To investigate the haplotype distribution of 23 Y-STR loci in 233 unrelated males in Tianjin Han nationality, and to explore forensic medicine applications. Methods Twenty-three Y-STR loci were genotyped by using PowerPlex® Y23 System and ABI-3500xl genetic analyzer. The gene diversity was calculated by counting the haploid genotype frequency of each locus. Results A total of 233 haplotypes were detected by 23 Y-STR loci. The genetic diversity value ranged from 0.3517 to 0.8918, and the cumulative genetic diversity (TGD) was 0.999920234. Conclusion Twenty-three Y loci in Tianjin Han population were polymorphic, and have important application value to individual identification and paternity testing in forensic science filed.

1 Materials and Methods
1.1 Materials
Blood samples were collected from two hundred and thirty-three irrelevant male individuals in Tianjin Han nationality when dealing with daily cases.

1.2 Instruments and Reagents
AB-9700 PCR Thermal Cycler (ABI Corporation, USA); PowerPlex®Y23 System (Promega Corporation, USA); ABI-3500xl Genetic Analyzer (ABI Corporation, USA), WEN ILS500 (Promega Corporation, USA).

1.3 Methods
Blood samples collected on FTA card were directly amplified using Powerplex Y23 System. The PCR reaction volume was 10μl. All the operating procedures were completed according to product manual from PCR amplification to data analysis.

1.4 Statistical Analysis
PX (haploid frequency) = n/N. The value of PX means the frequency of the haploid X. The value of n represents the number haploid X was observed, and the value of N was the number of the population.

GD (gene diversity)= N(1-∑Pi2)/(N-1). The value of Pi represents haplotype frequency, and the value of N was the number of the population.

2 Results and Discussion
2.1 Results
Two hundred and thirty-three haplotypes were detected through using the kit PowerPlex® Y23 System to analyze two hundred and thirty-three irrelevant males selected randomly from Tianjin Han population (Fig1, Fig.2). The genetic diversity value ranged from 0.3517 to 0.8918, and the cumulative genetic diversity (TGD) was 0.999920234.
Fig. 1 Allele frequencies and gene diversity of 23 Y-STR loci detected in 233 irrelevant males from Tianjin Han population

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2.2 Discussion

Y-STR analysis technology is very commonly used in forensic science field. There are many reports about Y-STR loci distribution at home and abroad. The recurrence probability of haplotypes detected by five or six Y-STR loci is a little higher. This situation appeared
occasionally to twelve Y-STR loci. The same haplotype was not found in this study using PowerPlex Y23 System including twenty-three Y-STR loci. However, for male individuals from the same parent line, the haplotypes of Y-STR loci were consistent, as gene information of Y-STR loci has the characteristic of paternal inheritance. Therefore, individual identification was not assured only by Y-STR testing. Y-STR testing can be used as an effective complement to the autosomal STR testing, which has important application value in the suspect familial identification, paternity testing, the male component detecting from mixed samples, and the judgment of multiple mixed male samples.

In this study, the polymorphism of locus DYS391 in twenty-three Y-STR loci was the lowest, and the GD value was 0.3517, which was in conformity with other domestic reports of DYS391 diversity. Except for locus DYS391, DYS438 and DYS437, the other 20 loci had a GD value greater than 0.5. These loci had great value, as the loci polymorphism is well distributed, in individual identification and paternity testing in forensic science field.