Maize Dwarf Mosaic Virus (MDMV) samples in Thailand collected from Kanchanaburi, Nakhon Pathom, Ratchaburi, Suphan Buri, Nakhon Sawan, Nakhon Ratchasima and Mukdahan can be transmitted by mechanical method and Aphid transmission. The nucleotide fragments corresponding to coat protein gene of 7 isolates of MDMV were synthesized by reverse transcription-polymerase chain reaction (RT-PCR) method by using CP gene specific primers, SsCP1/T22 and SsCP2/T22, to yield the DNA bands approximately 1,000 bp and 700 bp in size, respectively. Both DNA fragments were cloned into pGEM®-T Easy vectors and sequenced. The full length of coat protein gene of all 7 isolates contained 939 nucleotides in length and were translated to 313 amino acids. The sequence similarity of the 7 isolates were 97-99 % at the nucleotide and 96-99 % at amino acid level. In comparison to the previously reported sequences in GenBank (JGMV, MDMV, SCMV and SrMV), it was found that the nucleotide sequence was 79 % similar to MDMV-B while the amino acid was 92 % sequence homology to the MDMV-B sequence. Phylogenetic tree shown the sequence of the 7 isolates similarity with MDMV-B were 77.8 % at the nucleotide as well as homology with SCMV-A1, A2, B, D, E and MDMV-B were 76.5 % at amino acid level. Determination of resistant level of sorghum varieties against 3 MDMV isolates from Ratchaburi, Nakhon Sawan and Nakhon Ratchasima, almost of them showed the same resistant level. From this study, 7 isolates of MDMV in Thailand were the type strain of MDMV-B.