

was employed to study the genotype taxon and population genetics of 154 isolates of *S. typhi* from Xinjiang in recent 11 years. Seven kinds of enzymes were examined and determined. One hundred and fifty-four strains of *S. typhi* were classified into 69 electoretic types (ETs) and 10 clones (CLa-CLj). Among those 154 strains 80 epidemic isolates belonged to 21 ETs and 3 clones (CLe, f, j). ET17, 20, 21, 24, 26, 27 were the main ETs (61.30%), and CLf was the dominant clone (95.00%). Seventy-four non-epidemic isolates belonged to 48 ETs and 9 clones (CLa, b, c, d, f, g, h, i, j), no obvious dominant ET was found in them, and the main clone CLh accounted for 43.30%. It demonstrated that both outbreak and sporadic epidemics could be caused by many strains of ETs and clones, but the distribution of the former ETs was more concentrated and the preponderance of clones was more obvious. The analyses on structure of population genetics indicated that all of 7 enzymes were polymorphic. Genetic diversity among the enzyme loci was quite high, with an average of 0.35 per locus (H). The average number of alleles per locus (\bar{h}) was 6.14. There was no significant

difference in \bar{h} or H between the isolates of different sources ($P > 0.05$). It was clear that *S. typhi* of different sources in Xinjiang were originated from the same population. The results also showed that there was a dominant allele in every enzyme locus. Natural selection was the main role in the evolution of *S. typhi*.

Key words Multilocus enzyme electrophoresis *S. typhi* Population genetics

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南召县1953~1992年疟疾流行病学分析

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南召县山深蚊虫多,属间日疟高发区。1953~1992年疟疾发病490 891例,男271 463例(55.30%),女219 428例(44.70%),男女之比为1.24:1。分布于全县16个乡镇,发病率波动在1932.61/万~0.07/万之间,曾为严重危害我县人民身体健康的传染病。40年间农村发病占95.12%,最小年龄6个月,最高年龄84岁,18~45岁病例占总数的60%以上。经全民预防服药、普查普治和以消灭传染源为主的综合目标责任制的实施,1988年起发病率控制在1/万以下,为1992年11种传染病之第10位。

40年中五次发生间日疟爆发流行,分别为1956、1965、1970、1977、1981年。发病率依次为230.77/万、482.06/万、1932.61/万、427.80/万、269.52/万。1990年在较低发病率(0.12/万)的情况下,较1989年(0.07/万)又有回升。由此看来南召县疟疾发病有每5~10年一次大流行的趋势。

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