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Genome structure in soybean revealed by a genomewide genetic map constructed from a single population ☆

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ABSTRACT

A complete genetic linkage map of the soybean, in which sequence-based (SB) genetic markers are evenly distributed genomewide, was constructed from an F_{12} population composed of 113 recombinant inbred lines derived from an interspecific cross involving Korean genotypes Hwangkeum and IT182932. Several approaches were employed for the development of 112 novel SB markers targeting both the gaps and the ends of the linkage groups (LGs). The resultant map harbored 20 well-resolved LGs presumed to correspond to the 20 pairs of soybean chromosomes. The map allowed us to identify the important chromosomal structures that were not observed in the integrated genetic maps, to identify the new potentially gene-rich regions, to detect segregation distortion regions within the whole genome, and to extend the ends of the LGs. The results will facilitate the further discovery of agronomically relevant genetic loci in the heretofore neglected chromosomal regions and should also provide some important links between the soybean genetic, physical, and genome sequence maps in the regions.

Molecular genetic linkage maps provide effective tools for positioning genes and other sequence features on a genome. Such genetic mapping techniques require sizeable sets of genetic markers that are polymorphic between individuals or populations and that, for correct and thorough positionings, those markers also be evenly distributed on a genomewide scale. Recently, many genetic maps in which molecular markers are distributed genomewide without notable gaps have been constructed from an interesting mapping population for the genetic analyses of many major crop species and model plants [1]. However, the construction of such a genetic map remains difficult for the soybean, one of the principal crops cultivated worldwide, owing primarily to the relatively high chromosome number in the soybean genome, as well as its ancient polyploidy nature [2,3]. The soybean has a moderately sized genome of approximately 1100 Mb [4], which is packaged into 20 chromosome pairs [5].

Initial genomewide soybean genetic linkage maps of the molecular markers have been developed primarily on the basis of the analysis of anonymous sequence polymorphisms [e.g., restriction fragment length polymorphism (RFLP), amplified fragment length polymorphism, and random amplified polymorphic DNA (RAPD)] [6–12]. All these genetic maps, which are based on a single mapping population, consisted of more than 20 linkage groups (LGs), together with many unlinked markers. The first genomewide map consisting of 20 homologous LGs corresponding to the 20 observed chromosomal pairs was achieved from the alignment of 20+ LGs derived from each of three mapping populations [13]. The consensus (or integrated) map was based on the presence of common simple sequence repeat (SSR) loci across the maps. Unlike RFLP markers, which usually detect more than 2 loci in the soybean [14], the SSR markers employed therein map to 1 locus and are multiallelic in the majority of cases. An additional 420 SSRs were mapped in the initial three populations, as well as in two additional soybean mapping populations [15]. JoinMap software [16,17] was employed to combine the five maps into an integrated genetic map encompassing 2523.6 cM of Kosambi map distance across 20 LGs. The map harbored 1849 markers but included more than 10 intervals of at least 20 cM. During the course of this study, an additional 1141 single-nucleotide polymorphism (SNP) markers were also mapped [18]. The SNP markers were mapped into three populations, including the two employed in the creation of the 2004 integrated linkage map, and then combined into an integrated transcript map. The SNP markers filled many gaps in the 2004 integrated map. However, the map harbored several sequence-based (SB) marker-rare regions over a range in excess of 20 to 30 cM, which harbored clusters of RFLP markers. Taken together, a complete genetic map derived from a single population,

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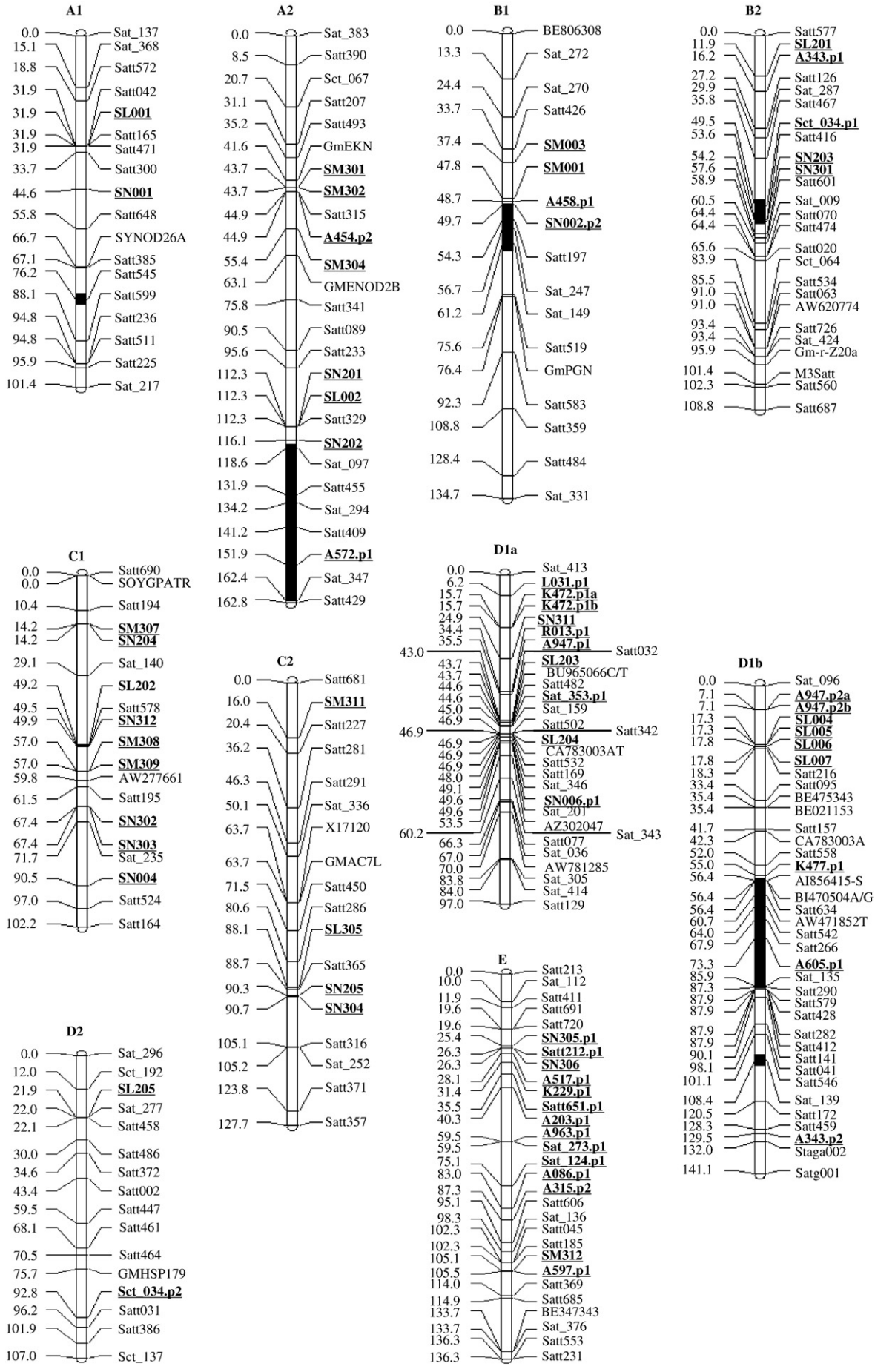
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15.1 Sat_368
18.8 Satt572
31.9 Satt042
31.9 SL001
31.9 Satt165
31.9 Satt471
33.7 Satt300
44.6 SN001
55.8 Satt648
66.7 SYNOD26A
67.1 Satt385
76.2 Satt545
88.1 Satt599
94.8 Satt236
94.8 Satt511
95.9 Satt225
101.4 Sat_217
A2
0.0 Sat_383
8.5 Satt390
20.7 Sct_067
31.1 Satt207
35.2 Satt493
41.6 GmEKN
43.7 SM301
43.7 SM302
44.9 Satt315
44.9 A454.p2
55.4 SM304
63.1 GMENOD2B
75.8 Satt341
90.5 Satt089
95.6 Satt233
112.3 SN201
112.3 SL002
112.3 Satt329
116.1 SN202
118.6 Sat_097
131.9 Satt455
134.2 Sat_294
141.2 Satt409
151.9 A572.p1
162.4 Sat_347
162.8 Satt429
B1
0.0 BE806308
13.3 Sat_272
24.4 Sat_270
33.7 Satt426
37.4 SM003
47.8 SM001
48.7 A458.p1
49.7 SN002.p2
54.3 Satt197
56.7 Sat_247
61.2 Sat_149
75.6 Satt519
76.4 GmPGN
92.3 Satt583
108.8 Satt359
128.4 Satt484
134.7 Sat_331
B2
0.0 Satt577
11.9 SL201
16.2 A343.p1
27.2 Satt126
29.9 Sat_287
35.8 Satt467
49.5 Sct_034.p1
53.6 Satt416
54.2 SN203
57.6 SN301
58.9 Satt601
60.5 Sat_009
64.4 Satt070
64.4 Satt474
65.6 Satt020
83.9 Sct_064
85.5 Satt534
91.0 Satt063
91.0 AW620774
93.4 Satt726
93.4 Sat_424
95.9 Gm-r-Z20a
101.4 M3Satt
102.3 Satt560
108.8 Satt687
C1
0.0 Satt690
0.0 SOYGPATR
10.4 Satt194
14.2 SM307
14.2 SN204
29.1 Sat_140
49.2 SL202
49.5 Satt578
49.9 SN312
57.0 SM308
57.0 SM309
59.8 AW277661
61.5 Satt195
67.4 SN302
67.4 SN303
71.7 Sat_235
90.5 SN004
97.0 Satt524
102.2 Satt164
C2
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16.0 SM311
20.4 Satt227
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46.3 Satt291
50.1 Sat_336
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63.7 GMAC7L
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88.7 Satt365
90.3 SN205
90.7 SN304
105.1 Satt316
105.2 Sat_252
123.8 Satt371
127.7 Satt357
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15.7 K472.p1b
24.9 SN311
34.4 R013.p1
35.5 A947.p1
43.0 Satt032
43.7 SL203
43.7 BU965066C/T
44.6 Satt482
44.6 Sat_353.p1
45.0 Sat_159
46.9 Satt502
46.9 Satt342
46.9 SL204
46.9 CA783003AT
46.9 Satt532
48.0 Satt169
49.1 Sat_346
49.6 SN006.p1
49.6 Sat_201
53.5 AZ302047
60.2 Sat_343
66.3 Satt077
67.0 Sat_036
70.0 AW781285
83.8 Sat_305
84.0 Sat_414
97.0 Satt129
D1b
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7.1 A947.p2b
17.3 SL004
17.3 SL005
17.8 SL006
17.8 SL007
18.3 Satt216
33.4 Satt095
35.4 BE475343
35.4 BE021153
41.7 Satt157
42.3 CA783003A
52.0 Satt558
55.0 K477.p1
56.4 AI856415-S
56.4 BI470504A/G
56.4 Satt634
60.7 AW471852T
64.0 Satt542
67.9 Satt266
73.3 A605.p1
85.9 Sat_135
87.3 Satt290
87.9 Satt579
87.9 Satt428
87.9 Satt282
87.9 Satt412
90.1 Satt141
98.1 Satt041
101.1 Satt546
108.4 Sat_139
120.5 Satt172
128.3 Satt459
129.5 A343.p2
132.0 Staga002
141.1 Satg001
D2
0.0 Sat_296
12.0 Sct_192
21.9 SL205
22.0 Sat_277
22.1 Satt458
30.0 Satt486
34.6 Satt372
43.4 Satt002
59.5 Satt447
68.1 Satt461
70.5 Satt464
75.7 GMHSP179
92.8 Sct_034.p2
96.2 Satt031
101.9 Satt386
107.0 Sct_137
E
0.0 Satt213
10.0 Sat_112
11.9 Satt411
19.6 Satt691
19.6 Satt720
25.4 SN305.p1
26.3 Satt212.p1
26.3 SN306
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31.4 K229.p1
35.5 Satt651.p1
40.3 A203.p1
59.5 A963.p1
59.5 Sat_273.p1
75.1 Sat_124.p1
83.0 A086.p1
87.3 A315.p2
95.1 Satt606
98.3 Sat_136
102.3 Satt045
102.3 Satt185
105.1 SM312
105.5 A597.p1
114.0 Satt369
114.9 Satt685
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133.7 Sat_376
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