

Title (en)

MULTIPLE GENETIC MARKER SELECTION AND AMPLIFICATION

Title (de)

SELEKTION UND AMPLIFIKATION VON MULTIPLLEN GENETISCHEN MARKERN

Title (fr)

SELECTION ET AMPLIFICATION DE MARQUEURS GENETIQUES MULTIPLES

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Application

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Abstract (en)

[origin: WO03031646A1] Methods of selection and amplification of genetic markers for genetic testing are provided, and in particular, to facilitate multiplex PCR amplification from limiting amounts of target nucleic acid (i.e. 1 ng, or less, nucleic acid or the amount of nucleic acid contained in 200 or fewer cells). The method of selecting a plurality of genetic markers as targets for nucleic acid amplification includes the step of selecting each of said plurality of genetic markers according to a heterozygosity index, wherein the heterozygosity index is 0.5 or greater. The method of nucleic acid sequence amplification includes a step of using a nucleic acid sequence amplification technique and at least nine primer pairs in combination to amplify a plurality of respective genetic markers from a limiting amount of nucleic acid samples. The methods of the invention are generally applicable to improved genetic diagnostic and screening methods such as prenatal diagnostic testing, fetal sex determination and genetic identification, such as by DNA fingerprinting, in organisms such as bacteria, humans and other animals where available target nucleic acid is limiting. The nucleic acid amplification method of the invention is also applicable to forensic analysis of degraded, old, ancient, difficult and or other low-abundance samples that have hitherto been difficult to amplify and identify.

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