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Short communication

A potato cDNA encoding a homologue of mammalian multidrug resistant P-glycoprotein

W. Wang, D. Takezawa and B.W. Poovaiah*
*Laboratory of Plant Molecular Biology and Physiology, Department of Horticulture, Washington State University, Pullman, WA 99164-6414, USA (*author for correspondence)*

Abstract

A homologue of the multidrug resistance (MDR) gene was obtained while screening a potato stolon tip cDNA expression library with ^{35}S-labeled calmodulin. The mammalian MDR gene codes for a membrane-bound P-glycoprotein (170−180 kDa) which imparts multidrug resistance to cancerous cells. The potato cDNA (PMDR1) codes for a polypeptide of 1313 amino acid residues (ca. 144 kDa) and its structural features are very similar to the MDR P-glycoprotein. The N-terminal half of the PMDR1-encoded protein shares striking homology with its C-terminal half, and each half contains a conserved ATP-binding site and six putative transmembrane domains. Southern blot analysis indicated that potato has one or two MDR-like genes. PMDR1 mRNA is constitutively expressed in all organs studied with higher expression in the stem and stolon tip. The PMDR1 expression was highest during tuber initiation and decreased during tuber development.

Multidrug resistance (MDR) is a phenomenon known to occur in mammalian tumor cells that hampers cancer chemotherapy [5, 6, 14]. The MDR gene codes for a membrane-bound P-glycoprotein that functions as an ATP-dependent efflux pump which extrudes a range of structurally different compounds from the cell, including cytotoxic natural products [6]. Multidrug-resistant cells are characterized by increased expression of the MDR gene and decreased intracellular drug accumulation. The MDR P-glycoprotein belongs to the ATP-binding cassette (ABC) superfamily of membrane-bound transport proteins [7]. A number of MDR-like genes have been cloned from both eukaryotes and prokaryotes [6, 14]. Eukaryotic P-glycoproteins are characterized by the presence of 12 transmembrane domains within the two similar halves, each half containing six transmembrane regions and an ATP-binding

site within the large intracytoplasmic loop. An *Arabidopsis* genomic sequence with homology to mammalian MDR-like genes has been reported [4].

A ^{35}S-labeled potato calmodulin isoform PCM6 [16] was used for screening a potato stolon tip cDNA expression library (λZAPII, Stratagene) to obtain calmodulin-binding clones [11]. After three rounds of screening, several positive clones were identified. Among these clones, a partial cDNA clone was sequenced (3172 bp, nt 953−4124, Fig. 1) and the sequence comparison using the GenBank database revealed that it had high homology to MDR-like genes. In order to clone the 5′ region, the cDNA library was rescreened using a ^{32}P-labeled *Eco*RI/*Spe*I fragment (nt 953−1710, Fig. 1) of the original clone as a probe. Out of five positive clones obtained, two cDNA clones (nt 1−3548, Fig. 1) contained longer 5′ regions and another three cDNA clones (nt 321−4160, Fig. 1) contained 26 additional nucleotides in the 3′ region as compared to the original cDNA. Since the most

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1                         TAAAAACCATTGGACATTGGAAATGGTCTGAA
33 ATGCAAGGTGTTGAACTTGTTGTCTCTGAAGACAAAAATTCAAACACCCCCACAACAACA
   M  Q  G  V  E  L  V  V  S  E  D  K  N  S  N  T  P  T  T  T    20

93 ACAACAACAAATAGTCATCAATTTCAAGAAACAAGAATGGAGGTTAAAAAAGAAGAAGGG
   T  T  T  N  S  H  Q  F  Q  E  T  R  M  E  V  K  K  E  E  G    40

153 GGTGATGTGGAGAAGCCAAGTAGTCCACCACCAGCAGTTGGTTTTGGTGAACTTTTTAGA
    G  D  V  E  K  P  S  S  P  P  P  A  V  G  P  G  E  L  F  R    60

213 TTTGCTGATGGTTTGGATTGTGTACTAATGATAATTGGTTCACTTGGTGCTTTTGTCCAT
    F  A  D  G  L  D  C  V  L  M  I  I  G  S  L  G  A  F  V  H    80
                                   S1
273 GGATGTTCTTTGCCTTTGTTTCTTAGATTCTTTGCTGATCTTGTTAATTCTTTTGGCTCT
    G  C  S  L  P  L  F  L  R  F  F  A  D  L  V  N  S  F  G  S    100

333 TATGCTAATGATGTTGATAAGATGACTCAAGAAGTTTTAAAGTATGCATTTTACTTTCTT
    Y  A  N  D  V  D  K  M  T  Q  E  V  L  K  Y  A  F  Y  F  L    120

393 GTGGTGGGTGCTGCAATATGGGCATCTTCATGGGCAGAGATATCATGCTGGATGTGGACT
    V  V  G  A  A  I  W  A  S  S  W  A  E  I  S  C  W  M  W  T    140
                  S2
453 GGTGAGAGACAAACAACAAAGATGAGGATCAAATACTTAGAGGCTGCTTTGAACCAAGAT
    G  E  R  Q  T  T  K  M  R  I  K  Y  L  E  A  A  L  N  Q  D    160

513 ATTCAATATTTTGATACTGAAGTTAGAACTTCTGATGTTGTTTCTGCAATTAACACTGAT
    I  Q  Y  F  D  T  E  V  R  T  S  D  V  V  S  A  I  N  T  D    180

573 GCTGTAGTGGTCCAAGATGCCATTAGTGAGAAGTTGGGCAATTTCATTCATTATATGGCT
    A  V  V  V  Q  D  A  I  S  E  K  L  G  N  F  I  H  Y  M  A    200

633 ACATTTTTGTCTGGATTTGTGGTGGGATTTACAGCAGTATGGCAATTAGCTCTAGTTACT
    T  F  L  S  G  F  V  V  G  F  T  A  V  W  Q  L  A  L  V  T    220
       S3
693 CTTGCTGTAGTTCCACTTATTGCTGTAATTGGTGCTATCTACACTGTGACATCAGCCAAA
    L  A  V  V  P  L  I  A  V  I  G  A  I  Y  T  V  T  S  A  K    240
       S4
753 TTGTCAAGTCAAAGTCAAGAAGCACTTTCAAAGGCAGGGAACATTGTTGAACAGACAGTA
    L  S  S  Q  S  Q  E  A  L  S  K  A  G  N  I  V  E  Q  T  V    260

813 GTTCAAATTCGGACGGTATTGGTGTTTGTTGGTGGTGAGGCAAAAGCATTGCAAGCATACACA
    V  Q  I  R  T  V  L  V  F  V  G  E  A  K  A  L  Q  A  Y  T    280

873 GCAGCACTTAGAGTTTCTCAAAAGATTGGATATAAAGAGTGGATTTTCAAAAGGATTAGGA
    A  A  L  R  V  S  Q  K  I  G  Y  K  S  G  F  S  K  G  L  G    300

933 CTTGGAGCTACATATTTTACTGTTTTCTGTTGTTATGCTCTTCTTTTATGGTATGGGGGC
    L  G  A  T  Y  F  T  V  F  C  C  Y  A  L  L  L  W  Y  G  G    320
                             S5
993 TATTTAGTTAGACATCATTTCACCAATGGAGGACTTGCCATAGCAACAATGTTTGCAGTC
    Y  L  V  R  H  H  F  T  N  G  G  L  A  I  A  T  M  F  A  V    340
                              S6
1053 ATGATTGGTGGATTGGCATTGGGACAATCTGCCCCTAGCATGACTGCATTTGCAAAAGCT
     M  I  G  G  L  A  L  G  Q  S  A  P  S  M  T  A  F  A  K  A   360

1113 AGAGTTGCAGCTGCCAAGATTTTCCGGATTATCGATCATAAGCCAAGCGTCGACAGAAAC
     R  V  A  A  A  K  I  F  R  I  I  D  H  K  P  S  V  D  R  N   380

1173 GCCAAGACGGGGTTGGAGTTAGACACTGTTAGTGGCCAGCTAGAGCTTAAGAATGTCGAG
     A  K  T  G  L  E  L  D  T  V  S  G  Q  L  E  L  K  N  V  E   400

1233 TTCTCTTATCCTTCAAGGCCTGAAATCAAGATTCTCAACAATTTCAACCTCGTTGTTCCA
     F  S  Y  P  S  R  P  E  I  K  I  L  N  N  F  N  L  V  V  P   420

1293 GCTGGAAAGACCATCGCTTTAGTCGGAAGCAGTGGTTCGGGGAAAAGCACTGTGGTATCC
     A  G  K  T  I  A  L  V  G  S  S  G  S  G  K  S  T  V  V  S   440

1353 CTTATCGAAAGATTTTATGATCCCACCTCAGGACAACTTATGCTTGATGGAAATGACATA
     L  I  E  R  F  Y  D  P  T  S  G  Q  L  M  L  D  G  N  D  I   460

1413 AAGACACTGAAATTGAAATGGCTAAGGCAGCAAATTGGCCTTGTAAGCCAAGAACCAGCA
     K  T  L  K  L  K  W  L  R  Q  Q  I  G  L  V  S  Q  E  P  A   480

1473 CTTTTCGCAACAAGCATCAAAGAAAACATACTATTAGGAAGGCCAGATGCAACACAAATT
     L  F  A  T  S  I  K  E  N  I  L  L  G  R  P  D  A  T  Q  I   500

1533 GAGATCGAAGAAGCTGCTAGAGTTGCCAATGCCCATTCTTTCGTAATCAAACTTCCTGAT
     E  I  E  E  A  A  R  V  A  N  A  H  S  F  V  I  K  L  P  D   520

1593 GGCTTTGATACTCAGGTAGGGGAGAGGGGATTACAATTATCAGGTGGACAGAAGCAGAGG
     G  F  D  T  Q  V  G  E  R  G  L  Q  L  S  G  G  Q  K  Q  R   540

1653 ATTGCTATAGCAAGGGCCATGCTTAAGAATCCAGCGATCCTTCTCTTAGACGAGGCAACT
     I  A  I  A  R  A  M  L  K  N  P  A  I  L  L  L  D  E  A  T   560

1713 AGTGCTTTAGATTCCGAATCAGAAAAGCTAGTGCAGGAGGCTCTAGACAGGTTCATGATC
     S  A  L  D  S  E  S  E  K  L  V  Q  E  A  L  D  R  F  M  I   580

1773 GGACGAACGACTCTTGTGATTGCTCATCGGCTGTCTACTATCCGGAAGGCTGACCTGGTG
     G  R  T  T  L  V  I  A  H  R  L  S  T  I  R  K  A  D  L  V   600

1833 GCTGTACTACAACAAGGCAGTGTCTCGGAGATTGGGAAGCCACGATGAGCTTATGAGTAAA
     A  V  L  Q  Q  G  S  V  S  E  I  G  S  H  D  E  L  M  S  K   620

1893 GGAGAGAATGGTATGTATGCCAAGCTCATCAAAATGCAAGAAGCAGCTCATGAAACCGCT
     G  E  N  G  M  Y  A  K  L  I  K  M  Q  E  A  A  H  E  T  A   640

1953 CTTAGTAATGCCAGAAAGAGCAGTGCAAGGCCCTCGAGTGCAAGGAACTCTGTAAGCTCA
     L  S  N  A  R  K  S  S  A  R  P  S  S  A  R  N  S  V  S  S   660

2013 CCAATCATCACTAGAAACTCTTCCTATGGTCGATCACCATACTCCCGCCGGTTGTCTGAC
     P  I  I  T  R  N  S  S  Y  G  R  S  P  Y  S  R  R  L  S  D   680
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2073 TTTTCTACCTCGGACTTCAGCCTCTCCCTTGATGCTGCATATTCTAATTACCGAAATGAA
     F  S  T  S  D  F  S  L  S  L  D  A  A  Y  S  N  Y  R  N  E   700

2133 AAGCTTGCATTCAAGGACCAAGCTAGTTCGTTTGGCCGGCTTGCAAAAATGAACTCTCCT
     K  L  A  F  K  D  Q  A  S  S  F  G  R  L  A  K  M  N  S  P   720

2193 GAGTGGACTTATGCTTTAATTGGTTCTATAGGCTCTGTCATCGTGTGGTTCACTTAGTGCT
     E  W  T  Y  A  L  I  G  S  I  G  S  V  I  C  G  S  L  S  A   740
                   S7
2253 TTCTTTGCATACGTCTTGAGTGCTGTTCTTAGCGTGTACTACAATCCGGATCATGCTTAC
     F  F  A  Y  V  L  S  A  V  L  S  V  Y  Y  N  P  D  H  A  Y   760

2313 ATGAGCGAACAAATTGCGAAATACTGTTATCTTTTGATTGGAGTTTCATCGGCTGCACTC
     M  S  E  Q  I  A  K  Y  C  Y  L  L  I  G  V  S  S  A  A  L   780
                          S8
2373 ATTTTCAACACTCTACAGCATTACTACTGGGATGTAGTGGGGGAGAATTTAACAAAACG
     I  F  N  T  L  Q  H  Y  Y  W  D  V  V  G  E  N  L  T  K  R   800

2433 GTGAGAGAGAAAATGCTGGCAGCAGTGCTTAAAATGGAAATGGCGTGGTTCGATCAGGAA
     V  R  E  K  M  L  A  A  V  L  K  M  E  M  A  W  F  D  Q  E   820

2493 GAGAACGATAGTTCAAGAATTGCAGCTAGGCCTCTCTCTGGATGCCAACAATGTTAGGTCA
     E  N  D  S  S  R  I  A  A  R  L  S  L  D  A  N  N  V  R  S   840

2553 GCCATTGGGGATAGAATCTCCGTCATTATGCAGAACTCAGCTCTCATGCTAGTCGCGTGC
     A  I  G  D  R  I  S  V  I  M  Q  N  S  A  L  M  L  V  A  C   860
                          S9
2613 ACTGCAGGATTCGTATTGCAGTGGCGTCTGGCCCTCGTCCTCATTGGGGTCTTCCCCGTG
     T  A  G  F  V  L  Q  W  R  L  A  L  V  L  I  G  V  F  P  V   880

2673 GTCGTTGCAGCAACAGTTTTACAGAAAATGTTCATGAAGGGATTCTCAGGAGACTTGGAA
     V  V  A  A  T  V  L  Q  K  M  F  M  K  G  F  S  G  D  L  E   900
       S10
2733 GCTGCTCATGCCAAAGCCACTCAACTTGCTGGAGAAGCTGTAGCTAATGTAAGAACAGTT
     A  A  H  A  K  A  T  Q  L  A  G  E  A  V  A  N  V  R  T  V   920

2793 GCTGCCTTTAATTCGGAGACGAAAATAGTCAATCTTTTCGACTCCAGCCTCCAAACTCCG
     A  A  F  N  S  E  T  K  I  V  N  L  F  D  S  S  L  Q  T  P   940

2853 CTTAGGCGTTGCTTCTGGAAGGGACAGATTGCGGGAAGTGGTTATGGGATTGCTCAATTT
     L  R  R  C  F  W  K  G  Q  I  A  G  S  G  Y  G  I  A  Q  F   960

2913 TTGCTTTATTCTTCCTATGCCCTTGGCCTTTGGTATGCCTCCTGGCTTGTCAAGCATGGG
     L  L  Y  S  Y  A  L  G  L  W  Y  A  S  W  L  V  K  H  G     980
       S11
2973 ATCTCTGACTTCTCGAAGACGATCCGTGTTTTCATGGTGCTCATGGTTTCTGCTAATGGT
     I  S  D  F  S  K  T  I  R  V  F  M  V  L  M  V  S  A  N  G   1000
                              S12
3033 GCAGCCGAAACATTGACCTTAGCCCCTGACTTCATCAAGGGTGGCAGAGCAATGCGTTCT
     A  A  E  T  L  T  L  A  P  D  F  I  K  G  G  R  A  M  R  S   1020

3093 GTTTTCGAACTCCTTGACCGTAAAACAGAAGTTGAGCCGGATGATCCAGATGCCACCGCT
     V  F  E  L  L  D  R  K  T  E  V  E  P  D  D  P  D  A  T  A   1040

3153 GTCCCTGATCGTCTTCGTGGTGAAGTGGAATTTAAGCATGTAGACTTCTCATATCCCACT
     V  P  D  R  L  R  G  E  V  E  F  K  H  V  D  F  S  Y  P  T   1060

3213 AGACCCGACGTGTCAATTTTCCGTGATTTGAATCTTCGTGCTCGAGCTGGAAAGACTCTT
     R  P  D  V  S  I  F  R  D  L  N  L  R  A  R  A  G  K  T  L   1080

3273 GCTCTTGTTGGACCAAGTGGATGTGGAAAGAGCTCAGTCATTTCACTTATAGAGCGGTTC
     A  L  V  G  P  S  G  C  G  K  S  S  V  I  S  L  I  E  R  F   1100

3333 TACGAGCCATCATCTGGACGTGTCATCATCGATGGCAAGGATATTCGTAAGTACAACCTT
     Y  E  P  S  S  G  R  V  I  I  D  G  K  D  I  R  K  Y  N  L   1120

3393 AAATCCTTGAGAAGACACATTGCTGTGAGTGCCACAAGAACCTTGCCTCTTTGCTACCACC
     K  S  L  R  R  H  I  A  V  V  P  Q  E  P  C  L  F  A  T  T   1140

3453 ATCTATGAAAACATCGCGTATGGACATGAATCAGCAACCGAGGCTGAGATAACCGAAGCA
     I  Y  E  N  I  A  Y  G  H  E  S  A  T  E  A  E  I  T  E  A   1160

3513 GCAACCTTGGCAAACGCCCACAAGTTCATATCTGCATTGCCTGATGGATACAAAACATTT
     A  T  L  A  N  A  H  K  F  I  S  A  L  P  D  G  Y  K  T  F   1180

3573 GTTGGAGAAAGGGGAGTTCAATTGTCTGGTGGACAAAAGCAAAGAATCGCCATTGCTCGT
     V  G  E  R  G  V  Q  L  S  G  G  Q  K  Q  R  I  A  I  A  R   1200

3633 GCTTTCCTAAGGAAAGCAGAGCTAATGCTGCTAGATGAAGCAACAAGTGCACTCGATGCA
     A  F  L  R  K  A  R  L  M  L  L  D  E  A  T  S  A  L  D  A   1220

3693 GAGTCTGAAAGATGTGTACAAGAAGCATTGGATCGCGCTTGTGCTGGTAAGACCACTATT
     E  S  E  R  C  V  Q  E  A  L  D  R  A  C  A  G  K  T  T  I   1240

3753 GTTGTTGCACACAGGCTATCTACAATCAGAAATGCACATGTGATCGCGGTCATAGACGAT
     V  V  A  H  R  L  S  T  I  R  N  A  H  V  I  A  V  I  D  D   1260

3813 GGGAAAGTAGCAGAACAAGGTTCTCATTCTCATCTGTTGAAAAACTACTCAGATGGTATT
     G  K  V  A  E  Q  G  S  H  S  H  L  L  K  N  Y  S  D  G  I   1280

3873 TATGCGCGTATGATACAACTACAACGATTTACACACGGAGAAGCTGTGAATATGGCAACA
     Y  A  R  M  I  Q  L  Q  R  F  T  H  G  E  A  V  N  M  A  T   1300

3933 GGATCAACGTCTTCCTCGCGTCCTAAGGAAGATCAAGATTGAGAAGAAAACGCGAATTGA
     G  S  T  S  S  S  R  P  K  E  D  Q  D  *                     1313

3993 AGCTCAAAATGAAAAAATACCAGTAGAAAAAAAAAGGAGTATACCTTGTGTAACACCCTT
4053 ATTATTTTTTGGACTGCTAATTTCTTGTTCACTGTTTCTAGTATAGTATAGTATAATATG
4113 TGCATTAATCCAAAATTATATTTATCCTTCAATTTTTCCGGCCCGCTA
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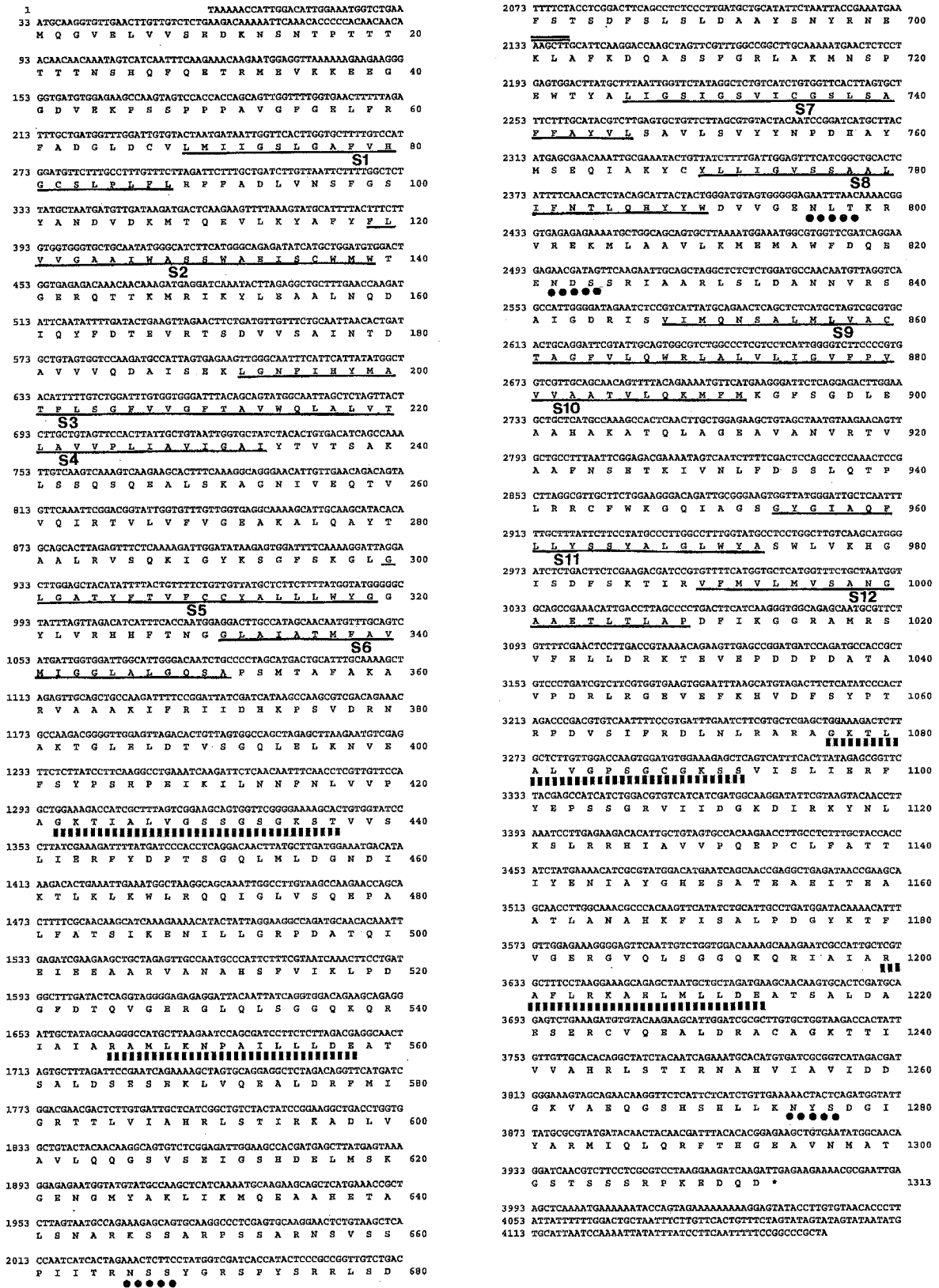
Figure 1. Nucleotide and deduced amino acid sequences of the PMDR1 gene. Putative transmembrane segments S1–S12 are underlined. Two potential ATP-binding sites (each consisting of two parts) are indicated by hatched regions. The dotted lines indicate the potential N-linked glycosylation sites corresponding to the sequences NXS/T. The *Hind*III site is indicated by a double line above the sequence.
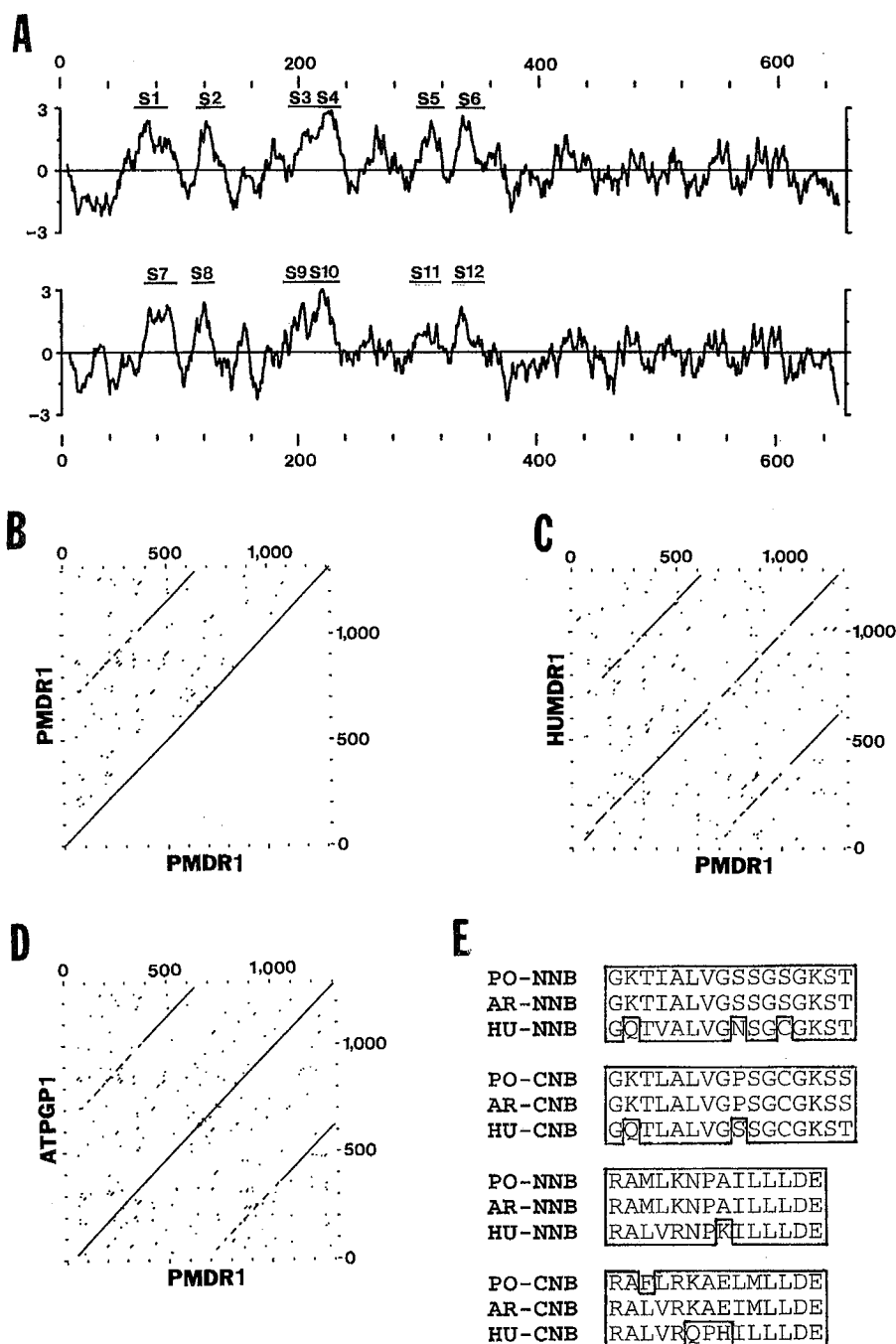
Figure 2. A. Hydropathy plot of the predicted amino acid sequence of the N-terminal half (top) and C-terminal half (bottom) of PMDR1. Kyte-Doolittle hydrophobicity values are marked on the left for a window of 11 amino acid residues. Putative transmembrane segments of S1–S12 are indicated. B. Dot matrix comparison showing internal duplication in the PMDR1 polypeptide. C. Dot matrix comparison of human MDR1 P-glycoprotein (HUMDR1) to the potato MDR-like gene product (PMDR1). Dot matrix analysis was performed for a window of 19 amino acid residues. D. Dot matrix comparison of *Arabidopsis* P-glycoprotein (ATPGP1) to PMDR1. E. Comparison of the potential ATP-binding sites of PMDR1 to those of *Arabidopsis* ATPGP1 and human MDR1 genes. Identical and functionally similar amino acid residues are boxed. PO, AR and HU indicate potato, *Arabidopsis*, and human, respectively. NNB and CNB represent the conserved sequences in the ATP-binding sites of the N-terminal half and C-terminal half, respectively.

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upstream ATG at position 23 is followed by a termination codon after only three nucleotides, we assign the ATG at nucleotide position 33 as the translation initiation codon, which is located 2 bases downstream from a purine residue in agreement with the eukaryotic initiation site [9]. The 186 bp of the 3'-untranslated region sequence does not contain an intact polyadenylation signal and an obvious poly(dA) tail and they may be present in the downstream region. The cDNA codes for a polypeptide of 1313 amino acid residues. The complete nucleotide sequence and the deduced amino acid sequence of PMDR1 are presented in Fig. 1.

The hydropathy profiles and the dot matrix comparison revealed that the N-terminal half of PMDR1 is similar to its C-terminal half (Fig. 2A, 2B), and their amino acid sequences share 36.8% identity and 59.8% similarity. The dot matrix comparison (Fig. 2C) between PMDR1 protein and human MDR1 P-glycoprotein [3] shows that their amino acid sequences share extensive homology (41.1% identity and 63.7% similarity). Fig. 2D shows the high homology between PMDR1 and the gene product of ATPGP1, a genomic clone which was isolated from *Arabidopsis* [4]. Their amino acid sequences share 85.7% identity and 92.4% similarity. However, a distinct variation exists in their N-terminal ends; the PMDR1 polypeptide has an extra 26 amino acid stretch in the N-terminal end as compared to *Arabidobsis* ATPGP1-encoded protein. The deduced amino acid sequence of PMDR1 revealed several significant structural features. The hydropathy plot presented in Fig. 2A shows a series of highly hydrophobic domains in the N-terminal and C-terminal halves and their hydropathy profiles are very similar (Fig. 2A). Each half of the PMDR1 polypeptide contains six putative transmembrane segments (Fig. 1, 2A) which are conserved in the corresponding regions of other MDR homologues. Another structural feature of PMDR1 polypeptide is the presence of two putative ATP-binding sites (Fig. 1). Two pairs of conserved amino acid sequences are present in the polypeptide at positions 422–437/545–558 in the N-terminal half and positions 1077–1092/1200–1213 in the C-terminal half. These amino acid sequences of the putative ATP-binding sites are highly conserved in proteins coded by MDR-like genes (Fig. 2E).

To determine the approximate copy number of PMDR1, Southern blot analysis of potato genomic DNA was carried out using the random-primed ^{32}P-labeled probe of the cDNA fragment (nt 953–3302, Fig. 1) [13]. Depending on the restriction enzymes, one or three hybridizing bands were observed, indi-
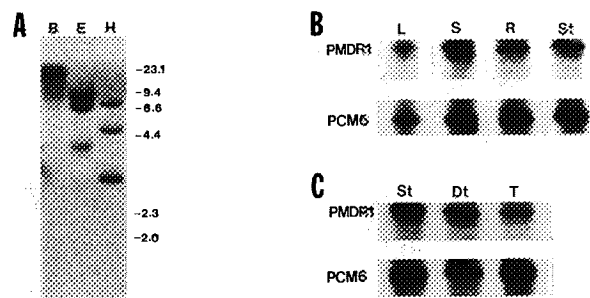
Figure 3. A. Southern analysis of PMDR1. 10 μg of potato DNA was digested with restriction enzymes and transferred onto a nylon membrane. The membrane was hybridized at 42 °C with ^{32}P-labeled probe in a solution containing 50% formamide, 6× SSPE, 5× Denhardt's solution, 0.1% w/v SDS, and 100 μg/ml herring sperm DNA. The membrane was washed at 60 °C in 0.5× SSC and 0.1% w/v SDS. The size of the standard markers is shown in kb. B, *Bam*HI; E, *Eco*RI; H, *Hin*dIII. B. RNase protection assay showing the expression of PMDR1 in different tissues of potato plants. 20 μg of total RNA was used in each reaction. L, leaf; S, stem; R, root; St, stolon tip. The expression of potato calmodulin isoform PCM6 is shown for comparison. It has been observed that PCM6 expression is lower in leaf as compared to other organs [16]. C. RNase protection assay showing the expression of PMDR1 during the early stages of tuber development. St, stolon tip; Dt, developing tuber; T, tuber. The expression of potato calmodulin isoform (PCM6) is shown for comparison.

cating that potato has one or two MDR-like gene(s) (Fig. 3A). To study the expression of the PMDR1 gene in different organs, total RNA was isolated from different organs of potato plants and developing tubers at two different stages of development [19]. The RNase protection assays were performed by using the standard protocol [13]. An *Spe*I/*Hin*dIII fragment of the PMDR1 coding region (nt 1711–2133, Fig. 1) was subcloned into pBluescript II KS(+) plasmid and used as a template for making the ^{32}P-labeled antisense RNA probe, and the reaction mixture was analyzed on 4% polyacrylamide gel containing 7 M urea. The ^{32}P-labeled antisense RNA probe for the potato calmodulin PCM6, which exhibits constitutive mRNA expression [16], was used for comparison. The results indicate that PMDR1 is constitutively expressed in all organs studied, with the higher expression in the stem and stolon tip (Fig. 3B). The expression was highest in the stolon tip during tuber initiation and decreased during tuber development (Fig. 3C).

A number of MDR or MDR-like genes have been isolated from different organisms [6, 14]. Although the functions of some of these genes have not been clearly identified, they are most likely to be membrane-bound transporter proteins with a wide substrate specificity.

Most of the studies on the functions and substrates of MDR P-glycoprotein were conducted with the tumor cells, which are invariably associated with increased production of P-glycoprotein. However, several studies have consistently shown that the MDR P-glycoprotein is expressed in many normal organs, suggesting that they may play a protective role in the transport or secretion and keep toxic metabolites and xenobiotics out of these normal tissues [2, 5, 6]. Since many cytotoxic compounds transported by P-glycoproteins of mammals and other organisms are hydrophobic natural compounds derived from plants [2, 6], it is likely that similar transport systems may also exist in plants. Because the deduced amino acid sequence and the structural features of potato MDR-like gene (PMDR1) share a striking similarity to the mammalian P-glycoprotein, it is possible that its function is also conserved.

Calcium channel blockers and calmodulin antagonists have been known to reverse the MDR phenomenon [5, 8, 17, 18]. However, the mechanism by which these agents reverse MDR effect is not fully understood [5]. Since the PMDR1 cDNA clone was isolated by screening a potato expression library using ^{35}S-labeled calmodulin, we believe that there is a direct interaction of Ca^{2+}/calmodulin with the PMDR1 gene product. Recently, Schlemmer et al. [15] reported that the murine MDR3 P-glycoprotein function is downmodulated by Ca^{2+}/calmodulin. Their results suggest that the murine MDR3 P-glycoprotein is a calmodulin-binding protein. These results and our present study suggest that Ca^{2+}/calmodulin may play a regulatory role in the function of the MDR P-glycoprotein. Ca^{2+} and calmodulin regulate many cellular processes and growth and development in plants [10, 12]. Balamani et al. [1] were able to block tuber induction by using Ca^{2+} chelators and calmodulin antagonists, suggesting a role for Ca^{2+}/calmodulin in tuberization. The high expression of PMDR1 mRNA in the stem and stolon tip (Fig. 3B and 3C) raises the possibility that calmodulin and its modulated proteins play a role in the tuberization process.

Acknowledgements

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