



应用微卫星DNA标记探讨我国长江中下游地区湖北钉螺群体遗传结构

李石柱1, 张丽1, 刘琴1, 吕山1, 王强1, 钱颖骏1, 杨坤2, 周晓农1*

1 中国疾病预防控制中心寄生虫病预防控制所, 卫生部寄生虫病原与媒介生物学重点实验室, 世界卫生组织疟疾、血吸虫病和丝虫病合作中心, 上海 200025; 2 江苏省血吸虫病防治研究所, 无锡 214064

Study on the Genetic Differences among *Oncomelania hupensis* Population in Middle and Lower Reaches of Yangtze River using Microsatellite DNA Markers

LI Shi-zhu1, ZHANG Li1, LIU Qin1, LV Shan1, WANG Qiang1, QIAN Ying-jun1, YANG Kun2, ZHOU Xiao-nong1*

1 National Institute of Parasitic Diseases, Chinese Center for Disease Control and Prevention; Key Laboratory of Parasite and Vector Biology, MOH; WHO Collaborating Center of Malaria, Schistosomiasis and Filariasis, Shanghai 200025, China; 2 Jiangsu Institute of Parasitic Diseases, Wuxi 214064, China

摘要

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摘要 目的 应用微卫星DNA分子标志分析中国长江中下游地区湖北钉螺群体的遗传结构。方法 利用6对微卫星DNA引物,对采集自湖沼型血吸虫病流行区的湖南汉寿县、湖北阳新县、江西星子县、安徽当涂县和江苏扬州邗江区的湖北钉螺的P84、T5-13、T5-11、T4-22、T6-27和P82等6个位点进行荧光标记通用引物PCR扩增。每个采集点采集20~50个钉螺标本,共165个。统计分析各群体的等位基因数(N_a)、近交系数(F_{IS})、期望杂合度(H_e)、观察杂合度(H_o)、多态信息含量(PIC)、群体间的遗传分化系数(F_{ST})和遗传距离,根据遗传距离进行聚类分析,并进行分子变异方差分析(AMOVA)。结果 5个湖北钉螺群体在6个微卫星位点等位基因数范围为3~33,平均为15.833。群体的平均 H_e 和 H_o 范围分别为0.600~0.883和0.308~0.759,两者在湖北群体最高,在江苏群体最低。群体的 F_{IS} 范围为0.143~0.539。成对群体间的 F_{ST} 范围为0.0006~0.0531,由于 F_{ST} 值较小,提示群体间未出现明显遗传分化。各群体的平均PIC为0.511~0.850,除江苏群体外,均为高度多态。分级AMOVA结算结果显示,变异主要存在于个体间,占总变异的95.2%。聚类分析结果显示,安徽群体与江苏群体首先聚为一支,然后依次同湖南、江西、湖北群体聚在一起。结论 湖北钉螺多样性较为丰富;聚类分析结果符合湖北钉螺的地理分布格局;5个群体之间遗传差异较小,微卫星DNA的变异主要存在于个体间。

关键词: 湖北钉螺 微卫星DNA 群体遗传差异

Abstract: Objective To identify the genetic structure of *Oncomelania hupensis* in the middle and lower reaches of Yangtze River by using microsatellite DNA molecular markers. Methods *O. hupensis* snails were collected from the provinces of Anhui, Hunan, Hubei, Jiangxi, and Jiangsu, of which 6 polymorphic microsatellite DNA loci (P84, T5-13, T5-11, T4-22, T6-27 and P82) were amplified with fluorescence labeled universal primer. 20-50 snail samples were collected at each spot, adding up to 165 samples. The number of alleles (N_a), inbreeding coefficient (F_{IS}), heterozygosity (H), fixation index (F_{ST}) of each group snails, genetic distance between groups, and the polymorphic information content (PIC) were calculated. Cluster analysis was then carried out based on genetic distance, and hierarchical AMOVA calculation was done. Results The number of alleles in each population ranged from 3 to 33, and the inbreeding coefficient ranged from 0.143 to 0.539. The average expected heterozygosity and observed heterozygosity ranged from 0.600 to 0.883 and 0.308 to 0.759, respectively, being the highest in Hubei population and the lowest in Jiangsu population. The range of F_{ST} value between paired populations was from 0.0006 to 0.0531. The small F_{ST} value suggested that genetic differentiation did not occur among the populations. The average polymorphic information content in the populations ranged from 0.511 to 0.850, showing a high polymorphism except the Jiangsu population. Hierarchical AMOVA calculations showed that inter-individual variation of the snails occupied 95.2% of the total variations. Cluster analysis revealed that Anhui group clustered first to Jiangsu, followed with Hunan, Jiangxi and Hubei. Conclusion There is a rich diversity in *O. hupensis*. Cluster analysis shows a consistency with the geographical distribution pattern. The genetic differences among the 5 snail populations are trivial with microsatellite DNA variation mostly present in individuals.

Keywords: *Oncomelania hupensis* Microsatellite DNA Population genetic difference

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