

# cDNA sequence of the 3'-coding region of PVY genome (the Chinese isolate)

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Several cDNA clones corresponding to coat protein (CP) gene of PVY (the Chinese isolate) were isolated from the PVY cDNA library by using the PCR product of the CP-coding sequence as a probe. The nucleotide sequence was determined by the chain termination method with Sequenase Kit from USB. The sequences reported in this paper comprise the entire coat protein region and part of viral NIb. Comparison of CP amino acid sequence of the Chinese isolate with those of PVY<sup>n</sup> (1) and PVY<sup>o</sup> (2) shows 93% of identity in both cases.

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## REFERENCES

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Q Q Q P F A T I A Q E G K A P Y I A S M A L R K L Y M D R A	30
G CAA CAG CAA CCT TTT GCA ACA ATA GCG CAG GAAGGGAG GCT CCT TAT ATA GCA ACC ATG GCA TTA AGG AAA CTG TAT ATG GAT AGG GCT	91
V D E E E L R A F T E M M V A L D D E F E F D S Y E V H H Q	60
GTC GAT GAG GAA GAG CTA AGA GCC TTC ACT GAA ATG ATG GTC GCA TTA GAT GAT GAG TTC GAG TTC GAC TCT TAT GAA GTA CAC CAT CAA	181
I A N D T I D A V G D N K K D A K P E Q G S I Q S N P N K G K	90
GCA AAT GAC ACA ATT GAT GCA GTG GGA GAC AAC AAG AAA GAT GCA AAA CCA GAG CAA GGT AGC ATC CAG TCA AAC CCG AAC AAA GGA AAA	271
D K D V N A G T S G T H T V P R I K A I T P K M R M P K S K	120
GAT AAG GAT GTG AAT GCT GGT ACA TCT GGG ACA CAT ACT GTG CCG AGA ATC AAA GCT ATC ACG CCC AAA ATG AGA ATG CCC AAA AGC AAG	361
G A T V L N L E H L L E Y A P Q Q I D I S N T R A T Q S Q F	150
CGA GCA ACC GTG CTA AAT TTA GAA CAC TTG CTC GAG TAT GCT CCA CAA CAA ATT GAT ATT TCA AAT ACT CGG GCA ACT CAA TCA CAG TTT	451
D T W Y E A V R M A Y D I G E T E M P T V M N G L M V W C I	180
GAT ACG TGG TAT GAA GCA GTG CGG ATG GCA TAC GAC ATAGGAGAA ACT GAG ATG CCA ACT GTG ATG AAT GGG CTT ATG GTT TGG TGC ATC	541
E N G T S P N V N G V W V M M D G N E Q V G Y P L K P I V E	210
GAA AAT GGA ACC TCG CCA AAT GTC AAC GGA GTT TGG GTT ATG ATG GAT GGG AAC GAA CAA GTT GGA TAC CCG TTG AAA CCA ATC GTT GAG	631
N A K P T L R Q I M A H F S D V A E A Y I E M R N K K E P Y	240
AAT GCA AAA CCA ACC CTT AGGCAA ATC ATG GCA CAT TTC TCA GAT GTT GCA GAA CGC TAT ATA GAA ATG CGC AAT AAA AAG GAA CCA TAT	721
M P R Y G L I R N L R D V G L A R Y A F D F Y E V T S R T P	270
ATG CCA CGA TAT GGT TTA ATT CGA AAT CTG CGG GAC GTA GGT TTA CGC CGC TAT GCC TTT GAC TTT TAT GAG GTC ACA TCA CGA ACA CCA	180
V R A R E A H I Q M K A A A L K S A Q P R L F G L D G G I S	300
GTG AGG GCT AGGGAA GCG CAC ATT CAA ATG AAG GCC GCA GCA TTG AAA TCA GCT CAA CCT CGA CTT TTC GGG TTG GAC GGT GGC ATC AGT	901
T Q E E N T E R H T T E D V S P S M H T L L G V K N M *	327
ACA CAA GAG GAG AAC ACA GAG AGG CAC ACC ACC GAG GAT GTC TCT CCA AGT ATG CAT ACT CTA CTT GGA GTC AAC AAC ATG TGA	985

\* indicates the proteolytic cleavage site between NIb and CP.