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硕 士 学 位 论 文

漳江口互花米草种群遗传结构与分布格局

The population genetic structure and the pattern of distribution of S*partina alterniflora* in Zhangjiang Estuary

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摘　要

本文主要以福建省漳州云霄漳江口国家级红树林保护区为研究对象，利用ISSR 分子标记技术分析该地区互花米草的遗传多样性，揭示该地区互花米草的种群遗传结构，同时比较了天津塘沽大桥、宁德三都湾、上海崇明东滩、珠海淇澳岛、泉州洛阳桥、广西合浦沙田港等 6 个互花米草种群的遗传多样性，探讨了互花米草克隆生长入侵的可能机制，为互花米草入侵管理和防治提供一定的科学依据。

从 100 条 ISSR 引物中筛选出可以扩增出清晰、重复性好的 18 条引物，对福建省云霄漳江口国家级红树林保护区 253 份材料扩增。互花米草的遗传多样性及分化系数由 POPGENE 软件分析表明，互花米草上、中、下游种群总的遗传多样性(Ht)是 0.744，其中种群内的遗传多样性(Hs)为 0.448 ，种群间的遗传分化系数（Gst)为 0.398 ，与 AMOVA 分析种群间遗传变异量 22.56%基本一致。

由 UPGMA 法获得了基于 Nei's 无加权计算互花米草各种群的遗传距离聚类图。互花米草上、中、下游 3 个种群的遗传距离在 0.3237-0.6412 之间变化。上游和中游遗传距离最小（0.3237），下游与上、中游遗传距离较大。显然，生境的异质性导致互花米草种群的遗传分化程度。

进一步对该地区 21 个互花米草斑块亚种群进行分析，Nei's 遗传多样性指数 H 为 0.7754, Shannon's 信息指数 I 为 0.8036。物种水平的遗传多样性(Ht)为 0.781，斑块亚种群内遗传多样性(Hs)是 0.520 ，遗传分化系数为 0.334，与 AMOVA 分析种群间变异量 25.02%基本保持一致。21 个斑块亚种群的遗传距离在 0.1778－0.5157 之间，其中第 3 斑块亚种群与第 4 斑块亚种群间的遗传距离最小（0.1778），第 14 亚种群与第 18 斑块亚种群间的遗传距离最大（0.5157）。从总体趋势上看，斑块亚种群的自然分布情况和遗传上关系大致相同，上、中、下游的亚种群大体聚集在一起。

分析表明，漳江口 21 互花米草斑块亚种群的 253 个基株可以分为 37 个分株。同一斑块亚种群中由 2-3 个分株组成，而非单一分株的克隆生长。究其原因，可能与斑块扩散过程中存在一定比例的有性繁殖发生有关。此外，分株的潮汐漂浮扩散能力强也可能是导致克隆斑块亚种群出现遗传分化的原因。

同一分株出现在不同的斑块亚种群中。其中，中游的斑块亚种群 10 中的分

株在下游斑块亚种群 21 中也存在，说明该地区互花米草的克隆扩散能力高达 10Km 以上。

对所采取的不同纬度下 389 份互花米草材料共扩增出 186 条带，扩增条带分子量大小在 0.1-2kb 之间,其中 164 条带具有多态性，其多态性百分率为 88.1%，各引物扩增条带数在 5-14 条不等，平均为 10 条。Nei's 遗传多样性指数 h 为 0.7347, Shannon's 信息指数 I 为 0.7564。物种水平的遗传多样性(Ht)为 0.755，种群内遗传多样性(Hs)是 0.435。互花米草分化系数为 0.423,基因流 Nm 为 0.341。 种群遗传距离在 0.1201－0.9530 之间变化。广西（GX）种群与泉州（QZ）种群间的遗传距离最小（0.1201）,种群的 UPGMA 聚类的结果表明,可以分成两大类群：

第一类群：天津塘沽大桥与其他 6 个种群的遗传距离最大，成为一个独立的分支；

第二类群：分类相对比较复杂，包括上海崇明东滩、宁德三都湾、 泉州洛阳桥、珠海淇澳岛、 漳州云霄保护区以及广西合浦沙田港，其中上海崇明东滩和宁德三都湾聚为一支，泉州洛阳桥和广西合浦沙田港聚为另一细支。珠海淇澳岛、 漳州云霄保护区再与两细支配聚合。

对漳江口以及其他 6 个纬度下互花米草种群的研究表明，互花米草在形态特性上随着纬度梯度的变化表现出极强的可塑性。

异质生境导致互花米草种群的遗传分化，这可能是互花米草种群具有高表型可塑性的遗传学基础。较高的表型可塑性和遗传分化能力是互花米草能够入侵广阔纬度区域的重要原因，同时也在适应不同环境时发挥了重要的作用。

关键词：互花米草；生物入侵；遗传结构；异质环境；

Abstract

Using ISSR DNA molecular markers, the genetic diversity and genetic structure of *Spartina alterniflora* populations from Zhang Jiang state-level nature reserve of mangrove forest (Zhangzhou, Fujian, ZZ), Tanggu brige of Tianjin (TJ), Luoyang brige of Quzhaou (Fujian, QZ), Chongming of Shanghai (SH), Sandu Bay of Ningde (Fujian, ND), Shatian port of Hepu (Guangxi, GX), and Qiao island of Zhuhai (Guangdong, ZH) were analysised to study the invasive mechanism of *Spartina alterniflora*.

We selected 18 primers from 100 ISSR Primers for PCR amplification, which may get clear, well-duplicated bands after gel electrophoresis. By the POPGENE software， genetic diversity and genetic differentiation coefficient of *Spartina alterniflora* populations (or sub-populations) from different location were calculated.

In Zhang Jiang state-level nature reserve of mangrove forest, the species level heredity multiple (Ht) of three *Spartina alterniflora* populations from upstream, midstream and downstream were 0.744, occupied in the group to inherit multiple (Hs) is 0.448 , Gst value was 0.398 which was consistent with the result of AMOVA analysis.

By the UPGMA based on the Nei' s non-weighting computation, the heredity distance map among three *Spartina alterniflora* populations were obtained. The heredity distance was from 0.3337 to 0.6412. In which, the heredity distance between upstream and midstream population was least (0.3237). Two populations could gather into one branch. The heredity distance between downstream and upstream or midstream population was more. It showed that heterogeneity habitat leaded to genetic differentiation within *Spartina alterniflora* populations.

Futher analyzed 21 *Spartina alterniflora* clonal patch subpopulations of ZZ, Nei's heredity multiple index h was 0.7754, Shannon's information I was 0.8036. Species level heredity multiple (Ht) were 0.781, occupied in the group to inherit multiple (Hs) is 0.520, Gst) value was 0.334 which was consistent with the result of AMOVA

analysis. The heredity distance among various populations were from 0.1778 to 0.5157. The heredity distance between NO.3 and NO.4 clonal patch subpopulation was least (0.1778)，the heredity distance between NO.14 and NO.18 clonal patch subpopulation was most (0.5157). From the general trend of the genetic relationship among subpopulations, the upstream ,midstream, downstream population gathered together, respectively.

By analyzing DNA bands and Using method of Sydes and Pekall(1998), we found that only 37 clonal ramets existed within 253 genets of 21 clonal patchs. A clonal patch is consisted of 2-3clonal ramets, not only same one ramets. It's probable that sexual reproduction existed in a clonal patch, or a ramet had strong spread ability by tidal water.

A ramet appeared different clonal patch. For example, a ramet in NO.10 clonal patch could spread in NO.21 clonal patch, showed spread ability of *Spartina alterniflora* was more than 10 Km. This is an evidence of strong invasive ability of *Spartina alterniflora*.

We obtained 186 bands by amplifying all 389 samples from different latitude distributions. The amplified bands molecular weight sizes were between 0.1-2kb. In which, 164 bands had polymorphism with polymorphism percentage 88.1%. Amplified bands number was from 5 to 14 , and the average band number was 10. Nei' s heredity multiple index h was 0.7347, the Shannon's information index I was 0.7564. Species level heredity multiple (Ht) were 0.755, occupied in the group to inherit multiple (Hs) is 0. 465. The *Spartina alterniflora* Gst value was 0.342. The heredity distance between various populations was from 0.1201 to 0.9530. The heredity distance between GX and ZH population was least (0.1201). The UPGMA cluster result indicated that *Spartina alterniflora* could divide into two big groups.

The first group only included TJ, which had biggest genetic distance with other six populations and became an independent branch. The second group included QZ, SH, ND, GX, ZH and ZZ. This group was complex and divided into three branchs. A branch included SH and ND, the second one included QZ and GX, and the third one