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Perspective

Next Generation Sequencing Problems in Children Pharmacogenomics

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DESCRIPTION

Pharamacogenetic is regarded as a major demonstration as to how personalized medicine is now applied. Although it happens a lot in ordinary clinical practice, genotyping to direct pharmacological treatment is exceedingly unusual. There are a number of reasons why the application of pharamacogenetic is less common than initially expected, including the inconsistent results reported for some variations and the absence of clinical implementation guidelines. Although attempts have been made to create task forces focused on clinical guidelines supported by research, more reproducible outcomes are now being produced.

A revolution in molecular genetics has occurred with the introduction of Next Generation Sequencing (NGS), which makes it possible to sequence a large number of genes up to the entire genome in a single reaction. This technology addresses another pharamacogenetic challenge, which is the speed at which a pharamacogenetic profile for a specific drug can be obtained in a specific patient. In addition to the excitement given by the enormous expansion of our sequencing capabilities, there are a number of factors to take into consideration regarding the accuracy and interpretation of the sequence data as well as the ethical implications of this technology. This paper will concentrate on the various NGS applications that can be helpful for child pharmacogenomics and the difficulties they present.

Pharamacogenetic is the study of how DNA variations affect drug response and understanding this relationship can help choose the best medication, dose, and length of treatment while also preventing negative drug reactions. There have been many demonstrations of how children and adults react different to medications. These include variations in medication metabolism and gene expression, both of which are a highly dynamic process operating from childhood to adolescence and adulthood. Despite the fact that there are still less research exclusively focused on the pediatric population than on adults, more and more genes are being discovered whose variations have an impact on the pharmacological treatment of childhood disorders. The identification of variants in novel genes as well as the validation of their functional effects will further increase our ability to predict drug treatment response in children; at the same time, the clinical implementation of this knowledge will demand an efficient diagnostic approach to first identify a pharmacogenomics profile in an individual patient in a short period of time, next to evidence-based clinical guidelines to facilitate decision making based on the genotype.

Sanger sequencing is currently the gold standard for identifying pathogenic variants, such as single nucleotide changes or minor indels and it has since been improved to assess changes in PCR-amplified DNA fragments with high sensitivity and specificity. The main drawbacks of Sanger sequencing are that each novel genetic test requires optimization and turnaround times for each gene analysis can be relatively long, especially in a field like pharamacogenetic where variants in multiple genes may be involved for a given drug, either independently or in interaction with each other. With both the introduction of Next-Generation Sequencing (NGS), genetic screening techniques underwent a technical revolution, making it possible to screen the entire exome the coding portions of our DNA and even the entire genome in a single experiment.

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