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BatchPrimer3: A free web application for allele specific (SBE and allele flanking) primer design for SNPs genotyping in molecular diagnostics: A bioinformatics study

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ABSTRACT

From 1990 to 2003 is the period needed to finish the human genome project. The ideas were and still introduce growing cheap, reliable and fast advance techniques for dealing with analysis of huge information of the human genome. Whereas that technique is contagious with a suitable analysis to differentiate between variants, linked to malady tendency and how drug responses. Single nucleotide polymorphism (SNP) considered the most common type of genetic variation between people. It is associated with various of diseases and sometime plays a role of prophylactic against a certain disease. Primer pairs considered the mainly implement player in polymerase chain reaction. So, they needed to design an efficient and good quality primer by many programs and applications still demanded. Many studies related to SNPs associated disease and mutations were depended on sensitive and inexpensive price method such as allele-specific (AS) polymerase chain reaction and single base extension.

Aims

To illustrate BatchPrimer3 application and how use it for primer design relying SBE and allele flanking techniques to SNPs genotyping along with population.

1. Background

The human genome contains > 3 billion pairs of bases which reside in each nucleated cell of the body (Venter et al., 2001; Consortium, 2001). Significant results have been obtained from the human genome project, the most important being the use of human variation data called the single nucleotide polymorphisms (SNP), which is the most abundant source of sequence variation in the human genome (Syvänen, 2001). SNP is a type of important genetic markers used for linkage studies to track genetic diseases (Brookes, 1999) Massive numbers of SNPs have been identified in different species and used in genetics and breeding (Varshney et al., 2005; Powell et al., 1996; Dvorak et al., 2007; Sobrino et al., 2005). Different SNPs are commonly found, play fundamental roles in the genetic variation among people, and can act as biomarkers, helping scientists identify genes associated with the disease (Al-Koofee and Mobarak, 2018). A number of different SNPs genotyping technologies have been developed based on various methods of allelic discrimination and detection platforms (Sobrino et al., 2005), such as ligation assay, restriction enzyme assay, allele-specific polymerase chain reaction assay, invasive cleavage assay and hybridization assay. Each of these technologies has a number of advantages and disadvantages. Primer design programs are essential in improving the polymerase chain reaction (PCR). Many web-based or standard-alone programs for PCR primer design are available but vary in quality and functionality (Abd-Elsalam, 2003; Yang et al., 2006). Primer extension is the most commonly used approach for SNP genotyping because it can be used in a wide variety of high-throughput detection platforms, i.e. fluorescence polarization, luminescence, fluorescence resonance energy transfer, electrophoresis, mass spectrometry, and arrays (Sobrino et al., 2005). A primer extension reaction involves two types of primer design, single base extension primers and allele-specific primers. Single-base extension (SBE) is a method for determining the identity of a nucleotide base at a specific position along nucleic acid. The method is used to identify a single-nucleotide polymorphism (SNP). In this method, an

Abbreviations: SNP, Single nucleotide polymorphisms; SBE, Single-base extension; CGI, Common gateway interface; BLAST, Basic local alignment search tool; T_m, Melting temperature; IUPAC–IUB, International union of pure and applied chemistry

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