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贵州头花蓼遗传多样性的ISSR分析

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 $_{\rm st}$ )为0.722 3,居群内Nei's基因多样性( $H_{\rm s}$ )为0.080 4,Shannon's多样性基因遗传分化系数( $I_{\rm st}$ )为0.044 2。UPGMA聚类分析显示48个居 st" 群可分为5大类。贵州境内西部,西南部与东南部的头花塞表现为交叉聚类Meantcl捡测层群间的遗传更离与她重距离之间无显著 的正相关关系(~0.262 9)。 结论:头花蓼种群遗传变异多存在于居群间,居群内的遗传分化较小居群间存在基因流(N<sub>m</sub>)受阻,聚类 显示部分迁徙居群没有出现随地理变化的遗传变异趋势。

中文关键词:<u>头花蓼 居群 遗传多样性</u> 遗传结构 <u>ISSR</u>

## $Genetic\ diversity\ of\ \textit{Polygonum\ capitatum\ } from Guizhou\ populations\ by\ ISSR\ markers$

Abstract:Objective: To detect genetic diversity of 48 population of Polygonum capitanum in Guizhou province. Method: The genetic diversity of 48 representational populations of P. capitanum including 240 individuals had been investigated by ISSR marker technique. Result: The genetic diversity had been revealed as follow: A total of 8 293 bands were produced in 240 individuals, of which 7 962 banes were common in the 48 population. The value of the average percentage of polymorphic bands (PPB) was 79.098, Nc18 centic diversity index ( $H_Q$ ) was 0.245 8, Shannon's information index (I) was 0.396 2, and genetic differentiation index ( $G_{sq}$ ) was 0.238 0 at population level, nace, (r<sub>g</sub>) was 0.245 x, Snamon's mormation faces (r)was 0.359 c, and generic differentiation ones (0<sub>gg</sub>) was 0.250 at population errespectively. The genetic differentiation index (6<sub>gg</sub>) was 0.072 2, genetic differentiation coefficient by Shannon's diversity (1<sub>gg</sub>) was 0.044 2 within the population levels. Groups cluster analysis based on the UPGMA method indicated that although the 48 populations could be divided into 3 groups and the *P. capitatum* seed sources. The groups cluster showed that a cross clustering of *P. capitatum* between the southwest and southeast populations in Guizbou province, and no significant correlation was found between geographical and genetic distance among them. Conclusion: The genetic diversity of *P. capitatum* is relatively high at the population levels, while low within the population levels, while low within the population levels, a significant degree of genetic differentiation occurs among the populations. The groups cluster analysis indicated they has not apparent genetic variation in regional pattern between the place of origin populations and the migrate populations.

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