This research was aimed to study genetic variation of Sugarcane mosaic virus (SCMV) genomes in Thailand. Three SCMV isolates were collected from naturally infected sugarcanes in sugarcane fields. By using reverse transcription–polymerase chain reaction (RT-PCR) technique with specific primers covering the whole genome, these three isolates were cloned and sequenced. Results showed that SCMV-KB isolate from Kanchanaburi province and SCMV-UT isolate from Suphan Buri province contained 3063 amino acids, while SCMV-UD isolate from Udon Thani province contained 3065 amino acids. Sequence comparison of full length genome revealed that the three isolates were of 98-99% and 98% identity of nucleotide and amino acid sequences, respectively. By comparison with GenBank databases, the three isolates were classified in SCMV group, they were similarity to the SCMV group of 79-80% and 89-90% identity of nucleotide and amino acid sequences, respectively, while they were similarity to the MDMV, SrMV and JGMV groups of 53-71% and 48-74% at nucleotide and amino acid sequence levels, respectively. The three isolates were displayed low genetic variations as indicated by their amino acid sequence similarity of more than 96%. With SCMV GenBank database comparison, the CI, HC-Pro, NlA-Pro, Nlb, Nla-VPg, 6K1 and P3 regions were found less variation with 87% similarity, while the P1, CP, 3'UTR, 5’UTR and 6K2 regions were displayed greater variation. Phylogenetic tree analysis shown that the 3'UTR, 6K2, P1 and 5’UTR could be used in grouping of SCMV by hosts, while CP gene could not be used in SCMV group classification between sugarcane and maize of Thailand. Base on this work, those results indicated that the three SCMV isolates in Thailand have low genetic variation and can be classified as the same strain of SCMV. Moreover, their genome variation may be affected by host relationship rather than by geographical location. Infectivity assays of these three SCMV isolates on sorghum and corn, the results were shown in the same virulence level and symptom expression on each host.