



## Genotypic structure of *Phytophthora infestans* in China with AFLP and SSR molecular markers

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The population structure of *Phytophthora infestans*, the causal agent of late blight of potato and tomato, has undergone major changes in the world over the past 20 years. Molecular marker, such as AFLP and SSR, provided a good tool to study genotypic structure of *P. infestans*.

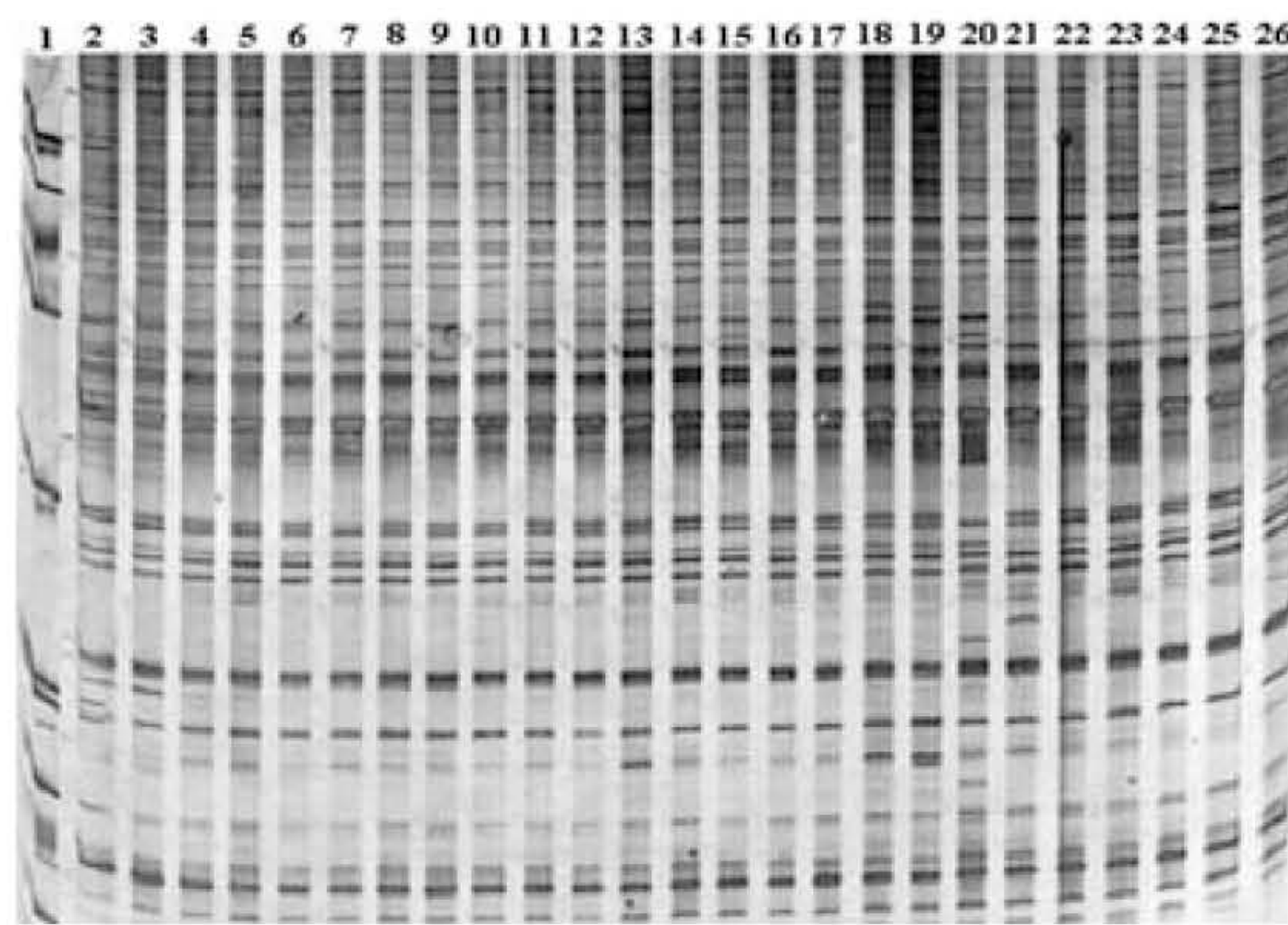


Fig. 1 AFLP fingerprints of *P. infestans* genomic DNA with the primer pair E16/M8

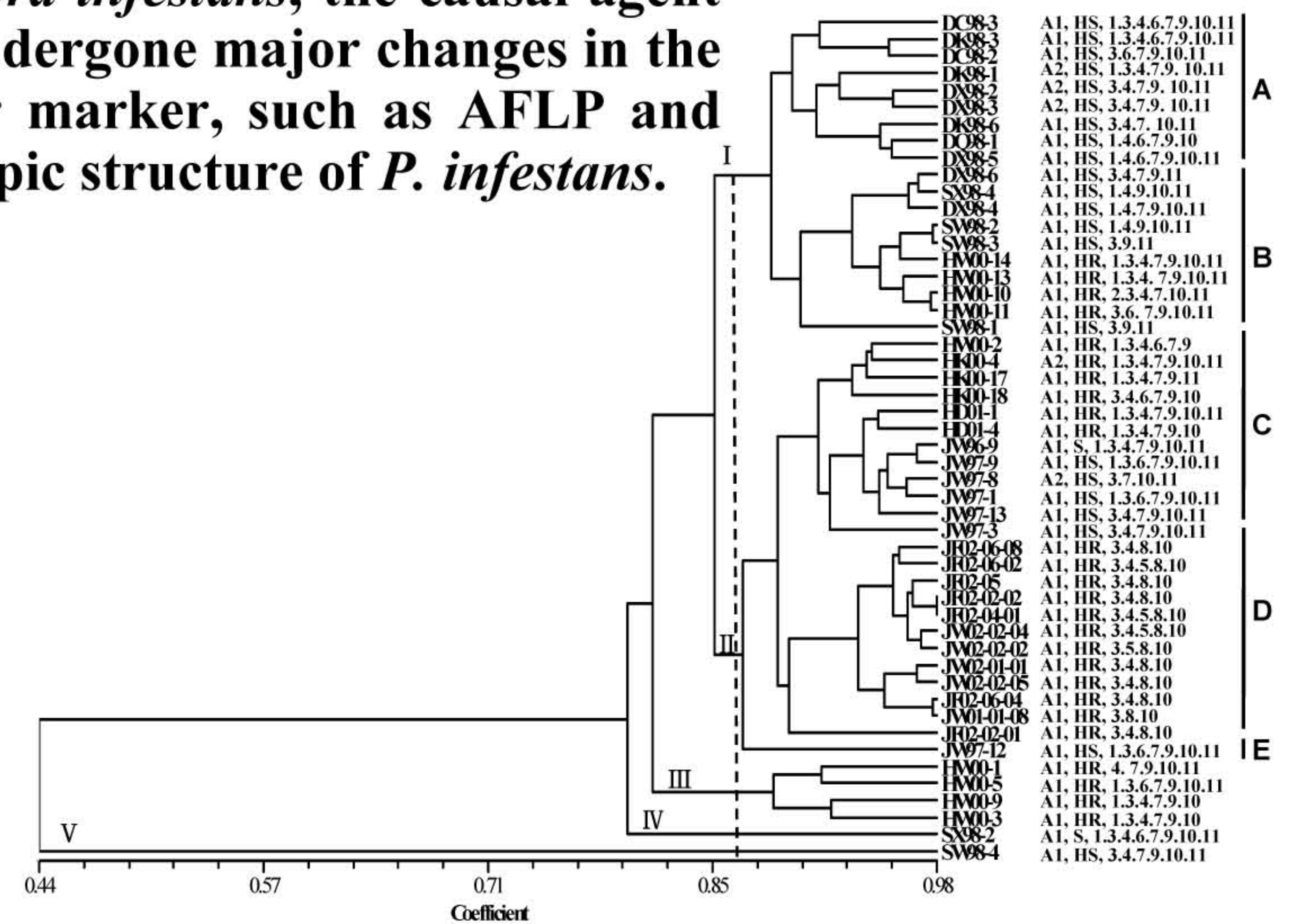


Fig 2. UPGMA tree constructed for 50 isolates of *P. infestans* using AFLP fingerprints produced by 12 primer pairs

The twelve combinations were used to amplify the genomic DNA of 50 isolates collected in China from 1997 to 2002. AFLP fingerprints of twenty-five representative isolates was shown in Fig.1 The total of 922 AFLP bands were obtained, and 530 of them, covering 57.5%, showed polymorphism. Cluster analysis using the unweighted pair-group method with arithmetic averages (UPGMA) separated 50 isolates into five AFLP groups (Fig. 2), which were correlated to groups defined by geographical origin, however, they were not correlated to groups defined by mating type, or response to metalaxyl and virulence. Parameters of genetic diversity calculated by POPGENE software indicated that the genetic diversity level of *P. infestans* population in China was not high.

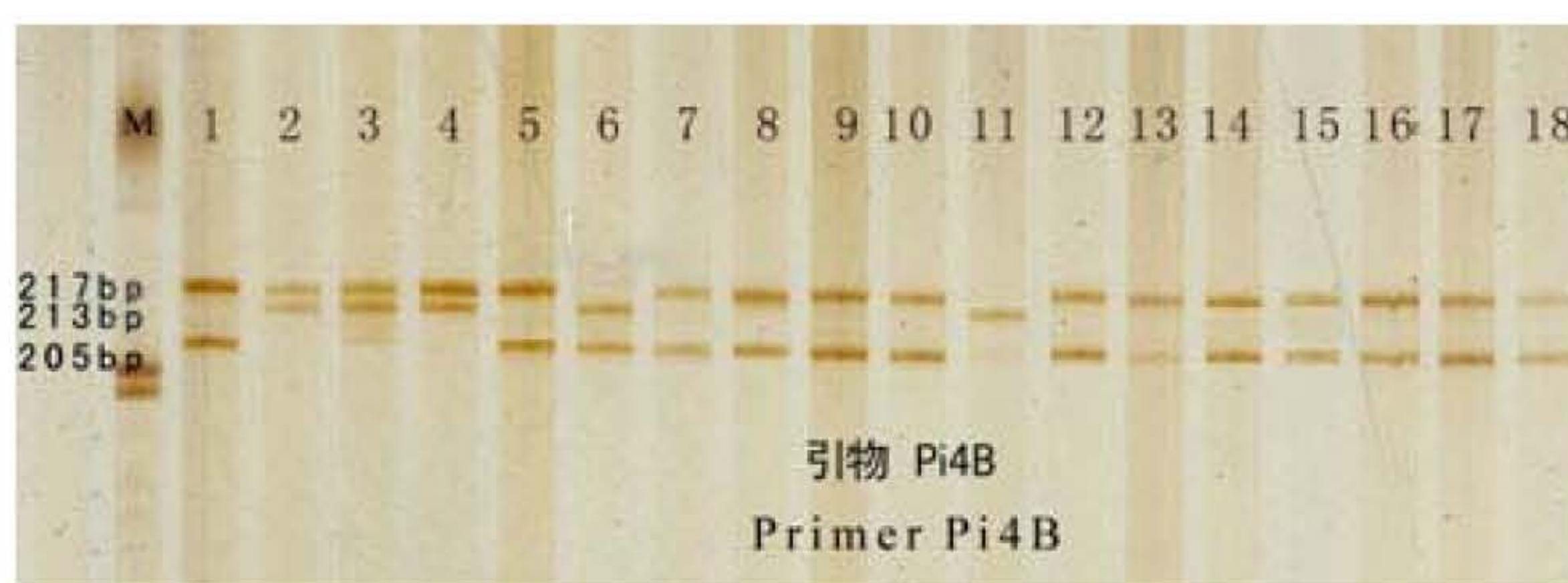


Fig. 3 DNA fingerprint of 18 isolates of *P. infestans*, based on SSR primer pair Pi4B

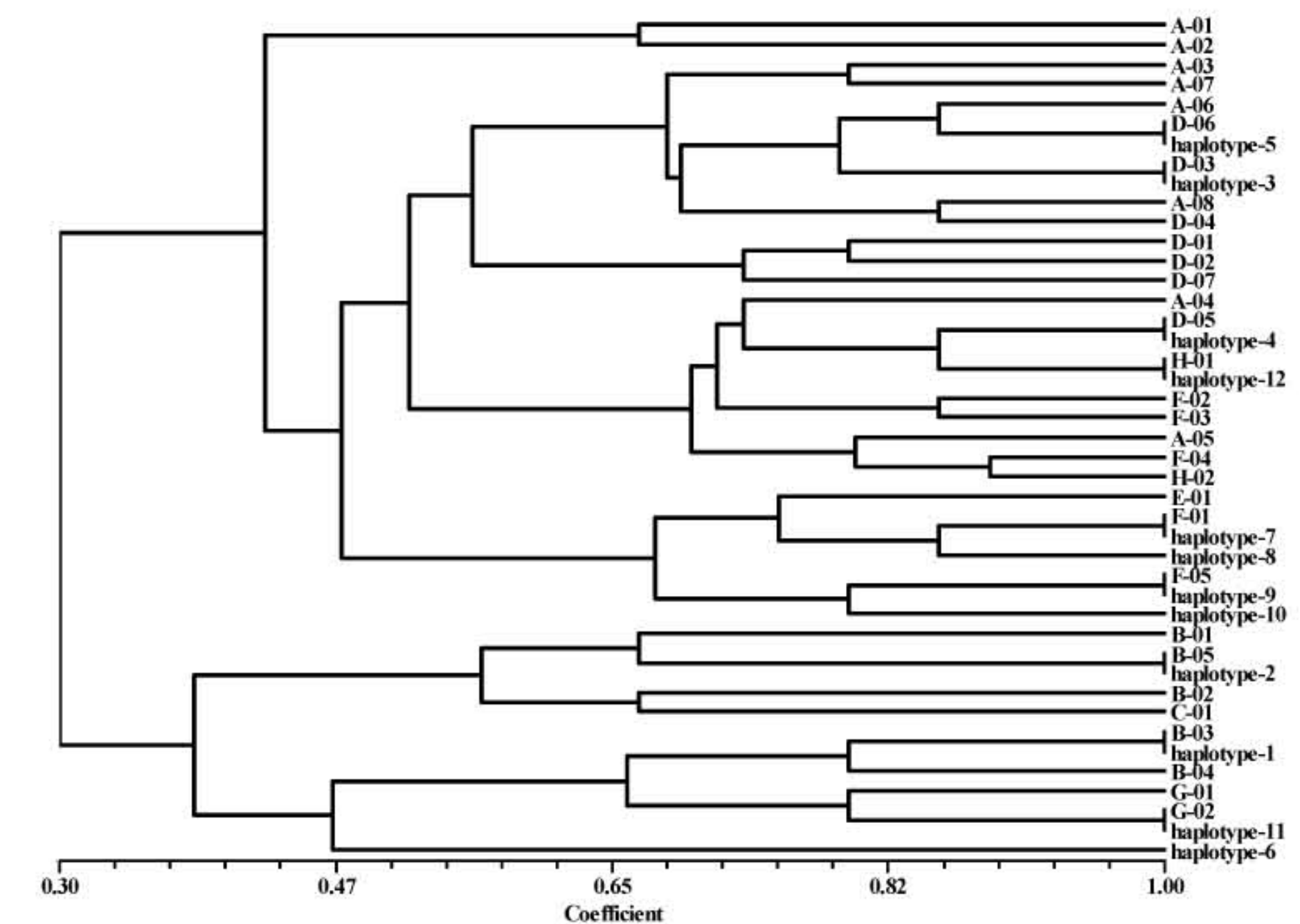


Fig. 2 Dendrogram of *P. infestans* for the definition of genotypes

SSR band patterns of 18 representative isolates of *P. infestans* were shown in Fig. 3. Dendrogram for determination of genotypes of haplotypes of the tested isolates was shown in Fig. 4. With the two microsatellites Pi4B and Pi4G, a total of twelve *P. infestans* genotypes were identified among the 271 isolates collected in China from 1996 to 2007. Among isolates collected from potato, 10 different SSR genotypes were detected of which two, F-01 and F-06, dominated the population. From tomato, only 2 SSR genotypes were found of which one, B-03, formed the major proportion of the population. Statistic analysis of allele genes generated by two primer pairs (Pi4B and Pi4G) indicated that diversity produced by the primer pair Pi4B were higher than that by Pi4G. The SSR genotypes of *P. infestans* collected from potato were entirely distinctive from those from tomato.