Genetic Analysis of Recombinant Inbred Lines for Sorghum bicolor × Sorghum propinquum

Wenqian Kong,*1 Huizhe Jin,*1 Cleve D. Franks,1,2 Changsoo Kim,* Rajib Bandopadhyay,*3 Mukesh K. Rana,*4 Susan A. Auckland,* Valorie H. Goff,* Lisa K. Rainville,* Gloria B. Burow,† Charles Woodfin,* John J. Burke,* and Andrew H. Paterson*5

*Plant Genome Mapping Laboratory, University of Georgia, Athens, Georgia 30602, and 1United States Department of Agriculture-Agricultural Research Service, Cropping Systems Research Laboratory, Lubbock, Texas 79401

ABSTRACT We describe a recombinant inbred line (RIL) population of 161 F5 genotypes for the widest euploid cross that can be made to cultivated sorghum (Sorghum bicolor) using conventional techniques, S. bicolor × S. propinquum, that segregates for many traits related to plant architecture, growth and development, reproduction, and life history. The genetic map of the S. bicolor × S. propinquum RILs contains 141 loci on 10 linkage groups collectively spanning 773.1 cM. Although the genetic map has DNA marker density well-suited to quantitative trait loci mapping and samples most of the genome, our previous observations that sorghum pericentromeric heterochromatin is recalcitrant to recombination is highlighted by the finding that the vast majority of recombination in sorghum is concentrated in small regions of euchromatin that are distal to most chromosomes. The advancement of the RIL population in an environment to which the S. bicolor parent was well adapted (indeed bred for) but the S. propinquum parent was not largely eliminated an allele for short-day flowering that confounded many other traits, for example, permitting us to map new quantitative trait loci for flowering that previously eluded detection. Additional recombination that has accrued in the development of this RIL population also may have improved resolution of apices of heterozygote excess, accounting for their greater abundance in the F5 than the F2 generation. The S. bicolor × S. propinquum RIL population offers advantages over early-generation populations that will shed new light on genetic, environmental, and physiological/biochemical factors that regulate plant growth and development.

As a botanical and genomic model for grasses, Sorghum bicolor L. Moench. (sorghum), a native of tropical Africa that is the most drought-resistant of the world’s top five cereal crops, is a logical complement to the largely sequenced genome of rice (Oryza). Sorghum has biochemical and morphological specializations to improve carbon assimilation at high temperatures (C4 photosynthesis), whereas rice uses C3 photosynthesis more typical of temperate grasses. Like rice, the most recent genome duplication in sorghum appears to be ~70 million years ago (Paterson et al. 2004), simplifying its comparative and functional genomics. With a high-quality DNA sequence (Paterson et al. 2009), the ~740 megabase pair sorghum genome is of high value for better understanding the genome of maize (Schnable et al. 2009) and in particular the impact of an ancient tetraploidy in maize shortly after its lineage diverged from that of sorghum (Swigonova et al. 2004). Sorghum is of particular importance as a diploid model for the Saccharinae clade of grasses that includes recently formed complex polyploids such as Saccharum (sugarcane, currently the world’s no. 1 biofuel crop), and Miscanthus, among the greatest-yielding of biomass crops in the U.S. Midwest (Heaton et al. 2008). Each of these polyploids share substantial genetic colinearity and synteny with sorghum (Kim et al. 2012; Ming et al. 1998), and Saccharum quantitative trait loci (QTL) often show positional correspondence

KEYWORDS quantitative trait locus simple-sequence repeat DNA marker recombination segregation distortion

Copyright © 2013 Kong et al.
doi: 10.1534/g3.112.004499

Manuscript received September 24, 2012; accepted for publication November 14, 2012
This is an open-access article distributed under the terms of the Creative Commons Attribution Unported License (http://creativecommons.org/licenses/by/3.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

1These authors contributed equally to this work.
2Present address: Pioneer Hi-Bred International, Plainview, TX 79072.
3Present address: Department of Biotechnology, Birla Institute of Technology (Deemed University), Mesra - 835 215, Ranchi Jharkhand, India.
4Present address: National Research Center on DNA Fingerprinting, National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi - 110 012, India.
5Corresponding author: Plant Genome Mapping Laboratory, University of Georgia, Athens, GA 30602. E-mail: paterson@plantbio.uga.edu
Figure 1  Genetic map of the S. bicolor × S. propinquum RILs. For each linkage group, genetic distances are shown on the right in Kosambi centimorgans; their corresponding physical chromosomes (from the current genome assembly, as cited) are shown on the left. Markers whose physical positions are unable to be located to their corresponding chromosomes are indicated by Y; markers whose genetic orders disagree with their physical positions are indicated by /C3. Bar and whisker plots on chromosomes 4, 8, and 9 indicate 1- and 2-LOD likelihood intervals for flowering QTL described in the text, with tick marks indicating likelihood peaks.
to those of sorghum (Ming et al. 2001, 2002). One of the few crops suited to all proposed approaches for renewable fuel production. i.e., from starch, sugar, and/or cellulose, sorghum itself is presently the no. 2 U.S. source of fuel ethanol from grain (after maize), and is promising cellulosic biofuel crop (Rooney et al. 2007).

*Sorghum bicolor* × *S. propinquum* is thought to be the widest euploid cross that can be made with the cultigen (*S. bicolor*) by conventional means, and interspecific populations from these species offer opportunities to genetically dissect a wide range of traits related to plant domestication and crop productivity, some of which have begun to receive attention (Chittenden et al. 1994; Feltus et al. 2006; Hu et al. 2003; Lin et al. 1995, 1999a,b). The opportunities offered by comparison of *S. bicolor* and *S. propinquum* have led to much effort to develop genomics resources, including a detailed genetic map (Bowers et al. 2003; Chittenden et al. 1994), bacteriogenic chromosome-based physical maps for both species (Bowers et al. 2005; Draye et al. 2001; Lin et al. 1999), expressed sequence tag (EST) resources (Pratt et al. 2005), and a genome sequence (Paterson et al. 2009). Among many other aspects of growth and development, *S. bicolor* and *S. propinquum* differ in characteristics related to perenniality, a life history strategy for which the *Sorghum* genus has become a model (Hu et al. 2003; Jang et al. 2009; Paterson et al. 1995b). Both consideration of how to expand agriculture to provide plant biomass for production of fuels or chemical feedstocks (Tilman et al. 2009), and strategies to rebalance food production with preservation of ecological capital (Glover et al. 2010), focus heavily on perenniality. Perenniality may also be a curse—*Sorghum halepense*, a wild perennial polyploid resulting from natural hybridization between *S. bicolor* and *S. propinquum*, finds occasional use as forage and even food (seed/flower) but is most noted as one of the world’s most noxious weeds, having spread from its west Asian center of diversity across much of Asia, Africa, Europe, North and South America, and Australia. Demonstration that most genes responsible for variations in size and number in *Sorghum* and *Oryza* of an important perennial organ, the rhizome, map to corresponding chromosomal locations (Hu et al. 2003), suggests that information about rhizomatousness from a few models (that are also major crops) may extrapolate broadly to a wide range of taxa.

By single-seed descent from the same *S. bicolor* × *S. propinquum* F2 population used in early-generation genetic analysis (Lin et al. 1995), we have produced and describe here a recombinant inbred line (RIL) population of 161 F5 genotypes that segregate for a wide range of traits, providing a valuable addition to the genetic resources available for this botanical and genomic model. The genetic control of flowering provides an example of how the RIL population contributes to improved knowledge of trait inheritance.

### TABLE 1 Comparison of regions of segregation distortion between *S. bicolor* (SB) × *S. propinquum* (SP) F5 RIL and F2 populations

| Chr. | Marker | cM | SB:SP Location, Mb | F5 | Marker | SB:SP LG | Location, Mb |
|------|--------|----|-------------------|----|--------|-----------|--------------|
| 1    | Xcup24 | 35.8 | 154.3 | 14.0 | None near | pSB195 | 203:15 | C | 14.2 |
| 2    | CA154181a | 50.6 | 129:24 | 58.3 | None near | pSB101 | 34:74 | B | 61.6 |
| 3    | CA199661a | 11.2 | 101:40 | 0.2 | None near | pSB075 | 111:35 | B | 66.1 |
| 4    | CA074959a | 35.0 | 100:23 | 3.5-6.2 | N.D. | A |
| 5    | TC48056a | 66.1 | 86:43 | 13.8-51.2 | N.D. | A |
| 6    | Xcup65 | 84.3 | 85:39 | 55.9 | N.D. | A |
| 7    | None near | | | | | |
| 8    | Xtxp265 | 77.2 | 117:37 | 64.9 | None near | pSB443b | 128:66 | A | 69.0 |
| 9    | N.D. | | | | | |
| 10   | mSbCIR329 | 0.0 | 134:26 | 0.2 | None near | pSB038 | 34:101 | F | 14.2 |
| 11   | N.D. | | | | | |
| 12   | Xisep1140 | 60.3 | 97:52 | 54.8 | N.D. | H |
| 13   | Xgap72 | 0.0 | 151:3 | 41.4 | None near | pSB064 | 33:81 | H | 6.5 |
| 14   | None near | | | | | |
| 15   | N.D. | | | | | |
| 16   | mSbCIR240 | 39.5 | 109:49 | 4.5 | None near | pSB095 | 104:60 | D | 50.7 |
| 17   | CA142735a | 26.5 | 115:46 | 31.7 | None near | pSB428a | 93:41 | D | 38.0 |
| 18   | TC59518b | 37.7 | 105:55 | 50.2-54.5 | None near | pSB643a | 65:20 | D | 4.3 |
| 19   | Xcup43 | 88.7 | 123:26 | 59.8 | None near | pSB784 | 19:50 | J | 5.9 |

N.D., no distortion (not significantly different from 1:1 segregation); RIL, recombinant inbred line; LG, linkage group. Physical location not on the corresponding chromosome of the linkage group: spicis are estimated by adjacent marker locations.

#### MATERIALS AND METHODS

**Genotyping and data analysis**

The mapping population comprised 161 F5 RILs derived by selfing of single F2 plants described previously (Lin et al. 1995) from a controlled cross between single plants of *S. bicolor* BTx623, and *S. propinquum* (unnamed accession). Leaf samples were frozen at −80°C and lyophilized for 48 hr. Genomic DNA was extracted from the lyophilized leaf sample based on Aljanabi et al. 1999. Polymerase chain reactions for simple sequence repeat (SSR) analysis were carried out under standard conditions for all primer pairs using 1 U of Taq polymerase with 10× polymerase chain reaction buffer (100 mM Tris-HCl at pH 9, 500 mM KCl, and 15 mM MgCl2), 2 mM dNTP, 3 mM MgCl2, 0.2 mM of each primer, and 20 ng of DNA template with a final reaction volume of 10 mL. The thermo-cycling was performed with the following program: (1) Preheat at 95°C for 3 min, (2) denaturation at 95°C for 30 sec, (3) annealing at 65°C for 1 min (−1°C cycle), (4) extension at 72°C for 1 min, (5) 10 cycles of steps (2)−(4), (6) denaturation at 95°C for 30 sec, (7) annealing at 55°C for 1 min, (8) extension at 72°C for 1 min, (9) 32 cycles of steps (6)−(7), and (10) final extension at 72°C for 5 min. The amplified products were visualized in 10% polyacrylamide gels with silver staining.
A total of 161 F5 individuals were genotyped. MAPMAKER (Lander et al. 1987) was used for map construction with the data type ‘ri self,’ which is suitable for the RIL configuration. Heterozygosity in codominant markers was treated as missing data by MAPMAKER because the ‘ri self’ configuration does not recognize it. Map distances, cM, were calculated using the Kosambi function (Kosambi 1944). Marker loci were grouped by two-point linkage analysis with a logarithm of odds ratio (LOD) threshold of 4.0 and a maximum distance of 30 cM. Local maximum likelihood orders of marker loci were confirmed using the ‘ripple’ command. The map was drawn using Adobe Illustrator. In 2009, 2010, and 2011, single 1.5-m plots of each RIL were transplanted (2009, 2011) or direct seeded at the University of Georgia Plant Science Farm, Watkinsville, GA, in a completely randomized design. Flowering dates were recorded for the first five flowers per plot. The average of the first five flowering days was calculated in Microsoft Excel. The means of the flowering dates over years were estimated using best linear unbiased prediction with SAS PROC MIXED. Lines, environmental effect, and their interaction were treated as random. The broad sense heritability (H) was calculated using the variance component method. 

\[ H = \frac{V_{G}}{V_{G} + V_{GE} + V_{residual}} \]

Heritability = 60.822/(60.822 + 102.57/3 + 1.5848/3) = 63.66. QTL analysis used composite interval mapping method in Windows QTL Cartographer V2.5_010 (Wang et al. 2012). Seed of the RIL population are distributed by the U.S. Department of Agriculture-Agricultural Research Service (USDA-ARS), Lubbock, TX (J. Burke).

### RESULTS

#### DNA markers and map construction

A total of 203 SSRs initially were selected and scored, derived from sugarcane ESTs (prefix “CA” or “TC”), previously mapped RFLP

### Table 2 Comparison of regions showing over-/underrepresentations of residual heterozygosity between S. bicolor × S. propinquum F5 RIL and F2 populations

| Chr. | Marker       | cM  | H:(SB + SP)\(^{*}\) | Location, Mb | F5                  | cM  | H:(SB + SP)\(^{*}\) | Location, Mb | F2                  |
|------|--------------|-----|--------------------|--------------|----------------------|-----|--------------------|--------------|----------------------|
| 1    | CA22647a     | 5.4 | 21:140             | 1.8          | pSB102               | 193:123 | 3.7                | SHO68        | 106:244\(^{c}\)    |
| 1    | TC71756a\(^{b}\) | 97.7 | 24:135             | 47.7/50.3-73.4 | pSB101               | 206:108 | 61.6               | pSB077       | 211:103              |
| 2    | CA296025c    | 18.2 | 26:133             | 6.0-2.0      |                      |           |                   |              |                      |
| 2    | mSBcIR222    | 37.4 | 26:131             | 4.7          |                      |           |                   |              |                      |
| 2    | Xcup63       | 51.6 | 25:136             | 59.1         |                      |           |                   |              |                      |
| 3    | CA152937a    | 50.2 | 24:132             | 9.1          |                      |           |                   |              |                      |
| 3    | TC48056a\(^{b}\) | 66.1 | 28:129             | 13.8-31.2    |                      |           |                   |              |                      |
| 3    | TC69429a\(^{b}\) | 93.4 | 21:135             | 55.9-10.4    |                      |           |                   |              |                      |
| 4    | Xcup61\(^{b}\) | 12.5 | 36:120             | 1.5-5.1      |                      |           |                   |              |                      |
| 4    | Xisep0203    | 42.5 | 26:123             | 10.0         |                      |           |                   |              |                      |
| 5    | Xxpo65       | 13.5 | 23:131             | 1.9          |                      |           |                   |              |                      |
| 5    | CA103773a    | 39.4 | 25:135             | 4.8          |                      |           |                   |              |                      |
| 5    | S14_284514_ag17\(^{b}\) | 52.1 | 41:116             | 13.5-42.0    |                      |           |                   |              |                      |
| 5    | CA100232a    | 55.6 | 31:130             | 54.3         |                      |           |                   |              |                      |
| 6    | Xxpo057      | 26.4 | 22:134             | 5.7          |                      |           |                   |              |                      |
| 6    | Xxpo040      | 0    | 28:129             | 0.9          |                      |           |                   |              |                      |
| 7    | Xxpo278      | 32.7 | 26:129             | 51.1         |                      |           |                   |              |                      |
| 7    | mSBcIR300    | 45.6 | 24:137             | 58.3         |                      |           |                   |              |                      |
| 8    | Xisep0829    | 47.8 | 31:122             | 59.4         |                      |           |                   |              |                      |
| 8    | Xxpo047      | 29.6 | 31:126             | 3.0          |                      |           |                   |              |                      |
| 8    | CA166256a    | 51.2 | 23:137             | 5.3          |                      |           |                   |              |                      |
| 8    | Xxpo321      | 68.1 | 22:134             | 50.5         |                      |           |                   |              |                      |
| 9    | TC50663d     | 0    | 20:120             | 3.0          |                      |           |                   |              |                      |
| 9    | TC65153a     | 43.3 | 23:114             | 54.5         |                      |           |                   |              |                      |
| 9    | Xgap206      | 63.6 | 21:137             | 59.2         |                      |           |                   |              |                      |
| 10   | Xcup49       | 0    | 30:130             | 0.2          |                      |           |                   |              |                      |
| 10   | CA217392a    | 26.8 | 21:132             | 1.6          |                      |           |                   |              |                      |
| 10   | CA191677a    | 81.9 | 21:139             | 58.6         |                      |           |                   |              |                      |

RIL, recombinant inbred line; LG, linkage group.

\(^{a}\) H:(SB + SP) indicates the ratio of heterozygotes (H) to the sum of parental genotypes (SB + SP).

\(^{b}\) Physical location not on the corresponding chromosome of the linkage group: apices are estimated by adjacent marker locations.

\(^{c}\) Deficiency of heterozygotes (all other cases are heterozygote excess).
probe sequences ["Xcup" (Schloss et al. 2002)], sorghum-sequenced genomic clones ["Xtxp" (Kong et al. 2000)], sorghum EST sequences ["Xisep" (Ramu et al. 2009)], previously developed SSRs ["Xgap" (Brown et al. 1996)], unpublished SSRs from Agropolis-Cirad-Genoplante ("mSbCIR"), and an unmapped scaffold in the genome sequence. Of those 203 markers, 135 segregating for 141 marker loci were mapped into 10 linkage groups corresponding to the 10 sorghum chromosomes. The remaining markers were excluded due to redundancy (i.e., cosegregation of multiple bands from the same primer) and weak and/or apparent artifactual amplifications. Among the 141 loci mapped in the F5 RILs, there is an average of 9 (5.6%) missing genotypes per locus, with 95% of the loci having less than 29 (18%) missing genotypes. Among 95 loci mapped in the F2 population, there is an average of 25 (6.8%) missing genotypes per locus, with 95% of the loci having less than 103 (27.8%) missing genotypes.

The genetic map of the RILs derived from annual S. bicolor and perennial S. propinquum (Figure 1) contains 141 loci on 10 linkage groups collectively spanning 773.1 cM. A total of 35 (24.8%) loci have dominant inheritance, with null alleles from S. propinquum at 14 loci and from S. bicolor at 21 loci, which is not a significant difference ($\chi^2 = 1.4, 1 \text{ d.f.}, P = 0.2367$). The average interval between consecutive loci is 5.48 cM, ranging from 0.0 cM between cosegregating markers to 25.7 cM in the largest gap (on chromosome 5). Construction of the map used a two-step strategy. First, to minimize ambiguity caused by

---

**Table 3 Biometric parameters of QTL for days to first flower in the S. bicolor x S. propinquum RILs**

| Chr. | LOD  | $a^*$  | R2  | Start, Mb$^b$ | End, Mb$^b$ | Population/Study (if Not Herein) |
|------|------|--------|-----|--------------|-------------|----------------------------------|
| 2    | 1    | −1.2   |     |              |             | S. bicolor x S. propinquum F2 (Lin et al. 1995) |
| 2    | 4.67 | −6.7   | 0.083 | 61.6         | 66.1        |                                  |
| 4    | 3.5  | −2.01  | 0.108 | 5.1          | 10.0        |                                  |
| 8    | 2.8  | 1.64   | 0.072 | 49.1         | 51.9        |                                  |
| 8    | 5.5  | c      | 0.134 | 50.5         | 55.5        | S. bicolor Bx623 x IS3620C (Brown et al. 2006) |
| 9    | 4.2  | −2.14  | 0.114 | 50.2         | 54.5        |                                  |
| 9    | 2.53 | −10.5  | 0.042 | 8.1          | 57.0        | S. bicolor x S. propinquum F2 (Lin et al. 1995) |
| 9    | 7.7  | —      | 0.195 | a            | 59.1        | S. bicolor Bx623 x IS3620C (Feltus et al. 2006) |

$^a$ Additive effect, calculated as S. bicolor Bx623 – other (S. propinquum or IS3620C as appropriate). To match this system, values reported in (Lin et al. 1995) were multiplied by −1.

$^b$ Based on flanking DNA marker locations in the published genome sequence (Paterson et al. 2009).

$^c$ Corresponding values not reported.

$^d$ Only a single nearby marker could be definitively mapped to the genome sequence, span of interval uncertain.
distorted loci, we constructed a framework map by selecting a subset of clearly scored markers that also did not deviate significantly from the expected Mendelian ratio (1:1) at \( P < 10^{-5} \) after Bonferroni correction. To assign linkage groups to chromosomes, we anchored framework markers to physical locations by blasting against the sorghum genome sequence. We then assigned and placed additional markers to the framework at LOD score of \( \geq 3.0 \) and carefully checked for double recombination events in the original scoring data.

**Comparison of genetic map to physical positions**

Comparison of the genetic map to physical positions of the mapped loci reveals the relationship between genetic distances and physical distances and the physical distribution of markers along the genome. Each marker on the genetic map was aligned to its corresponding physical position by virtue of the published \( S. \) *bicolor* genome sequence [Figure 1 (Paterson et al. 2009)]. The sorghum genome sequence information was given priority in ordering markers that were indistinguishable genetically. Overall, a total of 110 of 141 markers in 10 linkage groups are well aligned to their physical positions. The marker order in the genetic map occasionally deviates from that in the physical map. Distal markers on a linkage group tend to disagree more with the physical map than markers in the middle of a group, presumably due to a lack of flanking markers at the ends of chromosomes. A small number of markers show best matches to sequences that are on different chromosomes from where they map genetically. Factors that may contribute to the discrepancies between the genetic and physical maps include multiple amplifications of paralogous loci, sequence assembly errors; or cryptic structural differences between \( S. \) *bicolor* and \( S. \) *propinquum*.

The mapped SSR marker loci provide substantial coverage of the genetic map, with the exception of chromosome 6 for which markers only cover the lower one third of the chromosome (Figure 1). The unmapped region of this chromosome includes a large heterochromatic block (about 34 Mb) that contains the \( S. \) *propinquum Mal1* allele conferring short-day flowering (Lin et al. 1995). There is ample polymorphism between the parental genotypes in this region and we mapped the region in the F2 population (Lin et al. 1995). However, the RIL population was advanced in a temperate latitude, and artificial selection has largely eliminated photoperiodic flowering. This selection, together with limited recombination in this heterochromatic region, account for it being underpopulated with DNA markers in the RIL map.

Marker distribution is not even along the physical map: markers are concentrated in distal regions and sparse in central regions of the chromosomes. In an extreme case, chromosome 8, a recombinational distance of 4.7 cm spans a physical distance of approximately 46.3 Mb, covering a remarkable 83.4% of the chromosome. This phenomenon is in accordance with our previous observations (Bowers et al. 2005; Lin et al. 1995; Paterson et al. 2009) that the sorghum pericentromeric heterochromatin is recalcitrant to recombination, with the vast majority of recombination occurring in the distal euchromatin.

**Segregation distortion**

In the F5 RILs, all chromosomes except chromosome 7 contain regions with segregation distortion significant at the 5% level (Table 1). A total of 14 apices (peak genomic regions) of distortion were found, on chromosome 1 near cM 35.8, chromosome 2 near cM 50.6, chromosome 3 near cM 11.2, 35.0, 66.1, and 84.3; chromosome 4 near cM 77.2, chromosome 5 near cM 0.0 and 60.3; chromosome 6 near cM 0.0; chromosome 8 near cM 39.5; chromosome 9 near cM 26.5 and 37.7; and chromosome 10 near cM 88.7. All regions showed enrichment for \( S. \) *bicolor* alleles. Other than the chromosome 6 region under selection for day-neutral flowering, the most striking case of segregation distortion was on chromosome 1—the apex of this distortion was near the locus Xcup24 with a segregation ratio of 154:3 (homozygous \( S. \) *bicolor*; \( S. \) *propinquum*). This apex was genetically less than 1 cM from the most extreme case found in the F2 population from which these RILs are derived: the locus CSU507 on LG C (Bowers et al. 2003). In a larger set of F2 progeny previously described (Lin et al. 1995), we found similarly distorted segregation (203:15) in this region.

We compared the 14 regions of segregation distortion in the F5 RILs to the levels and patterns of segregation found in the F2 population from which these RILs are derived. Because different DNA markers were used in the two studies, this was done by aligning the F2 and F5 genetic maps to their physical locations on the \( S. \) *bicolor* genome (Paterson et al. 2009). A total of 11 regions of segregation distortion were found in the F2 (Table 1). Four of the 11 regions of segregation distortion in the F2 population favored the \( S. \) *propinquum* alleles, among which there are no longer distorted in the F5 RILs, and one region near the end of chromosome 2 contains overrepresentation of \( S. \) *bicolor* alleles (!) in the F5 RILs. Those regions with overrepresentation of \( S. \) *bicolor* alleles in the F2 generally also contain such overabundance in the F5 RILs, albeit a few cases lack nearby DNA markers. However, eight regions showing normal segregation in the F2 showed overabundance of the \( S. \) *bicolor* allele in the F5 RILs.

**Residual heterozygosity**

We compared regions of excess/deficiency of residual heterozygosity in the F5 RILs and the F2 population (Table 2). In the F2, eight regions show excess and two show deficiency of heterozygotes. All except two of these also show segregation distortion. In the F5, much higher homozygosity makes it difficult to distinguish heterozygote deficiency with statistical significance but 29 regions show excess, 7 (24%) of which also show segregation distortion. In the F2, the regions showing excess are all small (diagnosed by only 1 marker each); however, a large region of chromosome 1 shows deficiency of heterozygotes. In the F5, there are 3 large regions showing heterozygote excess in chromosomes 4, 5, and 7, respectively.

**Initial QTL mapping**

To explore the merit of the RIL population for QTL mapping, we focused on flowering, a trait associated with the tropical origin of \( S. \) *propinquum* that had a large confounding effect on many traits in F2 QTL mapping. In the RIL population, near-homozygosity for the flowering allele confers early flowering, a trait associated with the tropical origin of \( S. \) *propinquum* (Lin et al. 1995). However, a large region of chromosome 1 shows deficiency of heterozygotes. All except two of these also show segregation distortion. In the F5, much higher homozygosity makes it difficult to distinguish heterozygote deficiency with statistical significance but 29 regions show excess, 7 (24%) of which also show segregation distortion. In the F2, the regions showing excess are all small (diagnosed by only 1 marker each); however, a large region of chromosome 1 shows deficiency of heterozygotes. In the F5, there are 3 large regions showing heterozygote excess in chromosomes 4, 5, and 7, respectively.
The DISCUSSION

The *S. bicolor* × *S. propinquum* RIL population offers advantages over early-generation populations that promises to shed new light on the genetic, environmental, and physiological/biochemical factors that regulate plant growth and development. Dramatic variation in plant architecture, growth and development, reproduction, and life histories of the parental species that segregate among the progeny, together with homoyzogosity of the RILs and the ability to replicate them across a spectrum of natural and/or controlled conditions, makes this population of high potential importance for the discovery and validation of QTL. Many of these traits have been measured and will be reported under separate cover.

Advancement of the RIL population in a temperate environment (Lubbock, TX) may improve the ability to resolve QTL for traits that were previously below the significance threshold, also providing a more realistic assessment of variation that is relevant to temperate latitudes. For example, near-homozygosity for the *S. bicolor* allele along the salient portion of chromosome 6 reveals that we have largely eliminated genotypes with photoperiod sensitivity (“short-day flowering”), a trait associated with the tropical origin of *S. propinquum* that had a large confounding effect on many traits in F2-based QTL mapping. Eliminating the profound morphophysiological alteration associated with short-day flowering permitted us to identify two flowering QTL that eluded detection in our previous study with 370 F2 plants (Lin et al. 1995), one of which accounted for the observation that a few segregants flowered earlier than the early-flowering parent.

The advancement of the RIL population in an environment to which the *S. bicolor* parent was well adapted (indeed bred for) but the *S. propinquum* parent was not may have had some undesirable consequences as well. All segregation distortions in the F5 generation involved excesses of *S. bicolor* alleles, whereas the F2 generation showed similar numbers of cases of *S. bicolor* and *S. propinquum* excess. This finding suggests that in addition to the intended removal of short-day flowering, advancement of the population in temperate continental conditions may have caused some inadvertent selection against other traits of *S. propinquum*, a native of southeast Asia that inhabits streamside and moist places ([Anonymous 2006] zipcodezoo.com/Plants/S/Sorghum_propinquum/#footref_2). Although these biases favoring *S. bicolor* alleles may impact the ability to map QTL in a few regions of the genome, the population still exhibits a wide range of morphophysiological variations, with individual lines more comparable to one another by virtue of the near-absence of *Ma1*.

Benefiting from several additional cycles of recombination beyond our previous F2 population, comparison of this genetic map to the sorghum physical map and sequence highlight the striking bias in distribution of recombination across the sorghum genome. This is a good news—bad news scenario—relatively small amounts of physical DNA per cM may facilitate genomic analyses in the gene-rich portions of the genome, but large blocks of recombination-recalcitrant heterochromatin hinder access to other important genes.

Additional recombination that has accrued in the development of this RIL population may have also improved our ability to resolve apices (peak genomic regions) of heterozygote excess, accounting for their greater abundance in F5 than F2 generations, and occurrence in multiple locations on all chromosomes except the one (chromosome 6) for which about two-thirds of the physical length has been fixed due to selection against the *S. propinquum* short-day flowering allele.

A remarkably high 29 apices of heterozygote excess, together with rich genetic and genomic tools for these species, may make this an attractive system in which to further dissect the biology underlying interspecific heterozygote advantage.

ACKNOWLEDGMENTS

We thank members of the Paterson lab and two anonymous reviewers for many valuable contributions, and the U.S. Department of Agriculture (USDA) Agricultural Research Service, USDA Agriculture and Food Research Initiative, and U.S. Department of Energy–USDA Plant Feedstock Genomics Program for financial support. R.B. gratefully acknowledges financial support as a BOYSCAST Fellow from the Department of Science and Technology, Government of India (SR/ BY/L-08/2007). M.K.R. is thankful to the National Agricultural Innovative Project, Indian Council of Agricultural Research for providing financial support for his participation in this work.

LITERATURE CITED

Aljanabi, S. M., L. Forget, and A. Dookun-Saumtally, 1999 An improved and rapid protocol for the isolation of polysaccharide- and polyphenol-free sugarcane DNA. Plant Mol. Biol. Rep. 17: 281.

Anonymous, . 2006 *Sorghum propinquum*, pp. 600–601 in *Flora of China*, Vol. 22. Missouri Botanical Garden Press, St. Louis, MO.

Bowers, J. E., C. Abbey, S. Anderson, C. Chang, X. Draye et al., 2003 A high-density genetic recombination map of sequence-tagged sites for sorghum, as a framework for comparative structural and evolutionary genomics of tropical grains and grasses. Genetics 165: 367–386.

Bowers, J. E., M. A. Arias, R. Asher, J. A. Avise, R. T. Ball et al., 2005 Comparative physical mapping links conservation of microsynteny to chromosome structure and recombination in grasses. Proc. Natl. Acad. Sci. USA 102: 13206–13211.

Brown, S. M., M. S. Hopkins, S. E. Mitchell, M. L. Senior, T. Y. Wang et al., 1996 Multiple methods for the identification of polymorphic simple sequence repeats (SSRs) in sorghum (Sorghum bicolour (L.) Moench). Theor. Appl. Genet. 93: 190–198.

Brown, P. J., P. E. Klein, E. Bortiri, C. B. Acharya, W. L. Rooney et al., 2006 Inheritance of inflorescence architecture in sorghum. Theor. Appl. Genet. 113: 931–942.

Chittenden, L. M., K. F. Schertz, Y. R. Lin, R. A. Wing, and A. H. Paterson, 1994 A detailed RFLP map of Sorghum bicolor X S. propinquum, suitable for high-density mapping, suggests ancestral duplication of sorghum chromosomes or chromosomal segments. Theor. Appl. Genet. 87: 925–933.

Draye, X., Y. R. Lin, X. Y. Qian, J. E. Bowers, G. B. Burrow et al., 2003 Toward integration of comparative genetic, physical, diversity, and cytomorphic maps for grasses and grains, using the sorghum genome as a foundation. Plant Physiol. 125: 1325–1341.

Feltus, F. A., G. E. Hart, K. F. Schertz, A. M. Casa, P. Brown et al., 2006 Genetic map alignment and QTL correspondence between inter- and intra-specific sorghum populations. Theor. Appl. Genet. 112: 1295–1305.

Glover, J. D., J. P. Reganold, L. W. Bell, J. Borevitz, E. C. Brummer et al., 2010 Increased food and ecosystem security via perennial grains. Science 328: 1638–1639.

Heaton, E. A., F. G. Dohlenman, and S. P. Long, 2008 Meeting US biofuel goals with less land: the potential of Miscanthus. Glob. Change Biol. 14: 2000–2014.

Hu, F. Y., D. Y. Tao, E. Sacks, B. Y. Fu, P. X. Xu et al., 2003 Convergent evolution of perenniality in rice and sorghum. Proc. Natl. Acad. Sci. USA 100: 4050–4054.

Jang, C. S., T. L. Kamps, H. Tang, J. E. Bowers, C. Lemke et al., 2009 Evolutionary fate of rhizome-specific genes in a non-rhizomatous Sorghum genotype. Heredity 102: 266–273.

Kim, C., D. Zhang, S. A. Auckland, L. K. Rainville, K. Jakob et al., 2012 SSR-based genetic maps of *Miscanthus sinensis* and *M. sacchariflorus*, and their comparison to sorghum. Theor. Appl. Genet. 124: 1325–1338.
Kong, L., J. Dong, and G. E. Hart, 2000 Characteristics, linkage-map positions, and allelic differentiation of *Sorghum bicolor* (L.) Moench DNA simple-sequence repeats (SSRs). Theor. Appl. Genet. 101: 438–448.

Kosambi, D., 1944 The estimation of map distance from recombination values. Ann. Eugen. 12: 172–175.

Lander, E., P. Green, J. Abrahamson, A. Barlow, M. Daly et al., 1987 MAPMAKER: an interactive computer package for constructing primary genetic linkage maps of experimental and natural populations. Genomics 1: 174–181.

Lin, Y., K. Schertz, and A. Paterson, 1995 Comparative analysis of QTLs affecting plant height and maturity across the Poaceae, in reference to an interspecific sorghum population. Genetics 141: 391–411.

Lin, Y. R., L. H. Zhu, S. X. Ren, J. S. Yang, K. F. Schertz et al., 1999 A Sorghum propinquum BAC library, suitable for cloning genes associated with loss-of-function mutations during crop domestication. Mol. Breed. 5: 511–520.

Mace, E. S., and D. R. Jordan, 2011 Integrating sorghum whole genome sequence information with a compendium of sorghum QTL studies reveals uneven distribution of QTL and of gene-rich regions with significant implications for crop improvement. Theor. Appl. Genet. 123: 169–191.

Ming, R., S. C. Liu, J. da Silva, W. Wilson et al., 1998 Detailed alignment of Saccharum and Sorghum chromosomes: comparative organization of closely related diploid and polyploid genomes. Genetics 150: 1663–1682.

Ming, R., S.-C. Liu, J. E. Irvine, and A. H. Paterson, 2001 Comparative QTL analysis in a complex autopolyploid: candidate genes for determinants of sugar content in sugarcane. Genome Res. 11: 2075–2084.

Ming, R., T. A. Del Monte, E. Hernandez, P. H. Moore, J. E. Irvine et al., 2002 Comparative analysis of QTLs affecting plant height and flowering among closely-related diploid and polyploid genomes. Genome 45: 794–803.

Paterson, A. H., Y. R. Lin, Z. K. Li, K. F. Schertz, J. F. Doebley et al., 1995a Convergent domestication of cereal crops by independent mutations at corresponding genetic loci. Science 269: 1714–1718.

Paterson, A. H., K. F. Schertz, Y. R. Lin, S. C. Liu, and Y. L. Chang, 1995b The weeding of wild plants - molecular analysis of genes influencing dispersal and persistence of Johnsongrass, *Sorghum halepense* (L) Pers. Proc. Natl. Acad. Sci. USA 92: 6127–6131.

Paterson, A. H., J. E. Bowers, and B. A. Chapman, 2004 Ancient polyploidization predating divergence of the cereals, and its consequences for comparative genomics. Proc. Natl. Acad. Sci. USA 101: 9903–9908.

Paterson, A. H., J. E. Bowers, R. Bruggmann, I. Dubchak, J. Grimwood et al., 2009 The *Sorghum bicolor* genome and the diversification of grasses. Nature 457: 551–556.

Pratt, L. H., C. Liang, M. Shah, F. Sun, H. M. Wang et al., 2005 Sorghum expressed sequence tags identify signature genes for drought, pathogenesis, and skotomorphogenesis from a milestone set of 16,801 unique transcripts. Plant Physiol. 139: 869–884.

Ramu, P., K. Bantte, S. Senthilvel, C. Ashok Kumar, B. Jayashree et al., 2009 Exploiting rice–sorghum synteny for targeted development of EST-SSRs to enrich the sorghum genetic linkage map. Theor. Appl. Genet. 119: 1193–1204.

Rooney, W. L., J. Blumenthal, B. Bean, and J. E. Mullet, 2007 Designing sorghum as a dedicated bioenergy feedstock. Biofuels Bioproducts & Biorefining-Biofpr 1: 147–157.

Schloss, S. J., S. E. Mitchell, G. M. White, R. Kukatla, J. E. Bowers et al., 2002 Characterization of RFLP probe sequences for gene discovery and SSR development in *Sorghum bicolor* (L.) Moench. Theor. Appl. Genet. 105: 912–920.

Schnable, P. S., D. Ware, R. S. Fulton, J. C. Stein, F. S. Wei et al., 2009 The B73 maize genome: complexity, diversity, and dynamics. Science 326: 1112–1115.

Swigonova, Z., J. S. Lai, J. X. Ma, W. Ramakrishna, M. Llaca et al., 2004 On the tetraploid origin of the maize genome. Comp. Funct. Genomics 5: 281–284.

Tilman, D., R. Socolow, J. A. Foley, J. Hill, E. Larson et al., 2009 Beneficial biofuels—the food, energy, and environment trilemma. Science 325: 270–271.

Wang, S., C. J. Basten, and Z.-B. Zeng, 2012 *Windows QTL Cartographer 2.5*. Department of Statistics, North Carolina State University, Raleigh, NC.

Communicating editor: J. B. Holland