

## 不同地区溶藻弧菌的分子分型及毒力基因的分布特征研究

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**摘要:** 目的 研究不同地区溶藻弧菌的分子特征及毒力基因的携带情况, 分析溶藻弧菌之间的遗传相关性, 为进一步研究本菌的流行规律和制定防治措施提供依据。方法 对福建、湛江、广西、海南四个地区采集到的 127 株溶藻弧菌进行 RAPD 分子分型, 并对 *tlh*、*trh*、*tdh* 等 7 个毒力基因进行 PCR 检测。结果 将 127 株溶藻弧菌分成多个株系, 在毒力基因的检测中, *tdh* 和 *tlh* 的检测率均为 0, *toxR* 阳性菌和 *tlh* 阳性菌占主导地位, 其检出率分别为 100% 和 26.8%。结论 沿海地区养殖环境中溶藻弧菌污染状况比较严重, 且有相当比例的菌株携带毒力或疑似携带毒力。研究结果为深入探索溶藻弧菌的致病性、基因结构与功能 (或表型) 及其分子演化提供基础。

**关键词:** 溶藻弧菌; 分子分型; 毒力基因

## THE MOLECULAR SUBTYPING AND DISTRIBUTION OF VIRULENCE GENES IN *VIBRIO ALGINOLYTICUS* ISOLATED FROM DIFFERENT DISTRICTS

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**Abstract:** Object To study the molecular characteristics and the distribution character of virulence genes in *Vibrio alginolyticus*, to analyze the phylogenetic relationship between them so as to study the epidemic trend and support the policy-making. Methods The RAPD (random amplified polymorphic DNA) molecular markers were used to study the taxonomy of 127 *V. alginolyticus* from Fujian, Zhanjiang, Guangxi and Hainan. And 7 virulence genes were tested too, they are *tlh*, *trh*, *tdh* and so on. Results These strains can be divided into different groups according to the different genetic similarity and heredity distances. In the virulence genes detecting, there was no strain carrying *tlh* and *trh* genes, but the strains carrying *toxR* genes were 100%, and *tlh* genes were 26.8%, they were the two most genes detected on these 127 strains. Conclusion This study reveals the significant prevalence of *V. alginolyticus* in their habitats with high diversity of virulence genes. Representative *V. alginolyticus* isolates could be used for further investigation into their pathogenicity, functional genomics, and molecular evolution.

**Keywords:** *Vibrio alginolyticus*; molecular subtyping; virulence genes