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SNP Genotypes and Technology of the Effective Genes Analysis; Recommendations for Cardiology

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Editorial

Each patient has a combination of the genes bound to cardiovascular illnesses. Today there are 3000 illnesses to which individual genetic tests (Gene Tests Med. Gen. Information Resource 2013) are available. However to interpret such results, for example for polygenic diseases as an essential hypertension without computer systems is extremely difficult. Usually it is bound to a larger flow of information and shortage of clinical geneticists. Besides cognitive abilities of the cardiologist are limited by lack of knowledge in the field of bioinformatics and biotechnology.

Differences between genomic and clinical tests

Unprecedented depreciation of the chip-sequencing, made possible to conduct large researches of cardiovascular diseases. These technologies were always followed by 2 main problems:

I. choice of management of a huge array of genomic data;

II. choice of computing methods of the analysis [1-3].

Despite it, use of genomic results for 10 years became ubiquitous. Technically genetic tests don't differ from any other medical test. Genomic tests as all other clinical tests, are caused by the probabilistic size where a certain path physiological state is present (that is the diagnosis), or will be present (that is, the forecast) [4]. Anyway, genomic or usual tests are used for clinical decision-making in the context of an asymptomatic or pathological condition of the patient. As a result clinical genomic data have the same purpose as other medical tests: to provide information at diagnosis and treatment of the patient. However, genetic tests have also some difference from clinical:

a. high probability of the unforeseen obtained data;

b. confidentiality of the obtained information (only for family members);

c. The obtained data don't guarantee that the patient understands character of the provided information (for example: this category includes information on future risks of development of pathologies). Today there are some doubts that highly technological genetic tests of SNP won't be more expensive than medical researches [5]. Today the most important difference between genomic tests and clinical - the fact that medical institutions and medical industrial infrastructure believe that genetic and usual medical tests will be very different because of complexity of interpreting results.

Superfine phenotype, molecular information and their clinical context

To understand pathophysiology, clinical, imaging, functional, molecular, genomic, markers need to be connected, and further linked to outcomes. Such connection presents a formidable challenge to data storage, management and analysis, IT capacity, and accessibility. Innovative statistics will be needed addressing a multiplicity of potential biomarkers, identifying reliable and valid measurements.

Genomic test in CVD

Integration of biological markers for specific disease processes has the potential to identify patients at risk for first cardiovascular events (arterial hypertension, cerebrovascular or coronary heart diseases, cardiac arrhythmia, heart failure, diabetes type II) to allow to target therapies to patients who are most likely to benefit, and to allow better prediction of unwanted side-effects of therapy [6-7].

Technology of the effective genes analysis

The technology of the effective genes analysis is the combined method of the sequential analysis, ROC-curve and relative risk of RR (Altman's theorem) with use of basic mathematical algorithms

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(Bayes' theorem) in diagnostics of in vitro. Thus, using DNA identification, the developed algorithm can recommend an individual diet and a safe dose of drug (Warfarin, Klopidogrel, Simvastatin, Perindopril). The algorithm is capable to transform pathogenic genetic data to the diagnostic tool which in a combination with clinical observation and biometric data can create the clinical decision.

Recommendations

Despite numerous disadvantages of the genomic tests, the analysis of a big flow of genetic and clinical information it became real. We recommend considering several moments on the first steps. in - the first to pay attention to an analytical stage. To provide sensory management of all knots of system. It is necessary to consider in advance all working platforms which will be served by cardio-genetic lab. Use Bayesian approach to frame a matrix of recognition of the damaging alleles and haplotype. It is necessary to adhere to standard forms of biological data. To strengthen enough genetic information, clinical geneticist has to be able to structure a superfine phenotype. For stratification of risk of rising of the ABP (the high, increased, average risk) use multi-sample option. It will lead to specificity increasing while sensitivity will remain invariable. Use heuristic and statistical algorithms; they will be able to identify the damaging genotype, without conflicting to clinical information of the patient. We also recommend to limit access to genetic information. It is bound to the fact that information on existence of the inherited pathologies can affect a work arrangement and receiving insurance. In some countries laws of genetic non-discrimination (US genetic information nondiscrimination act GINA 2008) are adopted.

Despite a technological capability to process and make more exact clinical assessment of big data array, the problem of inaccessibility of resources and mechanisms of exchange of the annotated genetic information remains unresolved. Ability to authentically predict phenotypical results on the basis of a genotype, still remains a DNA lab task of the next generation.

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