Legume Anchor Markers Link Syntenic Regions Between *Phaseolus vulgaris*, *Lotus japonicus*, *Medicago truncatula* and *Arachis*

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ABSTRACT

We have previously described a bioinformatics pipeline identifying comparative anchor-tagged sequence (CATS) loci, combined with design of intron-spanning primers. The derived anchor markers defining the linkage position of homologous genes are essential for evaluating genome conservation among related species and facilitate transfer of genetic and genome information between species. Here we validate this global approach in the common bean and in the AA genome complement of the allotetraploid peanut. We present the successful conversion of ~50% of the bioinformatics-defined primers into legume anchor markers in bean and diploid *Arachis* species. One hundred and four new loci representing single-copy genes were added to the existing bean map. These new legume anchor-marker loci enabled the alignment of genetic linkage maps through corresponding genes and provided an estimate of the extent of synteny and collinearity. Extensive macrosynteny between *Lotus* and bean was uncovered on 8 of the 11 bean chromosomes and large blocks of macrosynteny were also found between bean and *Medicago*. This suggests that anchor markers can facilitate a better understanding of the genes and genetics of important traits in crops with largely uncharacterized genomes using genetic and genome information from related model plants.

THE legume family (Leguminosae) is the third largest family of higher plants and includes >19,000 species (LEWIS *et al.* 2005). Plants belonging to the family are diverse, and trees, shrubby perennials, annual herbs, ornamentals as well as agriculturally important crops are represented. Legumes play a critical role in natural ecosystems, agriculture, and agroforestry, where their ability to establish symbiosis with nitrogen-fixing rhizobial bacteria makes them efficient colonizers of low-nitrogen environments and desirable protein crops. *Phaseolus vulgaris* L. (common bean) is a particularly important source of protein. It serves as a

staple food known as the poor man's meat and contains dietary fiber, minerals, vitamins, and various health promoting compounds (GUILLON and CHAMP 2002; LETERME 2002). *Arachis hypogaea* (cultivated peanut) is in addition to being consumed in many human foods, the fifth most important oil crop and also a rich source of dietary protein for the chicken and pork industries (GRAHAM and VANCE 2003).

The legume family is divided into three subfamilies: Caesalpinioideae, Mimosoideae, and Papilionoideae. Most of the economically important legumes are members of the monophyletic subfamily Papilionoideae, which can be divided into four major clades. Although the legumes included in our study, *Lotus japonicus*, *Medicago truncatula*, bean, and *Arachis* are all in the Papilionoideae subfamily, they belong to three different clades: halogalegina, phaseoloid/millettioid, and aeschynomenoideae/dalbergioid. *Lotus* and *Medicago* are equally closely related to the bean and equally distantly related to *Arachis* (DOYLE and LUCKOW 2003). Also the agronomical and genome characteristics of the legumes in our study differ. Both of the model legumes are herbaceous plants of limited agricultural use with relatively small genomes of ~470 Mb, while the common

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bean and cultivated peanut are major grain legumes with larger genomes of 588 Mbp and 2813 Mbp, respectively (<http://data.kew.org/cvalues/homepage.html>). In the bean there are >29,000 domesticated and 1300 wild accessions in germplasm banks (BROUGHTON *et al.* 2003). However, the genetic base of the commercial cultivars of specific market classes is narrow. Less than 5% of the genetic diversity available has been used globally despite nearly a century of organized bean improvement (BROUGHTON *et al.* 2003). Several genetic maps representing different populations have been established on a backbone of RFLP markers (VALLEJOS *et al.* 1992; NODARI *et al.* 1993; FREYRE *et al.* 1998).

The cultivated peanut is an allotetraploid with an AABB genome complement. The polyploidization event in its origin left the tetraploid cultivated peanut reproductively isolated from its wild diploid relatives (HALWARD *et al.* 1993). This fact, combined with self-pollination, has entailed a narrow genetic base and a limited diversity for some traits of agricultural interest (MORETZSOHN *et al.* 2005). No linkage map is available for the cultivated peanut. The maps that have been published in *Arachis* were based on interspecific crosses of diploid *Arachis* species or a cross of a synthetic tetraploid with the cultivated peanut (HALWARD *et al.* 1993; BUROW *et al.* 2001; MORETZSOHN *et al.* 2005).

Characterizing syntenic relationships between model and crop legumes seems therefore to have wide applications. If collinearity (conservation of gene order) or synteny (conservation of linkage) is found between species, information from large-scale genome sequencing of the *Lotus* and *Medicago* gene-rich regions can be used to optimize the only limited genetic and genomic information available from the genomes of bean and *Arachis*. Following this rationale our objective was to investigate the level and structure of synteny between the legume models (primarily *Lotus*) and bean and *Arachis*. The aim was to design robust PCR-based markers requiring relatively simple laboratory equipment and for this purpose we focused on size markers on the basis of insertions/deletions, cleaved amplified polymorphic sequence (CAPS), and derived cleaved amplified polymorphic sequence (dCAPS) markers (KONIECZNY and AUSUBEL 1993; NEFF *et al.* 1998). The bioinformatics pipeline, which suggests comparative anchor-tagged sequence (CATS) loci for use within a set of related organisms (FREDSLUND *et al.* 2006a) and the automated primer design program PriFi (FREDSLUND *et al.* 2005) were used to identify and rank intron-spanning gene-based sets of degenerate primers. To identify conserved primer sites for use throughout the legume family, EST collections originating from *Lotus*, *Medicago*, soybean, and, to a limited extent, bean and *Arachis* were used as input. The pipeline then applied a number of filters optimizing the selection of single-copy orthologous genes and the likelihood of identifying polymorphisms between the mapping pa-

rents. Hence primers were designed for conserved exon regions allowing PCR amplification of an intron-spanning fragment, detection of polymorphism, and gene verification by sequencing of the intron and flanking exon regions, respectively (FREDSLUND *et al.* 2005, 2006a,b). Applying these criteria, a list of 459 universal Leg-primer sets was generated (<http://cgi-www.daimi.au.dk/cgi-chili/GeneticMarkers/table>).

We have tested 159 pipeline-generated primer pairs in bean and 124 in *Arachis* and converted ~50% into legume anchor markers. Subsequent comparison of the corresponding positions of these anchor markers on the linkage maps of *Lotus*, *Medicago*, bean, and *Arachis* showed different levels of genome conservation. A high level of macrosynteny was discovered between bean and *Lotus* where syntenic regions often span large regions, even entire linkage groups. Substantial regional synteny was also found between bean and *Medicago* and these regions occasionally cover segments with no apparent bean-*Lotus* synteny.

MATERIALS AND METHODS

Design of gene-based PCR markers: Homologous ESTs from mainly *Lotus japonicus*, *Medicago truncatula*, and soybean were aligned together with genomic sequence from *Lotus* or *Medicago*, and primer sites in conserved exon regions were identified. The bioinformatics pipeline was set to optimize for the following criteria: (1) the targeted gene was either single copy or represented by two copies in *Arabidopsis*, (2) primer design was based on ESTs where the topology of the gene tree was found to match the species tree indicating orthology of targeted genes, and (3) primer pairs anneal in conserved exon regions allowing PCR amplification of an intron-spanning fragment (FREDSLUND *et al.* 2005, 2006a,b). The resulting primers are called Leg primers. At first the work was done manually, later (starting with marker Leg060) the process was automated. In addition, the ESTs were compared to the full set of inferred protein-coding sequences of the reference species *Arabidopsis* to estimate the number of paralogous sequences. Only sequences expected to be single copy in the legumes were used.

Starting with Leg175, a fully automated bioinformatics approach was used for both, grouping closest homologs, sequence alignment, and primer design (FREDSLUND *et al.* 2005, 2006a,b). A number of primer sets (<http://bioweb.abc.hu/cgi-mt/pisprim/pisprim.pl>) developed by György Kiss's group in Gödöllő, Hungary, for the Grain Legume Integrated Project (GLIP) were also tested in bean. These primer sets were developed from essentially the same criteria. Three of them were mapped and given names of the type "mtmt_Gen_" followed by three numbers with spacing in between.

The criteria for selecting primers, from the bioinformatics pipeline, for experimental use/marker development were that they should be single copy in *Arabidopsis*. Homologous single-copy genes in any two genomes are likely to be orthologs, and only true orthologs are suitable for comparative studies. Moreover, the alignment underlying primer design should contain ESTs from at least three different species, or two species from different clades, to represent a broad span of sequence divergence and thereby make it likely that the PCR primers would perform well in distantly related legumes like *Arachis*. The predicted biological function of the gene, where the primers anneal, was never used as a criterion in the selection process.

DNA extraction and marker development: Genomic DNA from the mapping parents and for each of the recombinant inbred lines (RILs) were isolated from frozen, young leaf tissue using a modified cetyltrimethylammonium bromide (CTAB) method. Leaf tissue from a single leaf was crushed in liquid nitrogen using mortar and pestle. The tissue was then transferred to a 13-ml Sarstedt tube and CTAB extraction was carried out as described by SANDAL *et al.* (2006) except that the chloroform/isoamylalcohol step was repeated and 10 μ l (instead of 5 μ l) of RNase (10 mg/ml stock) were added. The DNA pellet was redissolved in $\sim$ 100 μ l of H₂O. Standard PCR conditions were used for the parental survey, where markers were amplified with 94° for 5 min, then 40 cycles of 94° denaturing for 30 sec, 48° (or 45°) annealing for 30 sec, and 72° extension for 2 min, followed by a 5-min final extension at 72°. The PCR reaction was carried out in a final volume of 20 μ l containing estimated 0.1 μ g of genomic DNA. Single PCR products were purified in the tube using a combination of ExonucleaseI (New England Biolabs, M0293L) and shrimp alkaline phosphatase (USB, 70092Y) in a buffer containing 20 mM Tris–HCl pH 8.0 and 10 mM MgCl₂. Multiple PCR products were gel extracted using the QIAquick gel extraction kit (Qiagen, 28706), and except for eluting in 30 μ l, the kit protocol was followed. Sequencing was done using ABI BigDye version 3.1. The identity of the amplification products was confirmed by Blastx searches against the Arabidopsis protein database at NCBI or comparison of the translated sequence from the amplification product to the translated sequence of the EST contig underlying primer design. Only amplification products reliably identified were considered further. If there was a significant size difference in the amplification product from the mapping parents, a size marker was made. Otherwise the web-based dCAPS Finder ver. 2.0 software (NEFF *et al.* 2002) was used for suggestion of enzymes for CAPS markers and design of mismatched primers for development of dCAPS markers based on reliable SNPs.

Map calculation and map drawing in bean: Linkage analysis was performed using JoinMap version 2.0 (STAM 1993). The linkage groups were numbered according to FREYRE *et al.* (1998). MapChart 2.2 was used to draw the map (VOORRIJS 2002), and map modifications were done in Microsoft PowerPoint. To test the quality of the data and the mapping, the color mapping procedure was used (KISS *et al.* 1998).

The map position of the bean sequences representing 18 different standard bean markers with a single best match (E -value $< 10^{-7}$) to a Lotus sequence with a known map position (supplemental Table S3) were placed on the bean–Lotus/Medicago/Arachis synteny map (Figure 3) along with the Leg markers. Some of these markers (D1032, Bng12, Bng228, and Bng200) were already positioned along with the Leg primers using the BAT93 $\times$ JaloEEP558 (B $\times$ J) RILs. Others had been mapped either in the B $\times$ J F₂ population or in other bean populations, and positioning of these on the B $\times$ J RIL map were made by manual evaluation according to shared markers and cM distances on the bean integrated linkage maps (http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?taxid=3885) (this applies to D1051, Bng72, Bng108, Bng148/R, Mng415, Bng57, Bng3, Hyp4-1, Bng179, Bng87, Bng95, Bng26, Bng206, and Bng1).

Linkage analysis in Lotus: For the anchor markers that could not be mapped in the Gifu $\times$ MG20 population, primers were tested for polymorphism between *L. japonicus* Gifu and the related species *L. filicaulis* (SANDAL *et al.* 2006). Lotus BAC/TAC sequences and the web-based computer program Tandem Repeat Occurrence Locator (TROLL) (<http://wsmartins.net/webtroll/troll.html>) were used for identifying microsatellites. Due to suppression of recombination and resulting poor resolution in parts of the Lotus genetic map

(SANDAL *et al.* 2006), some of the Leg markers were not mapped to a specific location on the Lotus map, but rather to a region. If this region was < 10 cM the marker was artificially put on the map on a location equivalent to the midpoint of the interval where it was mapped (this applies to 12M-Gm, 33M-Gm, Leg036, Leg055, Leg081, Leg183, Leg187, Leg191, Leg203, Leg213, Leg228, and Leg231). Leg markers mapping to a region > 10 cM are not shown on the Lotus map (this applies to Leg111, Leg177, Leg202, Leg206, and Leg762).

RESULTS

Gene-based PCR markers: To validate the application of the Leg primers for comparative mapping, a subset corresponding to single-copy genes in Arabidopsis was selected for generating legume anchor markers in bean and Arachis. The chosen Leg primers were used to amplify PCR fragments from the BAT93 and JaloEEP558 parents of the bean RILs (FREYRE *et al.* 1998), as well as the *A. duranensis* K7988 and *A. stenosperma* V10309 parents (MORETZSOHN *et al.* 2005) of the Arachis population, subsequently used for mapping. Following the flow scheme outlined in Figure 1 an overlapping set of 159 and 124 primer pairs was tested in bean and Arachis, respectively. To verify the identity of amplified fragments, the terminal exon sequences of the PCR fragments were compared to a translated version of aligned ESTs used for primer design or alternatively a Blastx search was performed (Figure 1). For bean, $\sim 70\%$ of the PriFi primer pairs on the basis of ESTs from four, three, or two different legume species amplified a product that was verified (supplemental Table S1). In Arachis $\sim 55\%$ of the primer pairs on the basis of four or three ESTs produced a PCR fragment that could be verified (supplemental Table S1). Following a positive confirmation of gene identity, sequence polymorphism between the mapping parents was used to develop the CAPS, dCAPS, or size markers applied for mapping the Leg-marker loci. In bean, 50% of the original primer sets tested were developed into markers and in Arachis the yield was 45% (Table 1). Prior to the development of the bioinformatics pipeline a number of markers were developed manually using the same principles, and adding these markers a total of 111 bean markers were made.

Gene-based genetic map of the bean: To develop the bean genetic linkage map, 77 lines from the recombinant inbred (RI) population B $\times$ J (FREYRE *et al.* 1998) were used. The segregation information collected from the 111 Leg markers in this study was analyzed, along with data from 150 framework markers from the core linkage map (FREYRE *et al.* 1998). Using JoinMap version 2.0 (STAM 1993) and a 3.5-LOD threshold, we were able to assign 104 Leg markers to 99 loci in 11 linkage groups, corresponding to the haploid chromosome number of bean (Figure 2). The linkage groups range from 40.8 cM (*Pv*LG10) to 99.8 cM (*Pv*LG2), and the total map length is 758 cM (Table 2). The number of

FIGURE 1.—Flow scheme of marker production. The Leg primers were tested on DNA from mapping parents. Single products were enzymatically purified before sequencing, verification of gene identity, and detection of polymorphism. Multiple products were gel extracted individually before sequencing. Only sequence confirmed PCR products were converted into markers.

Leg markers per chromosome range from 3 to 19 with an average of 9.5 and the average interval between Leg markers is 7.3 cM. The generated Leg markers include 15 polymorphic size markers, 48 CAPS, and 48 dCAPS markers. Marker information can be seen in supplemental Table S2.

Besides the described linkage groups, one Leg marker (7-Gm) showed linkage to one of the framework markers (DROD3a) and four Leg markers (Leg191, Leg194, Leg223, and Leg232) came out as unlinked loci.

Mapping in both the B × J and the DOR364 × G19833 (D × G) population, had previously proved useful for positioning microsatellites that were monomorphic in one or the other of the populations (BLAIR *et al.* 2003). In an attempt to improve the marker yield 17 different Leg-primer pairs, which amplified a correct but monomorphic product in B × J, were tested in the D × G mapping parents. However, a SNP polymorphism was detected in only two of the PCR fragments (data not shown) implying that a mapping population originating from more distantly related parents is optimal for this approach.

TABLE 1

Summary of primer efficiency for exhaustively tested primer pairs

	Primer pairs tested	Amplify correct gene	Markers developed
Bean (B × J)	159	113 (71.1)	80 (50.3)
Arachis (K × V)	124	67 (54.0)	56 (45.2)

Numbers in parentheses are percentages.

Allele frequencies in the B × J RI population: The allele frequency was calculated for each marker locus to evaluate the degree of deviation from the expected 0.5 transmission frequency for each parental allele at each locus of the RIL lines. All markers with segregation data were subjected to this analysis, including the framework markers and interestingly there were large regional differences in allele frequencies. At the bottom part of *PvLG7* there is a major segregation distortion. The maternal BAT93 alleles are overrepresented compared to the paternal JaloEEP558 alleles (supplemental Figure S1). The segregation distortion has a maximum at the bottom of *PvLG7* with 85% of the alleles originating from BAT93, but is normalized to the expected value of 50% at the middle of *PvLG7* after ~35 cM. This linkage group was previously reported to have a preference for the BAT93 allele (NODARI *et al.* 1993; FREYRE *et al.* 1998). On *PvLG10*, a modest but consistent segregation distortion was observed. *PvLG10* carries only 11 markers, but at all loci, the transmission frequency was higher for the BAT93 alleles. Moreover, on *PvLG1*, *PvLG4*, and *PvLG6* large regions of segregation distortion were found. On *PvLG1* and *PvLG6* the JaloEEP558 alleles were favored in regions of ~30 cM, whereas on *PvLG4* the BAT93 alleles were more prominent, again in a region of ~30 cM. The preference for the Andean JaloEEP558 alleles on linkage group *PvLG1* is consistent with the observations of FREYRE *et al.* (1998) and NODARI *et al.* (1993). Preferential transmission of parental alleles could be caused by an allele specific advantage in viability or fertility and Leg markers may represent or be linked to alleles selected during the eight generations used for development of the RILs (FREYRE *et al.* 1998).

Bean–Lotus synteny: To evaluate the extent of macro-synteny between Lotus and bean the individual positions of Leg markers on the two genetic linkage maps were compared. Most of the Leg-marker positions in Lotus were known from their presence on BAC or TAC clones, which were mapped in the intraspecific cross between *L. japonicus* ecotypes Gifu and *L. japonicus* Miyakojima MG-20 (HAYASHI *et al.* 2001; KATO *et al.* 2003) and the collinear *L. filicaulis* × *L. japonicus* Gifu map (SANDAL *et al.* 2006). Where map positions were absent, we took advantage of the Lotus genome-sequencing program. A corresponding BAC or TAC clone was included in the genome sequencing and genetically mapped using the

FIGURE 2.—Genetic linkage map of the bean. Each vertical bar represents individual bean linkage groups (LG). Marker names are shown on the right side of each linkage group, connecting lines indicate the position of each locus on the linkage map, and centimorgan values are given on the left side. Each of the Leg markers (red and in boldface type) represents a single-copy gene in the bean except for one marker (“Baja”), which is marked with #. Non-Leg markers are shown in italics.

TABLE 2
Synteny summary of the 11 *Phaseolus vulgaris* linkage groups

Bean linkage group	Length of LG (cM)	No. of anchor markers	Synteny identified				Approximate size (cM)
			<i>Lj</i> LG	<i>Mt</i> Chr	<i>Ara</i> LG	Cannon synteny block	
<i>Pv</i> LG1	56.3	9	5	1	—	1	2
			1	7	—	5	4
<i>Pv</i> LG2	99.8	23	4	4	3	7	34
			2	5	—	10	58
<i>Pv</i> LG3	95.0	15	4	—	—	8	15
<i>Pv</i> LG4	75.0	7	2	4, 6	5	—	65
<i>Pv</i> LG5	56.3	4	3	2	—	—	23
<i>Pv</i> LG6	71.6	15	6	2	—	3	37
			1	7	—	5	3
<i>Pv</i> LG7	70.7	9	5	1	9	2	64
<i>Pv</i> LG8	70.8	12	2	5	7	9	30
<i>Pv</i> LG9	42.9	9	1	3	2, 8	4	43
<i>Pv</i> LG10	40.8	4	3	—	—	—	8
<i>Pv</i> LG11	78.8	15	3	4, 8	3	6	70
Total	758	122 ^a					

The main affinities observed toward *Lotus japonicus* (*Lj*), *Medicago truncatula* (*Mt*), and *Arachis* (*Ara*) are given. The approximate sizes of the syntenic blocks in bean are based on bean–Lotus syntenic, allowing one nonsyntenic marker.

^aIncluding 104 Leg markers and 18 standard bean markers (http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?taxid=3885) with a single best-sequence match (E -value $< 10^{-7}$) to a Lotus sequence with a known map position in Lotus.

standard microsatellite marker procedure. A total of 81 of the legume anchor markers were positioned on the genetic map of both bean and Lotus (Figure 3). To add more loci, 99 of the previously developed standard bean markers from the Build 1.1 linkage map (http://www.ncbi.nlm.nih.gov/mapview/map_search.cgi?taxid=3885) that had sequence information attached was searched (Blastn) against the Lotus genome sequence. This approach found bean sequences representing 18 different bean markers with a single best match (E -value $< 10^{-7}$) to a Lotus sequence with a known map position on the Lotus genetic map (supplemental Table S3).

A total of 99 unique positions were shared between bean and Lotus, ranging from 2 (*Pv*LG5) to 20 (*Pv*LG2) shared markers per linkage group and an average of 9 common markers per linkage group. Extensive syntenic between Lotus and bean was found for about half of the bean linkage groups. In *Pv*LG4, *Pv*LG7, *Pv*LG9, and *Pv*LG11 the syntenic regions span entire linkage groups (with a maximum of one nonsyntenic marker) and in *Pv*LG2 and *Pv*LG8, half a linkage group. *Pv*LG5 and *Pv*LG10 have only 2 and 3 markers, respectively, shared with Lotus. Only 4 of the 11 bean linkage groups have markers that map to >2 different Lotus linkage groups, and even among these, 3 clearly show syntenic toward one particular Lotus chromosome. For example, 6 of 11 markers on *Pv*LG3 belong to *Lj*LG4, 7 of 12 markers on *Pv*LG6 belong to *Lj*LG6, and 5 of 8 markers on *Pv*LG8 belong to *Lj*LG2. *Pv*LG1 contains 9 shared markers mapping to 3 different Lotus linkage groups.

The syntenic marker positions on Lotus and bean chromosomes shown in Figure 3 indicate that only a

limited number of large-scale rearrangements occurred during the evolution of legume chromosomes. To evaluate this suggestion further, marker collinearity was investigated. Three examples of this analysis are shown in Figure 4. It is clear that the blocks of syntenic loci are only partly collinear and that smaller internal chromosome rearrangements have occurred in addition to the large scale rearrangements. Figure 4 (bottom) shows an example of one bean linkage group having blocks of anchor loci shared with two Lotus linkage groups and one Lotus linkage group having syntenic blocks shared with two bean linkage groups.

Bean–Medicago syntenic: Positions of Leg markers in Medicago were found by Blastn searches against the Medicago pseudomolecules (http://www.medicago.org/genome/cvnt_blast.php), using a combination of bean sequences amplified with the Leg primers and the Medicago EST sequence included in the CATS alignment for Leg-primer design. Search information is presented in supplemental Table S4. For the previously developed bean standard markers with sequence information known, the bean sequence was used (supplemental Table S3). Among the Leg markers, 65 had a match with E -value $< 10^{-7}$ in Medicago, and among the 18 marker sequences 10 had a match with E -value $< 10^{-7}$. All in all this amounts to 75 shared positions between bean and Medicago, ranging from 3 (*Pv*LG5 and *Pv*LG7) to 15 (*Pv*LG2) markers per bean linkage group and an average of 6.8 markers per linkage group (Figure 3). Substantial syntenic is seen. Two of the bean linkage groups, having 3 (*Pv*LG5) and 5 (*Pv*LG9) shared positions to Medicago, respectively, have only markers mapping to a single

FIGURE 3.—Synteny between bean, Lotus, Medicago, and Arachis defined by legume anchor markers. Synteny to *Lotus japonicus* (Lj) and *Medicago truncatula* (Mt) is given by the color code. The color scheme reflects the synteny observed between Mt and Lj. For example, pronounced synteny has been found between LjLG2 and MtChr5 (CANNON *et al.* 2006) and accordingly they were given the same color. The gene content of LjLG1 is for the main part shared between MtChr3 and MtChr7 and accordingly they were given similar colors. Two markers sharing the same position in the bean are indicated by a vertical bar, in the color window. The correspondence between Leg-marker positions in Lotus and the 10 large-scale synteny blocks described by CANNON *et al.* (2006) is indicated by dotted lines. The bean linkage groups (LG) are shown as previously presented in Figure 2. The locations of the 14 non-Leg markers marked with asterisks are only approximate and therefore no centimorgan position is given.

FIGURE 3.—Continued.

FIGURE 4.—Detailed examples of macrosynteny between bean (*Pv*) and *Lotus japonicus* (*Lj*). Each vertical bar represents individual bean and *Lotus* linkage groups (LG). Marker names are shown on one side of each linkage group and centimorgan values are given on the other side. Each of the Leg markers (shown in boldface type) represents a single-copy gene in the bean except for one marker, which is marked with #. Non-Leg markers are shown in italics. Lines connect anchor-marker loci. *Lj*LG5, *Lj*LG3, and *Lj*LG4 are shown in reverse orientation.

Medicago chromosome and at the bottom part of *Pv*LG2 a large syntenic segment spanning 52 cM is seen. Six of 11 bean linkage groups have markers that map to >2 different *Medicago* linkage groups, but 5 of these have

1 (*Pv*LG3 and *Pv*LG11) or 2 (*Pv*LG2, *Pv*LG6, and *Pv*LG8) uninterrupted syntenic regions of at least 3 markers. A total of 11 uninterrupted regions with ≥ 3 shared markers are distributed over the bean linkage groups.

FIGURE 5.—Detailed examples of macrosyteny between bean (*Pv*) and *Medicago truncatula* (*Mt*). Vertical bars represent individual bean linkage groups (LG) or segments of *Medicago* pseudochromosomes (hatched). Marker positions are given in centimorgans for bean and 1:100,000 bp for *Medicago*. Names of Leg markers are shown in boldface type whereas non-Leg markers are shown in italics. Lines connect anchor-marker loci. *MtChr4* and *MtChr5* are shown in reverse orientation.

Figure 5 shows two detailed alignments between bean and *Medicago*. In both examples, blocks of loci show synteny, but only partial collinearity indicating small internal chromosome rearrangements.

Bean–Arachis synteny: Positions of Leg markers in *Arachis* were found by mapping in a diploid F₂ mapping population, originating from a cross between *A. dura-*
nensis K7988 and *A. stenosperma* V10309 (MORETZSOHN

et al. 2005). Eighty-two Leg markers were mapped in *Arachis* and 38 of them have a linkage map position in bean. The number of shared loci between bean and *Arachis* range from zero (*PvLG1*) to eight (*PvLG3*), with an average of 3.5 shared loci per bean linkage group. In three of the bean linkage groups (*PvLG2*, *PvLG4*, and *PvLG8*) nondisrupted syntenic segments of ≥ 3 loci mapped to the same *Arachis* linkage group. Of these,

PvLG4 and *PvLG8* only shared markers to one *Arachis* linkage group. However, several of the bean linkage groups have a patchy pattern of loci shared with more *Arachis* linkage groups (Figure 3).

Figure 6 shows two detailed examples of macrosynteny between Medicago, bean, Lotus, and *Arachis*. The syntenic blocks between *Arachis* and Lotus consist of three and four markers, respectively.

Bean–Lotus–Medicago–Arachis synteny: Besides giving a quick overview of the pairwise synteny observed between bean, Lotus, Medicago, and *Arachis*, respectively, the color scheme given in Figure 3 reflects the previously described synteny blocks between Lotus and Medicago (CANNON *et al.* 2006). Accordingly, it is possible to relate the synteny detected by Leg markers to the chromosome correspondences between the two model legumes. In the large-scale sequence-based comparison reported by CANNON *et al.* (2006) 10 large-scale synteny blocks were identified. Notably most of the syntenic regions we have identified fall into these blocks. For example, three large syntenic segments between bean, Lotus, and Medicago were found on *PvLG2* and *PvLG9* (Figure 3 and Table 2). Our synteny analysis therefore supports and is supported by the large-scale sequence-based comparison.

Defining syntenic segments as uninterrupted regions with at least three markers, 48% of the bean linkage map is syntenic to Lotus (367 of 758 cM) and 35% is syntenic to Medicago (263 of 758 cM). However, bean has more markers shared with Lotus than with Medicago and therefore the numbers are not directly comparable.

Bean–Arabidopsis synteny: In our setup for primer design, we have used the GenBank accession number of the Arabidopsis ortholog as a reference for the alignment of legume EST sequences, and therefore we have shared positions for some 100 loci in bean and Arabidopsis. Five of the bean linkage groups (*PvLG3*, *PvLG5*, *PvLG6*, *PvLG8*, and *PvLG11*) have uninterrupted regions of ≥ 3 loci extending up to 33 cM (Leg133–Leg220 on *PvLG11*), which share linkage on an Arabidopsis chromosome (supplemental Figure S2). Given the ~ 112 million years thought to separate Arabidopsis from the legumes (BOWERS *et al.* 2003), the gene linkage is remarkable although macrosynteny has been observed before (GRANT *et al.* 2000). Moreover, our experimental setup focuses on single-copy and highly conserved genes, and this group of genes is optimal for identifying ancestral synteny.

DISCUSSION

Here we present the application of an automated and systematic approach for developing anchor markers in two distantly related legumes, bean and *Arachis*, chosen for testing the feasibility of the approach. Among the 159 Leg-primer pairs created by the bioinformatics pipeline, which were exhaustively tested in bean and an overlapping set of 124 Leg-primer pairs tested in *Arachis*,

113 (71%) amplified the correct product in bean and 67 (54%) amplified the correct product in *Arachis*. PriFi suggests and ranks 4 different primer pairs per alignment. For each of these we have only used the highest ranking and tested rankings from 187 to 22 without finding a difference in efficiency between high-ranking and low-ranking pairs. Use of ≥ 1 of the 3 alternative PriFi primer sets would therefore most likely increase the marker yield. Similarly, there were no major differences in efficiency between primer pairs based on ESTs from four, three, or two different legume species. The PriFi settings used to generate the 459 primer sets appear therefore to be robust. Since the *Arachis*-mapping parents were more polymorphic than the bean-mapping parents the marker yield was nearly the same, 50% *vs.* 45%. Here we present a bean linkage map with 104 new legume anchor-marker positions. The linkage map adds additional genetic resolution to the existing bean maps and expands the map with 1.9 cM at the outermost top of *PvLG6* and 4.1 cM at the top of *PvLG10*. Leg markers distribute over all of the 11 bean linkage groups, and in only five cases do 2 Leg markers share the same locus. This absence of clustering may indicate that suppression of recombination is rare in the B $\times$ J RILs. The distribution of Leg markers and thus the genetic resolution varies. For example, linkage group *PvLG2* has 19 Leg markers, whereas *PvLG10* has only 3 Leg markers. This difference might be a consequence of the bioinformatics setup designing Leg primers. The bioinformatics pipeline selects primers in regions of high sequence conservation and gives preference to highly expressed genes represented in EST collections. Neither conserved genes nor highly expressed genes are necessarily randomly distributed in genomes, and an inverse relationship between the frequency of single-copy genes and clustered retrotransposons has been observed (D. BERTIOLI, M. MORETZSOHN, L. H. MADSEN, N. SANDAL, S. LEAL-BERTIOLI, P. GUIMARÃES, B. K. HOUGAARD, J. FREDSLUND, L. SCHAUSER, A. M. NIELSEN, S. SATO, S. TABATA, S. CANNON and J. STOUGAARD, unpublished results). Most importantly our results provide proof of concept for the bioinformatics-driven identification of anchor-tagged loci that, together with positional information from homologous loci in Lotus, Medicago, and *Arachis*, provide a basis for comparative genomics and an overview of the synteny among these four legumes.

Synteny: One of the ideas behind the model-legume concept was to exploit synteny between model and crops to accelerate isolation and comparative characterization of genes from the less characterized crop legumes. This approach requires that the target genome regions contain the same genes in approximately the same order in models and crops. A substantial effort has been invested in investigating this question. Regional synteny between Medicago and/or Lotus models and pea (AUBERT *et al.* 2006), alfalfa (CHOI *et al.* 2004a), red clover (SATO *et al.* 2005), lens (PHAN *et al.* 2006, 2007), and lupin (NELSON *et al.* 2006; PHAN *et al.* 2006) lend support to this

FIGURE 6.—Detailed examples of macrosynteny between bean (*Pv*), *Lotus japonicus* (*Lj*), *Arachis* (*Ara*), and *Medicago truncatula* (*Mt*). Vertical bars represent individual bean, *Lotus*, and *Arachis* linkage groups (LG) or segments of *Medicago* pseudo-chromosomes (hatched). Marker positions are given in centimorgans for bean, *Lotus*, and *Arachis* and 1:100,000 bp for *Medicago*. Names of Leg markers are shown in boldface type whereas non-Leg markers are shown in italic. Lines connect anchor-marker loci. *MtChr5*, *LjLG2*, *AraLG7*, and *AraLG2* are shown in reverse orientation. Only the top part of *AraLG2* is shown.

approach. In the present analysis, we have anchor-tagged loci covering 758 cM of the bean genetic map and a set of 99 shared loci made it possible to compare this map with the genetic map of Lotus. All of the 11 bean linkage groups had noninterrupted regions of at least two markers also showing linkage in the Lotus genome, and in several of the bean linkage groups synteny spanned entire linkage groups. All in all, the legume anchor markers revealed a broad conservation of gene linkage (macrosynteny) between bean and Lotus.

Seventy-five loci were shared between bean and Medicago and substantial conservation of gene linkage between bean and Medicago was found (Figure 3). However, even though Medicago and Lotus phylogenetically are equally distant from bean, the conserved bean–Medicago segments are generally shorter than observed for bean–Lotus. Looking at uninterrupted syntenic regions >20 cM, five can be found between bean and Medicago [*PuLG2* (two regions), *PuLG6*, *PuLG9*, and *PuLG10*] whereas seven are seen between bean and Lotus [*PuLG2* (two regions), *PuLG4*, *PuLG7*, *PuLG8*, *PuLG9*, and *PuLG11*]. In certain regions linkage is more conserved between bean and Medicago than between bean and Lotus, for example, the region in *PuLG3* flanked by *Leg187* and *Leg164N*. Here five *Leg* markers all map to *MtChr8*, whereas the same region maps to four different Lotus linkage groups. Likewise, in *PuLG6* the region flanked by *Leg217* and *Leg081* have four *Leg* markers all mapping to *MtChr7*, whereas in Lotus, they map to three different linkage groups. However, in *PuLG2*, *PuLG4*, *PuLG7*, and *PuLG11* macrosynteny between bean and Lotus is more pronounced than between bean and Medicago.

Despite the fact that bean and Arachis have similar numbers of chromosomes (11 and 10, respectively), the wild Arachis species have genome sizes that are considerably larger than the genomes of bean and Lotus. *A. duranensis* has a gametic DNA content (1C) of 1243 Mbp (<http://data.kew.org/cvalues/homepage.html>). Moreover, Arachis is a rather distant relative of bean and Lotus, so the evidence of macrosynteny documented between Arachis, bean, Lotus, and Medicago is remarkable. In both of the detailed examples shown in Figure 6, the loci shared between Lotus and Arachis span a larger region in Lotus than in Arachis. Given the difference in DNA content between these two species, this seems surprising. However, whereas the average physical equivalent of 1 cM corresponds to 1.97 Mbp in Arachis (MORETZSOHN *et al.* 2005), Lotus chromosome 1 has a mean ratio of 0.77 Mbp/cM (PEDROSA *et al.* 2002).

A comparative map spanning cold- and warm-season legumes was presented by CHOI *et al.* (2004b). In their study, marker segregation was analyzed in *M. truncatula*, *M. sativa*, *P. sativum*, *V. radiata*, and bean. Using a limited number of markers, 8 of 11 bean linkage groups were included from their already-described relation to *V. radiata* (mung bean) (BOUTIN *et al.* 1995). No markers

were directly shared between bean and Medicago and bean–Medicago synteny was inferred using several bridging legume species. The bean–Medicago relations presented here are documented by directly corresponding shared loci and include all of the 11 bean linkage groups. In addition, 9 of the bean linkage groups show synteny to >1 Medicago linkage group, and in this study we have precise indication of which regions on the individual bean linkage groups share homology to which Medicago chromosomes.

Macrosynteny between bean and Lotus was described by ZHU *et al.* (2005). A circle diagram included 8 of 11 bean linkage groups and the relations to Lotus were inferred through positions shared between Lotus and Medicago. In contrast to ZHU *et al.* (2005), we present markers directly bridging the genomes of bean and Lotus and thereby we define regions of shared macrosynteny directly on each of the 11 bean linkage groups.

Previous studies have demonstrated substantial macrosynteny between Lotus and Medicago (CHOI *et al.* 2004b; YOUNG *et al.* 2005; CANNON *et al.* 2006), and in a bioinformatics approach comparing 121 Mbp of non-redundant map-anchored genomic sequence from the Lotus build with 149 Mbp from the Medicago build, 10 large-scale synteny blocks were identified (CANNON *et al.* 2006). On the bean–Lotus/Medicago/Arachis synteny map (Figure 3), the color code reflects the described synteny between Lotus and Medicago. As seen, in large parts of the bean genome, the synteny to Lotus and Medicago converges on the 10 large-scale synteny blocks defined by direct sequence comparison. We infer that large syntenic segments are conserved in the genomes of legumes and that anchor markers can link these segments between different species and directly to the genome sequence of the model legumes.

Given the extensive linkage observed between bean and the two model legumes in this study, we therefore conclude that Lotus and Medicago will have a significant potential for future identification of tightly linked markers for marker-assisted selection and map-based isolation of candidate genes.

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