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9个多态性STR基因座用于完全性葡萄胎的亲代来源鉴定 The Polymorphism of Nine STR Loci on the Genetic Original Identification of Complete Hydatidiform Mole

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摘要
选取9个多态性STR基因座，应用多重PCR技术和聚丙烯酰胺凝胶电泳结合银染显色的方法，对33例病理学诊断为完全性葡萄胎的组织标本及夫妇双方外周血标本进行分子病理学分析研究，判定其DNA来源。结果表明，33例病理学上的完全性葡萄胎有27例DNA为单纯性父方来源，占81.8%(27/33)，其中，纯合子完全性葡萄胎为22例，占66.7%(22/33)，杂合子完全性葡萄胎5例，占15.1%(5/33)；其余6例的DNA来自双亲，占18.2%(6/33)。葡萄胎的组织病理学诊断与其分子病理学诊断存在差异，提示9个多态性STR基因座分析法适用于鉴定葡萄胎DNA来源，具有准确可靠、快速、简便等优点，为进一步研究其恶变趋势提供可靠线索。

Abstract: To explore the genetic origin of hydatidiform mole (CHM), 33 cases of CHM were collected mainly from Harbin Red Cross Central hospital from 1998.6 to 2001.5 and studied by multiplex-PCR, products were separated using denaturing polyacrylamide gel and were detected by silver stain for 9 different STR loci analysis. Among 33 samples of CHM, DNA from only paternal origin was found in 27 cases (81.8%, 27/33), and from both parents in 6 cases (18.2%, 6/33); and in the former, the homozygous CHM and the heterozygous CHM were 22 cases (66.7%, 22/33) and 5 cases (15.1%, 5/33), respectively. There was difference between analysis of microsatellite DNA polymorphism and pathological diagnosis in hydatidiform moles' classification. The results suggest that the analysis of 9 polymorphic STR loci is suitable for genetic original identification of hydatidiform moles.

关键词 完全性葡萄胎 多态性STR基因座 分子遗传学 分子病理学 Key words complete hydatidiform mole polymorphic STR loci molecular genetics molecular pathology

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