

## 云南汉族HLA-DRB1多态性分析及与9个汉族群体的比较

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**摘要** 主要应用聚合酶链反应—微孔板杂交(Polymerase Chain Reaction and Microtitre Plate Hybridization, PCR-MPH)的方法对云南129个无亲缘关系的汉族样品进行了HLA-DRB1的遗传多态性分析,对MPH初分出的DRB1\*15组的样品进行了单链构象多态(Single-Strand Conformation Polymorphism, SSCP)检测。共发现36种等位基因,其中等位基因频率大于0.05的有DRB1\*1501(0.1240),DRB1\*09012(0.0969),DRB1\*08032(0.0930),DRB1\*1202(0.0891),DRB1\*1201(0.0814),DRB1\*1401(0.0775),DRB1\*0701(0.0620)。云南汉族HLA-DRB1等位基因频率与中国其他9个汉族群体进行 $\chi^2$ 检验,结果显示与云南汉族比较 $\chi^2 > 10$ 的有西安汉族(DR8,  $\chi^2 = 13.9712$ )、上海汉族(DR4,  $\chi^2 = 10.1632$ )、广东汉族(DR9,  $\chi^2 = 12.6121$ )和南京汉族(DR4,  $\chi^2 = 10.5796$ )。从遗传距离分析发现,在9个国内汉族群体中云南汉族与辽宁汉族有最近的距离(0.0541),而与广东汉族最远(0.1851)。云南汉族在构成上可能与辽宁汉族更为接近,尽管地处南方,但已不属典型的南方汉族。这也可能因云南汉族与当地的少数民族存在基因交流,从而形成了一个较为特殊的群体。

**关键词** [云南汉族](#) [HLA-DRB1基因多态](#) [聚合酶链反应—微孔板杂交](#) [单链构象多态](#) [遗传距离](#)

分类号

## Polymorphism of HLA-DRB1 in Han Population in Yunnan and Comparison with 9 Han Populations

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### Abstract

In this study, 129 samples of Han population in Yunnan province were detected by polymerase chain reaction and microtitre plate hybridization (PCR-MPH). The samples of DR\*15 subgroup being detected by PCR-MPH were further analyzed by Single-Strand Conformation Polymorphism (SSCP). By first polymerase chain reaction and microtitre plate hybridization (PCR-MPH), all of the 129 samples were divided into the following subgroups, viz. DR\*01, DR\*03, DR\*04, DR\*0701, DR\*08, DR\*09012, DR\*1001, DR\*11, DR\*12, DR\*13, DR\*14, DR\*15, DR\*1602 and DR\*1604. The samples of DR\*04, DR\*08/12, DR\*03/11/13/14 were further detected by second PCR-MPH and the ones of DR\*15 by SSCP. 36 kinds of alleles on HLA-DRB1 were detected in these samples. Among them, DRB1\*1501(0.1240), DRB1\*09012(0.0969), DRB1\*08032(0.0930), DRB1\*1202(0.0891), DRB1\*1201(0.0814), DRB1\*1401(0.0775), DRB1\*0701(0.0620), are the most frequent. The  $\chi^2$  test of HLA-DRB1 alleles was done between Yunnan Han and the other 9 Han populations. In detail, comparing with Yunnan Han on the  $\chi^2$  test, the  $\chi^2$  values of few alleles in the few Han populations was more than 10, they were Xian Han (DR8,  $\chi^2 = 13.9712$ ), Shanghai Han (DR4,  $\chi^2 = 10.1632$ ), Guangdong Han (DR9,  $\chi^2 = 12.6121$ ) and Nanjing Han (DR4,  $\chi^2 = 10.5796$ ). Comparing with 9 Han populations, the genetic distance between Yunnan Han and Liaoning Han was the nearest (0.0541), Guangdong Han was the farthest (0.1851). In the 9 Han populations, the genetic distance between Shanghai Han and Nanjing Han was the nearest (0.0122), and the one between Tianjin Han and Shanxi Han was also nearer (0.0219). Based on above analysis, the conclusion may be deduced that the resource of Yunnan Han may be close to Liaoning Han and it was not a typical southern Han population though Yunnan Han

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are resident in the South. Some gene flow may be exit between Yunnan Han and the local minorities and made Yunnan Han become a special population.

**Key words** [Yunnan Han population](#) [HLA-DRB1](#) [Polymorphism](#) [PCR-MPH](#) [SSCP](#) [Genetic Distance](#)

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