不同地区库蚊复组群体的同工酶遗传多样性研究Genetic Diversity of I soenzyme in Culex pipiens complex Field Populations Sampling from Distinct Area of China

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采用水平切片淀粉凝胶电泳的方法,对分布于我国5省的8个库蚊复组(Culex pipiens complex)野生群 体的遗传多样性进行研究,分析了4个酶系统7个基因座(ME、MDH-1、MDH-2、MDH-3、GPD、EST-2、EST-3)的酶谱 资料。结果显示: (1)群体内存在不同程度的遗传变异(He为0.098~0.41); (2)较低的基因流水平 (Nm=0.64) 使遗传漂变起主要作用,造成群体之间的遗传分化(Gst=0.303),而总群体的遗传多样性相对富集 于群体之内(Hs/Dst=2)。(3)库蚊群体的遗传结构属于距离隔离模式。(4)群体间的遗传一致性(或遗传距离) 反映出群体间的遗传分化程度,也表明与地理位置存在对应关系。Abstract: Eight field populations of Culex pipiens complex collected from five provinces (Guangdong, Henan, Shandong, Beijing and Yunnan) in 2001 were used to study genetic diversity by starch gel electrophoresis. Data from seven ▶ <u>本刊中 包含"库蚊</u>复组"的 loci (ME、MDH-1、MDH-2、MDH-3、GPD、EST-2、EST-3) of four isozymes were analyzed by software Biosys2.0 and FSTAT(Version 2.9.3). The results were as follows: (1) The values of He (from 0.098 to 0.41) indicated genetic variabilities of different degree in populations. (2) The low level of gene flow (Nm=0.64) could not prevent

genetic drift to cause the gene differentiation between populations. The genetic diversity between populations attributed to the genetic diversity of total populations is small (Gst =0.303), and the great part is accumulated within populations (Hs/Dst=2). (3) The genetic structure of Culex pipiens complex population was the isolation-by-distance model. (4) The genetic identity (or genetic distance) revealed the scale of genetic differentiation between populations which related to the collection sites.

关键词 库蚊复组 遗传多样性 同工酶 Key word Culex pipiens complex genetic diversity isoenzyme 分类号

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Abstract

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