RH[1] lines
- ~300 RH[1] lines with retention frequency of 20-80% were selected
- Repeat junction markers (RJM: *Wanjugi et al. 2009*) designed from BAC end sequences (BES) indicate resolution of ~400kb for this panel

RJM markers and NimbleGen for D-genome RH mapping

- 12.14 million 454 reads were generated from *Ae. tauschii* genomic DNA
- 1.4X genome coverage
- ~ 300,000 RJM primers were designed for high-resolution RH mapping
- NimbleGen array using these RJM markers is under development (Figure 3)



Langdon (AB genome) AL8/78 (D genome)

Figure 3: Pilot NimbleGen array for D-genome RH mapping containing 75K RJM markers.

Table 1: 3B RH: Much higher resolution than genetic mapping

Comparison of resolution between RH and genetic maps across the 3B deletion bins (adapted from Saintenac *et al.* 2008)

Deletion bins	3BS3-0.87-1.00	3BS8-0.78-0.87	3BS9-0.57-0.75	3BS2-0.56-0.57	3BS1-0.33-0.55	C-3BS1-0.33	C-3BL2-0.22	3BL2-0.22-0.28	3BL1-0.31-0.50	3BL10 .50-0.63	3BL7-0.63-1.00	Chr
Marker no.	7.0	155.0	9.0	3.0	44.0	28.0	27.0	29.0	47.0	4.0	187.0	540.0
Size bin (Mb)	56.0	39.0	78.0	4.0	95.0	142.0	124.0	33.0	39.0	73.0	208.0	992.0
Map size (cR)	79.7	572.9	69.2	36.7	113.7	115.6	99.1	58.9	37.0	41.3	459.6	1871.9
Resolution (Mb cR^{-1})	**0.7**	**0.1**	**1.1**	**0.1**	**0.8**	**1.2**	**1.3**	**0.6**	**1.1**	**1.8**	**0.5**	**0.5**
Map size (cM)	5.2	33.1	13.4	--	1.6	0.9	1.6	1.6	6.2	3.5	104.2	179.1
Resolution (Mb cM^{-1})	**10.8**	**1.2**	**5.8**	**--**	**61.3**	**167.1**	**80.0**	**21.3**	**6.3**	**21.2**	**2.0**	**5.5**
Map size ratio (cR cM^{-1})	**15.3**	**17.3**	**5.2**	**--**	**73.4**	**136.0**	**63.9**	**38.0**	**6.0**	**12.0**	**4.4**	**10.5**

Table 2: Available wheat RH panels

Chromosomes	Species	RH lines available	Purpose
Single chromosome panel			
1A, 1B, 1D, 3B, 4A*, 7B**	Durum , Hexaploid	1,000-3,500	Physical mapping/ Cloning gene (s)
Whole genome panel			
A and B genome	Durum, Hexaploid	3,000	Physical mapping/Field phenotyping
D-genome	*Ae. tauschii* (Synthetic), Chinese spring	>4,000	Physical mapping

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** In collaboration with Dr. Odd-Arne Olsen, Norwegian University of Life Sciences , Norway

BAC contigs can easily be mapped using fewer RH lines

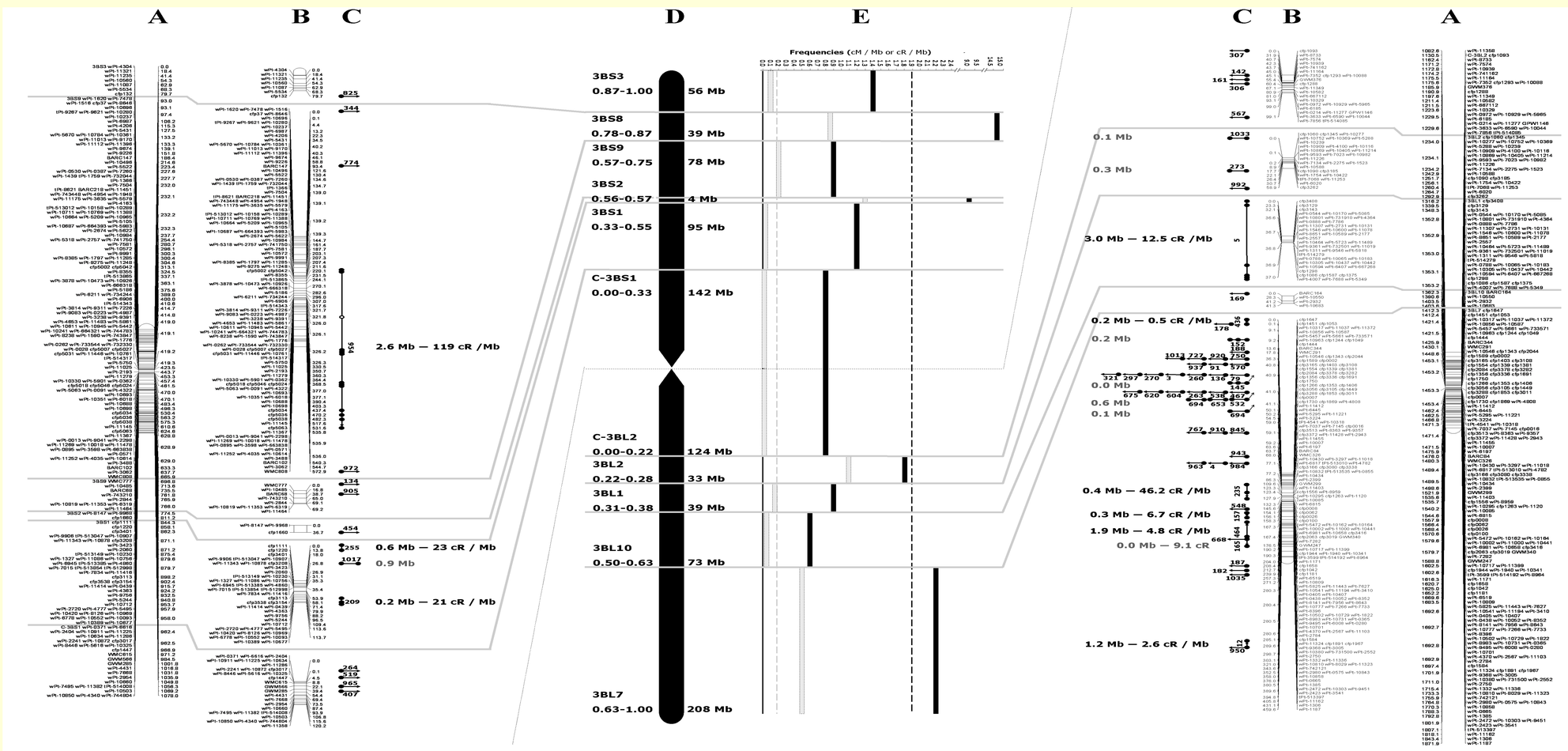

Figure 2: RH Mapping (based on 92 lines) *vs* Genetic Mapping (based on ~ 400 DH lines) *vs* Physical Mapping (based on 11 terminal deletion lines) of 3BS and 3BL. Complete *(A)* and deletion bin *(B)* Radiation Hybrid map for the short (left) and long (right) arms of chromosome 3B. *C*- BAC contig distribution based on anchored markers; contigs that contained a breakage event are indicated by vertical arrows pointing in the resolved map orientation and cR / Mb resolution within the contig is calculated; horizontal lines connecting multiple dots indicate contigs that had no breakage event and the size of the contig is reported; horizontal arrows indicate contig for which only a single marker was employed. *D*- Deletion bin map of 3B. *E*- Map resolution potential of different chromosome locations based on genetic mapping (grey lines) as reported by *Saintenac et al. 2008* and as obtained through RH (black line).

References

1. Wanjugi H, *et al.* (2009) Genome.52:576-587
2. Saintenac C, *et al.* (2009) Genetics 181: 393-403

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