



中文标题 检索 药刊检索

苗药大果木姜子的遗传分化及其化学变异的相关性分析

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中文摘要:目的: 基于苗药大果木姜子原植物来源的9个居群分析其遗传结构及其与化学成分变化的相关性。方法: 采用ISSR分子标记方法研究9个居群的遗传结构, 运用GC-MS分析其挥发油主要成分。结果: 挥发油主成分分析显示居群间具有显著水平的成分差异, 各主成分的变异系数以云南富宁居群为最小, 以广西乐业居群最大。3SSR分析表明, 在居群水平上来粮的多态位点百分率(P)平均值为42.41%, 期望杂合度(H)为0.181 0, Shannon多样性指数(H')为0.293 8, 居群内Nei's基因多样性(H_d)为0.188 9, 基因分化系数(G_{st})为2.269 1。遗传结构与挥发油主成分的相关性分析显示, 大果木姜子主成分的化学变异系数与遗传分化的4个指标相关性不显著。结论: 大果木姜子原植物种群的遗传变异多存在于居群内, 居群间的遗传分化较小。化学成分与遗传多样性相关性不明显, 暗示其他因素可能是导致其植物居群间发生化学变异的原因。

中文关键词: 大果木姜子 米楠 化学成分变异 遗传多样性 相关性分析

Researches on relationship between genetic differentiation and chemical variation of *Cinnamomum migao*

Abstract: Objective: To study the relationship between the genetic diversity and chemical variation of *Cinnamomum migao*. Method: ISSR marker technique was used to research the genetic structure of 9 population, GC-MS was used to analyze the main ingredients of the volatile oil in *C. migao*. Result: The analysis on the main ingredients of the volatile oil showed that there were significant or extremely significant differences in 9 populations. The minimum variation index of population was Yunnan Funing and the maximum variation index of population was Guangxi Yueye. ISSR marker analysis showed that the average of polymorphic loci percentage (P) was 42.41%, expected heterozygosity (H) was 0.181 0, Shannon's information index (H') was 0.293 8, the Nei's genetic diversity (H_d) in the group was 0.188 9, genetic differentiation index (G_{st}) was 2.269 1. The relationship between the genetic diversity and chemical variation showed that there was no significant correlation between the main ingredients of the volatile oil and 4 indexes of genetic structure of *C. migao*. Conclusion: The genetic diversity of *C. migao* was relatively high at the population levels, while it is low within the population levels, the relationship between chemical variation and genetic diversity was not obvious, that may indicate that other factors causes the chemical variation of *C. migao*.

keywords: *Cinnamomum migao* chemical variation genetic differentiation correlation analysis

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