Fig.1 The phylogenetic tree of *M. Graminicola* population from China and France of NCBI based on the COI gene constructed. The *mtCOI* sequences were imported into MAFFT for multiple sequence matching, and then the compared sequences were imported into Gblock of PhyloSuite software for trimming, and the optimized data were used for optimal model selection by ModelFinder software Bayesian. Inference with GTR+F+G4 model for mtCOI sequence was conducted in MrBayes 3.2.6 plugin in PhyloSuite. The scale is 0.020.
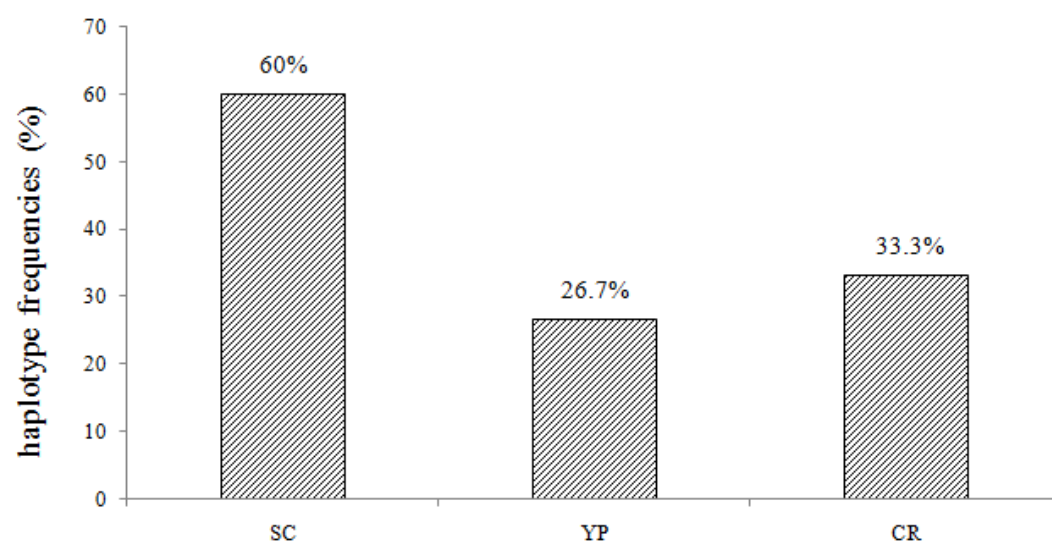
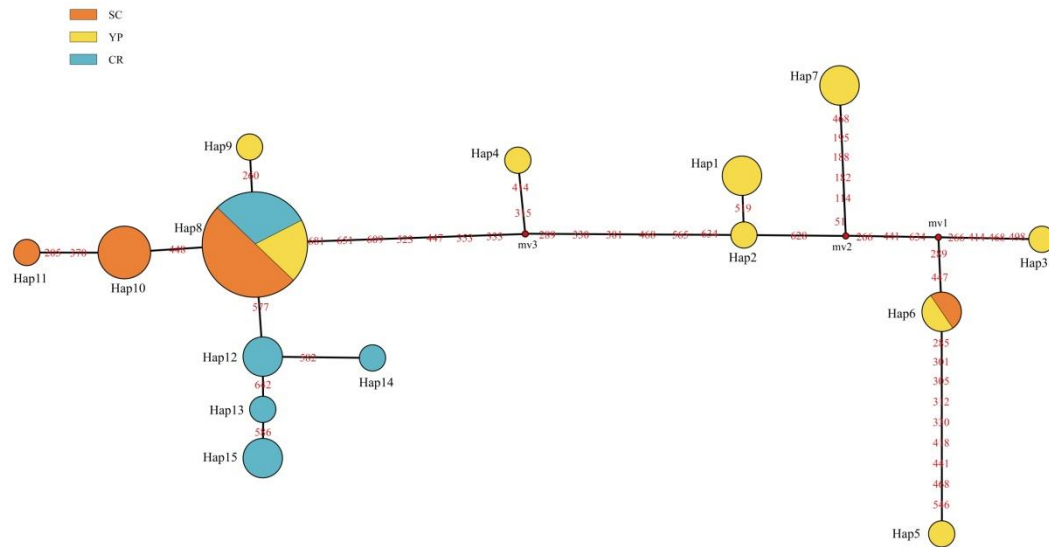Fig.2 Histogram of haplotype frequencies in each *M. Graminicola* groups

Fig.3 Median-Joining haplotype network of 54*M. graminicola* populations based on *mtCOI* gene using NETWORK 5.0 soft. Each numbered circle (Hap1-Hap15) represents a unique haplotype, and the size of the circle is proportional to the overall frequency of each haplotype in the entire sample of the species. Each line connecting the haplotypes refers to a mutational step. Marks on the lines indicate the number of steps. Colors correspond to different sampling locations and names are given in abbreviationsby initials of the group.
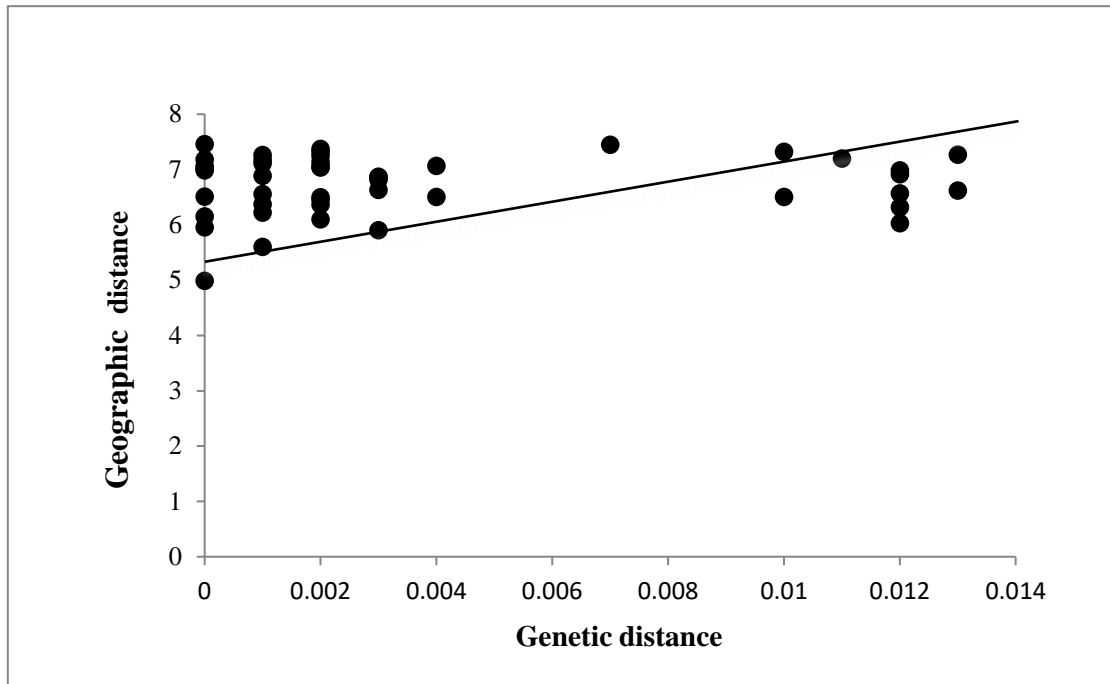
Fig.4 Correlation between genetic distanceand geographical distance in the *M. graminicola* populations based on *mtCOII* gene using SPSS soft. Genetic distance and geographical distance of the populations are in Appendix 1 and Appendix 2, respectively.