BW-introgression at 41.5 cM on chromosome 6

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The primer pair, P6-41F1/R1, at 41.5 cM was designed using the information for COSII marker At1g03150. A large PCR fragment (about 1,000 bp) was obtained for M82 (putative susceptible to *R. solanacearum*) and H7996 (resistant to *R. solanacearum*). These two sequences were compared and four SNPs and two indels were detected. The sequence for WVa700 is the same as M82, the sequences for RILs and BV-resistant germplasm are being determined.

H7996 P6-41, partial sequence: 905 bp;

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1      TTCCAGTGTA GATTTTAAAG TTCATCAGTT TTTTGGGTGA TATAGCTGAC GACTGATGAT
61     TATTTAATTT ATATACAGAT TGAGTTAAGT AAATTAGAAA TATCAAATAT AAGCTTGAAG
121    GTAGGACTAA AGGGTGGTAG ATAGGAGCCA ATTAAGTAGA AAGAGTCTAG AGTCCTTTAA
181    GAATACAGAA AATCTGAAGA TTAAGCAAAA ATTGCAAGAA TTGAAAATAA TATGCCTAAA
241    GCTCTCCCCT AACTCTTACC TTCTTTTTCA AGAGCAAATT GTTTTCTAAA GGTGGATGGA
301    GGAAATGGGA TTTTCTCGAG GAATATTCTT CAGCAGCACT GTTTGATGCA GGGTATACAT
361    TAACTTTGAC TTTATAGCTT CTTTTTTTTT TGTCATATAG TTGGCAAAGA ATTGATTGAA
421    TTTAGATCAA ACAATAGGTT GTAGCAAGGA ATGGCAAGGA TAAGCATTCT GAATTTCATT
481    TCTCTTTCAA GAATTGGGGA TGGAAAGTAG ATTTCATGGG CTGGTGTAGG CGGATTTCAC
541    TAATTCTATT CCCCTAGATG CTAACACTAT GTTTTTGAAA ATTTCCAGCA ACAGATCCTA
601    GGTCCAAGGC AGATGCAAGT AATCATTCTC TTATACTCCC TTCCGTGAAG AGGTTTCATT
661    TACTCGTTGT TGGTTTTCTT TTAAAAAGGA AAAAGTCGGA CTTTATTGGT GACAAAGTGG
721    TTAGAATGTA AATATGTACT TAGTTTGGCA CCGGCTGGTG TATTCTGGCC TCTTCATGGG
781    CGACAAAGTG GTTAGAATGT CAATTATNNN NNNNTCTTAT TATGGTTACT GTCTGGTGCA
841    TTTTNNNNNN NNNNNNNNNN TTTTGAAAAA TTACTCCTAA GAAAAACATT TGTTTTTTTA
901    AAAAC
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M82-P6-41,partial sequence: 907 bp;

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1      TTCCAGTGTA GATTTTAAAG TTCATCACTT TTTTGGGTGA TATAGCTGAC GACTGATGAT
61     TATTTAATTT ATATACAGAT TGAGTTAAGT AAATTAGAAA TATCAAATAT AAGCTTGAAG
121    GTAGGACTAA AGGGTGGTAG ATAGGAGCCA ATTAAGTAGA AAGAGTCTAG AGTCCTTTAA
181    GAATACAGAA AATCTGAAGA TTAAGCAAAA ATTGCAAGAA TTGAAAATAA TATGCCTAAA
241    GCTCTCCCCT AACTCTTACC TTCTTTTTCA AGAGCAAATT CTTTTCTAAA GGTGGATGGA
301    GGAAATGGGA TTTTCTCGAG GAATATTCTT CAGCAGCACT GTTTGATGCA GGGTATACAT
361    TAACTTTGAC TTTATAGCTT CTTTTTTTTT TTGTCATATA GTTGGCAAAA AATTGATTGA
421    ATTTAGATCA AACAATAGGT TGTAGAAAGG AATGGCAAGG ATAAGCATTC TGAATTTCAT
481    TTCTCTTTCA AGAATTGGGG ATGGAAAGTA GATTTCATGG GCTGGTGTAG GCGGATTTCA
541    CTAATTCTAT TCCCCTAGAT GCTAACACTA TGTTTTTGAA AATTTCCAGC AACAGATCCT
601    AGGTCCAAGG CAGATGCAAG TAATCATTCT CTTATACTCC CTTCCGTGAA GAGGTTTCAT
661    TTACTCGTTG TTGGTTTTCT TTTAAAAAGG AAAAAGTCGG ACTTTATTGG TGACAAAGTG
721    GTTAGAATGT AAATTATGTA CTTAGTTTGG CACCGGCTGG TGTATTCTGG CCTCTTCATG
781    GGCGACAAAG TGGTTAGAAT GTCAATTATG TAGTTGTCTT ATTATGGTTA CTGTCTGGTG
841    CATTTTGGTA TGTTAAACGA TGTTTTGAAA AATTACTCCT AAGAAAAACA TTTGTTTTTT
901    TAAAAAC
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Alignment of M82 (Top) by H7996 (G1=H7996, bottom)

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1       TTCCAGTGTAGATTTTAAAGTTCATCACTTTTTTGGGTGATATAGCTGACGACTGATGAT
        ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
1       TTCCAGTGTAGATTTTAAAGTTCATCAGTTTTTTGGGTGATATAGCTGACGACTGATGAT

61      TATTTAATTTATATACAGATTGAGTTAAGTAAATTAGAAATATCAAATATAAGCTTGAAG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61      TATTTAATTTATATACAGATTGAGTTAAGTAAATTAGAAATATCAAATATAAGCTTGAAG

121     GTAGGACTAAAGGGTGGTAGATAGGAGCCAATTAAGTAGAAAGAGTCTAGAGTCCTTTAA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121     GTAGGACTAAAGGGTGGTAGATAGGAGCCAATTAAGTAGAAAGAGTCTAGAGTCCTTTAA

181     GAATACAGAAAATCTGAAGATTAAGCAAAAATTGCAAGAATTGAAAATAATATGCCTAAA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181     GAATACAGAAAATCTGAAGATTAAGCAAAAATTGCAAGAATTGAAAATAATATGCCTAAA

241     GCTCTCCCCTAACTCTTACCTTCTTTTTCAAGAGCAAATTCTTTTCTAAAGGTGGATGGA
        |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
241     GCTCTCCCCTAACTCTTACCTTCTTTTTCAAGAGCAAATTGTTTTCTAAAGGTGGATGGA

301     GGAAATGGGATTTTCTCGAGGAATATTCTTCAGCAGCACTGTTTGATGCAGGGTATACAT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
301     GGAAATGGGATTTTCTCGAGGAATATTCTTCAGCAGCACTGTTTGATGCAGGGTATACAT

361     TAACTTTGACTTTATAGCTTCTTTTTTTTTTTGTCATATAGTTGGCAAAAAATTGATTGA
        ||||||||||||||||||||| ||||||||||||||||||||||||||| ||||||||||
361     TAACTTTGACTTTATAGCTTC.TTTTTTTTTTGTCATATAGTTGGCAAAGAATTGATTGA

421     ATTTAGATCAAACAATAGGTTGTAGAAAGGAATGGCAAGGATAAGCATTCTGAATTTCAT
        ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
420     ATTTAGATCAAACAATAGGTTGTAGCAAGGAATGGCAAGGATAAGCATTCTGAATTTCAT

481     TTCTCTTTCAAGAATTGGGGATGGAAAGTAGATTTCATGGGCTGGTGTAGGCGGATTTCA
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
480     TTCTCTTTCAAGAATTGGGGATGGAAAGTAGATTTCATGGGCTGGTGTAGGCGGATTTCA

541     CTAATTCTATTCCCCTAGATGCTAACACTATGTTTTTGAAAATTTCCAGCAACAGATCCT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
540     CTAATTCTATTCCCCTAGATGCTAACACTATGTTTTTGAAAATTTCCAGCAACAGATCCT

601     AGGTCCAAGGCAGATGCAAGTAATCATTCTCTTATACTCCCTTCCGTGAAGAGGTTTCAT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
600     AGGTCCAAGGCAGATGCAAGTAATCATTCTCTTATACTCCCTTCCGTGAAGAGGTTTCAT

661     TTACTCGTTGTTGGTTTTCTTTTAAAAAGGAAAAAGTCGGACTTTATTGGTGACAAAGTG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
660     TTACTCGTTGTTGGTTTTCTTTTAAAAAGGAAAAAGTCGGACTTTATTGGTGACAAAGTG

721     GTTAGAATGTAAATTATGTACTTAGTTTGGCACCGGCTGGTGTATTCTGGCCTCTTCATG
        ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
720     GTTAGAATGTAAA.TATGTACTTAGTTTGGCACCGGCTGGTGTATTCTGGCCTCTTCATG
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