Framework molecular markers of the *B. rapa* (R500 x FPsc) genetic map

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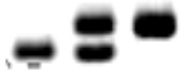
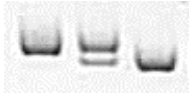
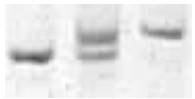
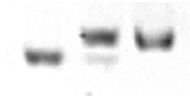
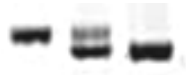
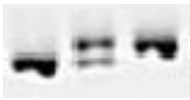
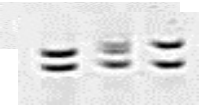
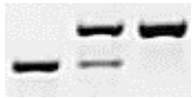
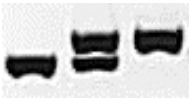
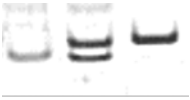
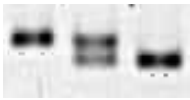
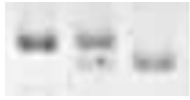
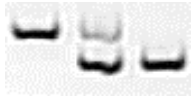
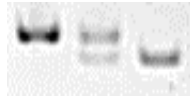
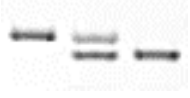
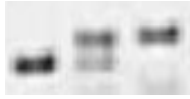
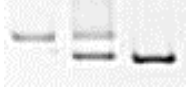
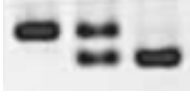
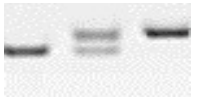
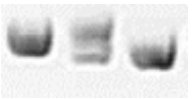
B. rapa Chr[1]	Marker[2]	Map Position[3] (cM)	Forward Primer Sequence	Reverse Primer Sequence	Fragment Size (bp) FPsc	Fragment Size (bp) R500	Image[4] F H R	Gel Run-time (min)[5]
A01	RP97	0.0	TGCTTGAGACGCTGCCACTTTGTTC	CATTCCTCCCCACCACCTTCACATC	190	225		30-60
A01	RP803	9.8	TCGGCTTCCAAGGGTAAGAT	CTCGTCCGTACCGTTCTCTT	180	160		90
A01	RP801	26.5	ATGCTCAGCCTCACATAGCA	ATGTTGGCTCTCCAAGATGC	NA	NA	NA	NA
A01	RP101	56.1	CTCCTGTCCTCAACTATGTTTCCTT	TTGATTAGAAATAGAAGAAGAGAGA	290	350		40
A01	RP185	60.9	CCCTTTGTTTCTTCTTTATTCA	TCAACTATTCTATCACATCTCCA	350	300		80
A01	RP323	66.3	AATCAAAGCATGCTCTTTCGATC	ATTACCTGCTAAGAGAGAACA	160	180		60
A01	RP2313	70.9	GATAAAGGTTGGAGGCGTGA	TTCCCACCTTGAATCTCCAC	250	235		60-90
A01	RP2045	86.7	AGTTCCTTGAGGTACCCTTGC	GTCGGTGGCCTGACCTTC	170	140		60

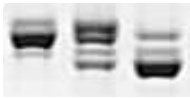
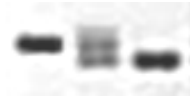
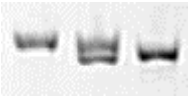
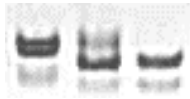
A01	RP819	114.7	GGACCTCTCATGGAGTCGAA	AACACCGGTTCGCAAGTAAT	160	180		90
A01	RP821	129.3	GAACGTAACACATTGCTGGTG	TGAGACTTCACAATTCAATCCA	190	220	NA	60
A02	RP757	0.0	GTGGTGAACGTGCTTAAGAT	ACGAGCTGGTTGAAAGTTTA	180	160		60
A02	RP851	8.4	AACAAACACCTTGCCGTTTC	GGATCGGGAGGTAGGAGAAG	200	250		60
A02	RP325	26.5	CAGCATGGTATGTAACTAT	ACCACTTTTATTGAGAATC	200	240		60
A02	RP565	48.3	ACCACAGTAATCAAATAGAG	GCTTGGATTAAGATAGAGTA	300	350		30
A02	RP1041	53.8	TATCTCAAGTACGAATAATAGAA	GAAGATTAAATATTATTGGCTTA	NA	NA	NA	NA
A02	RP103	85.2	AACGAACAACAACCAGCAAGGAGAG	GATCTGAAAACCCTAGCCGTCAATG	NA	NA	NA	NA
A02	RP1285	114.6	GCGCTATAAAGCACGAGGAC	TTCTCAAACGGCAATCTATGAA	250	230		100
A02	RP1533	126.9	ATAGTTAAGTGAAACATTGGT	AAGTAGAGTACTCCCCACTC	250	230		60
A02	RP859	137.4	GAGGGTTGCTCACCAGAAAA	AACCAGCAGCATGAGTTTCA	180	200		60

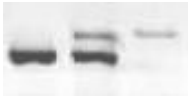
A02	RP401	151.5	TATTAGAAGTAAATATCCGAGTA	GACTAATGCTATTACAAAGAA	500	425		30
A03	RP105	0.0	TAATTTCCGTTTCGCCTCCACTTAT	TTGCTTTAATCAGGATGCTCTTGTC	125	175		70
A03	RP307	9.1	GAGTTTGGCATCTAGAGCTGAG	TCCTCTCTCAAAAACCATGAAG	165	180		70
A03	RP485	13.4	TCTCAAAAACCATGAAGTA	TAGAGCTGAGGTGAAATC	150	165		70
A03	RP2043	44.4	CCCTGGAAGTAGCCAAAGTG	CACACCACGGAACACAAAAG	115	100		80
A03	RP761	65.8	GCATCTCAGCCTTACAACTT	AGCAAGAACCCAGAAACATA	150	165		90
A03	RP911	69.9	CCGAGAGATGGACATGATGA	AGTGGGGCCATGGAAAGT	185	200		85
A03	RP263	88.0	CTTTCTGTCTCTCCCTCATTC	CGCTGTTATCCGACTCCA	190	210		60
A03	RP759	131.3	GTCATCTCCAGGTAAATCCA	TCTTGAACAACCTCTCCCTA	190	250		30
A04	RP2303	0.0	TCTCCCTTGGCTGATATGCT	GAGATGATCCACATTCCCTCA	230	210		60
A04	RP767	7.2	AAGAACGTCAAGATCCTCTGC	ACCACCACGGTAGTAGAGCG	80	130		30

A04	RP2317	16.0	GGTAACTGGGTTATCACCAAAGA	TCACAACCGCTGTCTGATTC	220	200		60
A04	RP2319	45.0	AGTGGATCCATGGGAAGAGA	TCTTGTGGTTGGTGGAAGTG	200	220		60
A04	RP763	58.6	GAAATGAGCGACAGTGTGAT	ACAAACGACCAGTTCATAGG	NA	NA	NA	NA
A04	RP611	61.4	AACTGTCGTAAATTGTTAGT	ATTGTAGATTTTGACAAGAG	NA	NA	NA	NA
A04	RP277	72.8	AGAACTACAGGAACAACC	CAAGATGCTTCTACTTCA	170	150		60
A04	RP1549	92.5	CACTGCCTCCAGATTGCAT	CGCGACTTTCGTTTCTCTCT	190	200		90+
A05	RP117	0.0	CTAGGGTTATGGTTTGAATCAGACA	TCGTATAGCTCAAATCAAATGTTCA	150	250		60
A05	RP121	34.3	CCTGCATTTGGAAAACAAAACATTA	TTCATCACTTCCTCCTCAAATACCG	150	225		30
A07	RP1141	41.2	AGTGTGTTGTGATGATTAAG	TATATGTCTTGCCTTTGATA	235	220		60-90
A05	RP311	44.1	ACGCAAGGGTTTAACTGTGG	TATCGCTCTTGTCTTGGCCT	NA	NA	NA	NA
A05	RP293	56.2	AGTTATATGGTTGCTACATT	AACAAATAGAGAATCTTTGA	200	175		70

A05	RP777	77.3	CGTCCGTAGCGCTATTTTTCAGA	ACGTTGTCGATCGCCCAGTTC	160	140		90
A05	RP2181	101.4	GGCCTTGCCCATAACACTAA	TCAGATGGAACGGAGAGAAGA	280	230		30
A05	RP2039	116.5	GAGCGGAGTTACCAAAGTTGTC	TCACTTACGTGGGTCAGCAC	220	180		60
A05	RP123	131.5	AAATTGTTTCTCTTCCCCAT	GTGTTAGGGAGCTGGAGAAT	150	130		60
A06	RP127	0.0	GCAGGCGTTGCCTTTATGTA	AACAAATAGAGAATCTTTGA	NA	NA	NA	NA
A06	RP1985	35.0	CTCGTGATCCAGTTATCTAT	GAAAATAATACAAGTGAAAGAC	190	160		60
A06	RP1993	42.8	GTCAACAAGATGTAACTTCA	AGTCAATCATGTAAGAATAATTT	210	180		30
A06	RP313	54.1	GATGGTTTACATAGTTTCGT	TCTACGGATTGTAATCTAAA	150	175		60
A06	RP2301	63.4	ATCGAGTCTGATATGGTCATCA	CTTCACTTGGTCACCACCTTC	220	190		30
A06	RP281	91.8	GAGACACACAGAAAGACTAT	ACTCATCTTGTTCCATTAT	150	120		60
A06	RP299	94.3	TAAATCACAACTCCCATC	CTTCTCTCATTGACAACTC	125	135		80

A06	RP943	115.2	ATTATTCCTTTGTATGTAAATTTTGCT	TTTTTATCTTCATCTATGATTTTTGGA	220	200		60
A06	RP749	136.7	AGTTGGCCCCATTTCATTGTTAT	CATCTTGACGGCCTCCATCTCCA	150	170		70
A07	RP2293	0.0	CACCTCTGCATCCCTCTCTG	GCTCCATCTCTATGACAGAAACC	165	145		60-90
A07	RP781	34.4	TTCAAAGGATAAGGGCATCG	TCTTCTTCTTTTGTTGTCTTCCG	120	140		50
A07	RP673	57.6	TTTGTTATTAACTTCCATGT	AAATAATTTGCCTACCTTAT	NA	NA	NA	NA
A07	RP1761	76.0	GGTGCCATTGCTAAACCTGT	AGCAAAGGGTTTCGCTACTC	210	195		90
A07	RP437	106.0	AGTGTTAAACATAATTAGCATAG	CGTTTCCTCTATCCACCAC	300	350		65
A08	RP989	0.0	CAATCTTAATCCTCGGGAACC	TGCAAGCGATAAGACTGCTG	160	140		60-90
A08	RP365	4.5	GATTCAAAACAAAACAAGT	TGAACTGGGGAAAAGAAAGCAAAGA	180	160		65
A08	RP1511	13.5	CAGTCACCTGATAAGATATG	GATCATTACTACATAACACAAAC	NA	NA	NA	NA
A08	RP161	34.8	AAGAGCAAGAGCCAAGACAGCCTAC	TGGTGATGGAGAAGTACATGGACGT	NA	NA	NA	NA

A08	RP67	55.8	TGAAATGCTCACTTTGGGTTC	AGTGAGAATCAAAACATATAA	150	160		60
A08	RP151	94.9	TGGTGGCTTGAGATTAGTTC	ACTCGAAGCCTAATGAAAAG	160	140		60-90
A09	RP1889	0.0	GCATATAGAGGACCAAGAGTAACG	CTTCGGCCCTTTTTGTGAT	155	140		60-90
A09	RP741	27.5	GGGAGAAATAAAGAATCTAA	ATCAGAAACAAACAAATATAAG	NA	NA	NA	NA
A09	RP1929	52.9	TCTCGTCGCTCTGAATTGTG	TTGTGAAATCAAAGCAAAAAGG	200	215		60
A09	RP181	78.2	GGAGCAGTTTGGAGTTGTAG	TGACCTGTGAGAAGGCAC	250	200		70
A09	RP73	96.6	GTCTCTTGATCTTGCTAAT	AGAACATGATAAGTTTAACG	170	160		95
A10	RP2089	0.0	TCGTTGACTTACACACCACAA	CCGAACAAATACCCGAATGT	190	170		90
A10	RP1919	21.8	TCCATTTTACGCATGACAGC	CTGCCATAACTTCGGGCTTA	170	185		60
A10	RP1043	36.2	CATGACTATGCTTTAATGTT	GGCTTTCTTCAAGTAGTAAT	260	240		60
A10	RP791	53.3	TGAGTTTATCACACTCAGG	CTTCACTTCCTAGGTAACAT	NA	NA	NA	NA

A10	RP89	70.2	GTATTATTGTCGCCGTGCAG	CAATAGTCTCTGTATCCATGAACTCC	350	500		30

Credits: The FPsc (Fast Plants, self-compatible) Genetic Resource Development Team at the University of Wisconsin-Madison has worked since 2007 to create, characterize, and disseminate plant-based genetic and molecular resources to teachers and students interested to explore topics ranging from traditional Mendelian genetics and evolutionary principles to emerging genomic sciences and bioinformatics. The molecular genetic markers described here are the primarily the results of work conducted by UW undergraduates Devin Walsh-Felz, Melissa Mohn, Katie Wang, Abby Busler, and Dave Anderson under the direction of Scott Woody and Richard Amasino, Department of Biochemistry, UW-Madison. Funding to support these efforts has been provided by grants from the National Science Foundation and the Howard Hughes Medical Institute awarded to R. Amasino. For more information see http://fpsc.wisc.edu.

Footnotes:

[1] FPsc markers were assigned to *B. rapa* chromosomes in accord with the convention adopted by the Multinational *Brassica rapa* Sequencing Consortium (Choi *et al.,* 2007, Theor Appl Genet 115:777–792). Concordant BLAST search results obtained by using the BRAD genome sequence database (http://brassicadb.org) using fwd and reverse primer sequences were used to validate placement and orientation (north to south) of markers on the *B. rapa* molecular map.

[2] The majority of molecular markers described here have been developed by using *Bacterial A* rtificial *C* hromosome (BAC) sequences (http://brassica.nbi.ac.uk/) and *W* hole *G* enome *S* equence (WGS; http://brassicadb.org/) data reported for the "Chiifu" variety of *B. rapa* , targeting *S* imple S*equence R* epeat (SSR) motifs within the *B. rapa* genome. A number of markers using oligonucleotide primer sequences that have been shown to detect (PCR fragment length) polymorphisms in other *B. rapa* mapping populations (Suwabe *et al* ., 2006, Genetics 173:309-319; Iniguez-Luy *et al* ., 2007, Theor Appl Genet 120:31-43; Del Carpio *et al* ., 2011, Theor Appl Genet 122:1105-1118) have been tested and found useful for mapping purposes in the R500 x FPsc F2 mapping population and may be included herein.

[3] Genetic map distance between and among linked markers was determined by using the R/QTL mapping program (www.rqtl.org/) to compare genotypes of 145 F2 segregants (290 chromosomes) derived from an initial cross between R500 and FPsc parental lines.

[4] Images shown are of PCR products obtained by using marker-specific oligonucleotides to amplify from FPsc (F), R500 x FPsc F1 heterozygote (H) and R500 genomic DNA templates.

[5] Suggested run-times are based on our experience using 2-3% agarose gels, NaB buffer, 250 V applied force for the times indicated to achieve adequate resolution of PCR fragments.

NA: Data presently not available. This documanet will be updated periodically to include additional information regarding listed markers as well as new

markers that may be added to the FPsc genetic map.