Figure S5. The phylogenetic trees. (A) Accessions grouped relative to P/A frequencies. The phylogenetic tree was created based on neighbor-joining method with p-distance model by PAUP* 4.0. (B) The accession tree was constructed by using all SNPs of non-P/A genes among genomes, based on the Neighbor-joining method. The 80 accessions could be generally divided into 8 clades, representing the eight geographic regions where they were sampled. The numbers after each accessions were: (1) Central Asia; (2) East Europe; (3) Caukasus; (4) N-Africa and Spain; (5) Russia; (6) Southern Italy; (7) Southern Tyrol and (8) Tuebingen. The locational distribution could be found on 1001genomes website.