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Current methods of mutation detection

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Abstract

Mutation detection is important in all areas of biology. Detection of unknown mutations can involve sequencing of kilobases of DNA, often in many patients. This has lead to the development of methods to screen DNA for mutations as well as methods to detect previously described mutations. This review discusses current methods used for such purposes with special emphasis on genetic diseases of humans. However, savings can be made by similar means in other areas of biology where repetitive or extensive sequencing for comparative purposes needs to be done. This review covers the methods used for detection of unknown mutations, namely the ribonuclease, denaturing gradient-gel electrophoresis, carbodiimide, chemical cleavage, single-strand conformation polymorphism, heteroduplex and sequencing methods. Once mutations have been defined they can be searched for repeatedly by methods referred to as diagnostic methods. Such methods include allele-specific oligonucleotide hybridization, allele-specific amplification, ligation, primer extension and the artificial introduction of restriction sites. We can now choose from a range of excellent methods, but the choice

will usually depend on the background of the laboratory and/or the application in hand. Screening methods are evolving to more satisfactory forms, and the diagnostic methods can be automated to screen whole populations inexpensively.

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Keywords

Detection of mutations; Mutation detection; Mismatch; Heteroduplex

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