In Thailand, downy mildew is one of the most important diseases of corn production and has been reported to be caused by several *Peronosclerospora* species, especially *P. maydis*. Corn varieties have been genetically improved and introduced to farmers; fungicides are also routinely used to control corn downy mildew. These factors induce adaptation by the pathogen. The aim of this study was to determine the genetic variation of *P. maydis* isolates based on physiological race and Simple Sequence Repeats (SSRs) markers. Forty-eight isolates of downy mildew fungi were tested for pathogenicity on six differential varieties by using leaf strip inoculation under greenhouse conditions. The results showed that the fungal isolates could be separated into eight physiological races. Then, virulence data of fungal isolates and races were analyzed using the Canberra and UPGMA methods in the NTsys program. The results revealed that the eight downy mildew races could be divided into three groups at a similarity coefficient of 90%. Furthermore, genetic variation of corn downy mildew fungi was observed by using nine primers of SSRs markers. Forty-three polymorphic bands were generated and analyzed using the Jaccard and UPGMA methods. The analysis separated 29 isolates into 16 groups with a cophenetic correlation ($r$) of 0.97. Therefore, plant breeders should consider the inoculum source and genetic variability of corn downy mildew fungi when corn breeding programs are conducted.