Commentary

Next-Generation Sequencing: The Future of Precise Medicine?

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DESCRIPTION

In the recent years, NGS have opened a route to a new dimension of molecular study, enabling the determination of the nucleotides (A, C, G, and T) orders in the entire genome of the species and has helped researchers in their molecular genetic studies. These technologies cost- effective for the DNA sequencing since high throughput data yield can be produced in massively parallel technology involving simultaneous sequencing of a large number of template DNA. NGS describes platforms that produce large amounts (typically millions) of DNA reads, commonly known as short reads compared to the traditional Sanger sequencing method (150bp to 1,000 bp). NGS can be divided into three main categories for the human study; Whole-Genome Sequencing (WGS), Whole-Exome Sequencing (WES) and transcriptomic study (RNA-seq).The benefits of NGS have driven the clinical understanding of human physiology, anatomy and subsequently system biology of human diseases to a new dimension of study and thus have made significance improvements in monitoring the health treatment.

The structure and nature of protein interaction networks is one of the best interests and is a considerable subject in the understanding of system biology, which is due to the availability of the dataset of protein interactions for the majority of protein study. Protein-Protein Interaction (PPI) networks act as a powerful tool for exploring protein functions and disease-gene relationship as shown in the Figure 1. This method may allow researchers to link the genes with their associated biological pathways and the corresponding diseases, which is used to improve the biomedical applications. Major advantages of studying PPI is may assign the unknown roles to uncharacterized proteins, availability of detailed information within a signaling pathway, and define the relationships between genes that arise from multi-molecular complexes. Network analysis may underline the existence of genes interaction harboring molecular alterations in common or rare diseases. However, one potential drawback of PPI is the underlying mechanisms of complex and rare diseases, which are come from the interaction of multiple genes with the environmental factors, cannot be revealed by such approaches.

Plant epigenetics has numerous applications in agriculture, food security, and environmental sustainability. Understanding the epigenetic mechanisms that underlie plant growth and development can help breeders to develop crop varieties that are more resistant to environmental stresses, diseases, and pests.

In the last few years, there has been an increasing area to exploit the concepts of network biology to understand disease module. Disease module can be explained by the existence of specific regions for the disease proteins based on the network study. The identification of these modules is the starting point for the discovery of drug targets and has provided deep insights into the molecular level for underlying diseases mechanism. For example, network approaches form the big data analysis to identify disease module have successfully in Parkinson's disease, progressive supranuclear palsy and cancer therapy. However, not all big data analysis can be directly translated into the clinical or drug developments due to the several factors such as experimental design, the total size of cohort study using patient and healthy control, and the relationship or the mechanism of the disease itself. This approach may need the larger collaboration of different research institutes and pharmaceutical industry depending on their expertise to help minimize costs and risks for drug developments, thus, lead to the precise medicine.

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