Editorial

iMedPub Journals
http://www.imedpub.com/

Genetics and Molecular Biology Research

2018
Vol.1 No.1:3

From Targeted Testing To Targeted Analysis: The Era of Comprehensive Clinical Genomics Analysis Is Coming

Hongxing Liu[1,2*] and Yu Zhang[1]

[1]Pathology & Laboratory Medicine Division, Hebei Yanda Lu Daopei Hospital, Langfang, China

[2]Translational Medicine Research Center, Beijing Lu Daopei Institute of Hematology, Beijing, China

[*]**Correspondence author:** Liu Hongxing, Translational Medicine Research Center, Beijing Lu Daopei Institute of Hematology, Beijing, China; Tel: +86 10 5894 3651; E-mail: starliu@pku.edu.cn

Received date: Jan 24, 2018; **Accepted date:** Jan 27, 2018; **Published date:** Jan 31, 2018

Citation: Hongxing L, Yu Z (2018) From Targeted Testing To Targeted Analysis: The Era of Comprehensive Clinical Genomics Analysis Is Coming. Genet Mol Biol Res Vol No: 1 Iss No: 1: PDF No: 3

Editorial

With the widely application of next generation sequencing (NGS) technology in clinic and the progress of molecular mechanisms research in tumour, more and more molecular markers have been identified and used in clinical diagnosis and treatment decisions [1-4].

Detection of dozens or hundreds of genes by targeted sequencing has been widely used in the diagnosis and treatment of various oncological and genetic diseases, and reports of genomics analysis based on whole exome sequencing (WES), whole genome sequencing (WGS), and transcriptome sequencing (RNA-seq) is also significantly increased.

Advantages and challenges of genomics analysis

With the significant decrease of cost and the improvement of analytical capabilities, the application of WES, WGS and RNA-seq increased gradually which provides more comprehensive genetic information.

Compared with traditional medical testings, genomics analysis brings new concepts and challenges. Traditional medical testings (biochemistry, immunology and targeted sequencing, etc.) basically belong to targeted testing that require the designation of a limited number of targets and corresponding tests which are expected to be relevant to the disease or phenotype. Genetic testing is the first to proceed with a methodologically comprehensive omics-based analysis that covers the real whole of genome, exome and transcriptome rather than specific targets. However, the huge amount of data generated by the omics sequencing (about 12G for 100 × WES data ad about 90G for 30 × WGS data) which brings a great challenge to the analysis and interpretation of information.

Interpretation of the connotation of genomics analysis

In previous targeted testings, each test provides a limited amount of information, and there is generally no information redundancy. However, genomics testing is different; you can first obtain more comprehensive information in one respect, and then extract abundant information to guide the diagnosis and treatment of diseases from different angles according to the needs. Genomics has brought revolutionary advances from "targeted testing" to "targeted analysis" in terms of testing and analysis modes.

We can use the genomics testing to analyze genetic disease and genetic predisposing factors of tumor, somatic mutation, genetic pharmacogenomics, minor histocompatibility antigens (mHAg), tumor neoantigen prediction as well as telomere length and chimeric rate [5-11].

The era of comprehensive clinical genomics analysis is coming

Now the cost of WES is close to the cost of targeted sequencing of dozens or hundreds of genes, but the amount of information is greatly increased. The advantages of omics testing and analysis are that it can provide a variety of information of clinical diagnosis and treatment for patients by analysis of multiple aspects in one testing and analysis of several times in one testing, which can achieve the most economical cost and the information-price-performance ratio. At the same time, genomics data can also be used as a treasure trove of information, accumulating valuable resources for further medical research.

References

1. Zhang Y, Wang F, Cen X, Hongxing L (2015) Mutaome profile of 10 common mutated genes in refractory and relapsed acute myeloid leukemia. J Leuk Lymph 24: 261-264.
2. Wang F, Zhang Y, Chen X, Hongxing L (2015) Mutaome analysis including 10 common mutated genes in newly diagnosed acute myeloid leukemia patients. J Leuk Lymph 24: 161-164.
3. Liu M, Zhang Y, Wang F, Chen Xue, Nie D, et al. (2017) Mutaome analysis of common mutated genes in patients with myelodysplastic syndromes. J Clin Path Res 37: 2332-2338.

4. Zhang Y, Liu M, Liu HX (2017) Gene mutations and its clinical significance in myelodysplastic syndrome. J Clin Path Res 37: 2237-2242.

5. West AH, Churpek JE (2017) Old and new tools in the clinical diagnosis of inherited bone marrow failure syndromes. Hematol Am Soc Hematol Educ Prog 2: 79-87.

6. Arber DA, Orazi A, Hasserjian R (2016) The 2016 revision to the world health organization classification of myeloid neoplasms and acute leukemia. Blood 127: 2391-2405.

7. Liu HX, Zhou FY, Zhang Y (2016) Advances in personalized medicine of hematologic neoplasms and related pharmacogenetics. J Leuk Lymph 25: 385-388.

8. Roy DC, Perreault C (2017) Major vs minor histocompatibility antigens . Blood 129: 664-666.

9. Efremova M, Finotello F, Rieder D, Trajanoski Z (2017) Neoantigens generated by individual mutations and their role in cancer immunity and immunotherapy. Front Immunol 28:1679.

10. Liu HX, Zhang Y, Chen X (2017) Advances in telomere and telomerase in hematological diseases. J Leuk Lymph 25: 12-14.

11. Lee M, Napier CE, Yang SF, Reddel RR, Pickett HA, et al. (2017) Comparative analysis of whole genome sequencing-based telomere length measurement techniques. Methods 114: 4-15.