Genetic diversity is important for a species and/or population survival. Diseases represent a permanent threat for domestic, captive and wild animal populations. Therefore, genetic diversity in genes involved in resistance/susceptibility to infectious and other diseases is of great interest. In this study, microsatellites and single nucleotide polymorphisms (SNPs) in immunity-related genes were used as markers to describe genetic diversity of three different breeds of the domestic horse (*Equus caballus*): Camargue, Murgese and Icelandic horses. 30 microsatellite and 21 SNP markers developed in this laboratory were genotyped in all three populations by using direct sequencing and PCR-RFLP techniques, respectively. Intra-population characteristics as well as genetic distances among the populations were obtained using the Arlequin3.1software. Microsatellite analysis revealed similar genetic diversity in all three populations studied. Average observed heterozygosities (Ho) ranged from 0,683 of Icelandic horse to 0,715 of Murgese and the mean number of alleles (N_A) varied form 6,37 of Murgese to 7,63 of Camargue. In Icelandic horse population 13 breed-specific alleles with a frequency _ 0,2 were found, suggesting a larger genetic heterogeneity of this breed. Similarly, genetic distances represented by the F_{TS} coefficient showed larger genetic differences of Icelandic horse (F_{TS} = 0,15 – 0,17) from those observed between the Camargue and the Murgese populations (F_{TS} = 0, 05) . Analysis of immunity-related gene SNPs revealed high genetic diversity in the South-European breeds (Ho = 0,313 in Murgese and 0,317 in Camargue) and significantly lower in Icelandic horse (Ho = 0,252). However, genetic distances based on SNP analysis showed only subtle differences among breeds with the highest value between Murgese and Icelandic horse (F_{TS} = 0,12). Neutrality tests of the SNP markers did not reveal any significant Tajima´s d value in any population. In conclusion, the parameters of genetic diversity of the populations studied in microsatellite loci were different from those in the immunity-related gene SNPs, suggesting that information provided by population analysis of candidate gene polymorphisms is different from data obtained by standard microsatellite studies.