

P4 Medication and the Genetic Sequence Interaction Studies

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DESCRIPTION

Tailored medicine, also known as accuracy medicine, is a clinical approach that divides people into different groups based on their risk of sickness or expected reaction, with clinical decisions, practises, mediations, and products being tailored to the particular patient. The phrases "tailored medication," "exactness medication," "defined medication," and "P4 medication" are all used interchangeably to convey this idea, but some authors and organizations also use these expressions on their own to highlight certain details. While the practice of treating patients appropriately has roots that can be traced back to the time of Hippocrates, the term has recently gained popularity as a result of the development of new diagnostic tools and informatics advancements that help understand the atomic basis of infection, particularly genomics [1].

This provides a clear evidence foundation on which to define gathering connected patients. Recent developments in personalized medicine rely on research that validates a patient's primary science, such as their DNA, RNA, or protein, which eventually results in a disease that can be validated. For instance, tailored approaches, like genome sequencing, can reveal Genetic changes that influence illnesses ranging from cystic fibrosis to malignant development. Another method, RNA-seq, can reveal which RNA atoms are specifically associated with various diseases. RNA levels can fluctuate due to the climate, unlike DNA [2, 3]. Hence, sequencing RNA can provide a more thorough understanding of a person's health. Recent studies have linked RNA articulation, interpretation, and protein amounts to genetic differences between individuals [4].

The principles of personalized medicine can be used to develop innovative new approaches to the delivery of medical care. Tailored medical care is based on the principles of systems science and makes use of futuristic tools to analyze health risks, create personalized health plans, and support patients in reducing risks, preventing illness, and accurately treating it when it does occur [5]. The Veterans Administration's decision to provide personalized, patient-driven consideration for all veterans is contributing to the growing acceptance of the concept of tailored medical services. In some cases, individualized medical care can be tailored to a patient's genetic markup rather than the markup of the disease-causing specialty; examples include drug-safe microorganisms or viruses [6, 7].

Analysts frequently conduct a test known as a "Genome-Wide Affiliation Analysis" to help doctors determine whether a transformation is linked to a specific infection (GWAS). A GWAS study will examine a single infection and arrange the genomes of several people who have that particular illness in order to look for shared changes in the genome. Modifications that were not conclusively linked to an infection by a GWAS study might subsequently be used to evaluate that disease in future patients by looking at their genome organization to find that same change. Several common and complex disorders have a higher likelihood of developing when certain characteristics are combined [8].

A person's risk for a certain ailment can also be predicted using personalized medicine, based on one or simply a few characteristics. By focusing on the assessment of disease risk using this methodology's comparable sequencing innovation, the doctor is able to begin preventive treatment before the illness manifests itself in their patient. For instance, if it is discovered that a Genetic alteration increases a person's risk of developing Type 2 Diabetes, that person can start making lifestyle adjustments that would lessen their potential for contracting the illness in the future.

The ability to examine a patient on an individual basis will take into account a more precise diagnosis and clear treatment strategy. Genotyping is the process of using organic tests to determine a person's DNA configuration. A person's genome can be measured against a reference genome, such as that of the Human Genome Project, in order to examine the current hereditary variants that can indicate possible diseases.

REFERENCES

- 1. Pruthi RK, Rodriguez V, Allen C, Slaby JA, Schmidt KA, Plumhoff EA. Molecular analysis in a patient with severe factor VII deficiency and an inhibitor: report of a novel mutation (S103G). Eur J haemat. 2007; 79(4):354-359.
- Ramezanpour N, Zaker F, Biswas A, Dorgalaleh A. Inhibitor in congenital factor VII deficiency; a rare but serious therapeutic challenge–a systematic literature review. J Clin Med. 2021; 10(2):211.

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- Tamary H, Fromovich Y, Shalmon L, Reich Z, Dym O, Lanir N, etal. Ala244Val is a common, probably ancient mutation causing factor VII deficiency in Moroccan and Iranian Jews. Thromb and haemos. 1996; 76(09):283-291.
- Swain SS, Sharma D, Hussain T, Pati S. Molecular mechanisms of underlying genetic factors and associated mutations for drug resistance in Mycobacterium tuberculosis. Emer microb and infec. 2020; 9(1): 1651-63.
- Rinder H, Thomschke A, Rüsch-Gerdes S, Bretzel G, Feldmann K, Rifai M, et al. Significance of ahpC promoter mutations for the prediction of isoniazid resistance in Mycobacterium tuberculosis. Eur J Clin Microbiol Infec Dis. 1998; 17:508-511.
- Phelan JE, O'Sullivan DM, Machado D, Ramos J, Oppong YE, Campino S, et al. Integrating informatics tools and portable sequencing technology for rapid detection of resistance to antituberculous drugs. Geno med. 2019; 11:1-7.
- Oppong YE, Phelan J, Perdigão J, Machado D, Miranda A, Portugal I, et al. Genome-wide analysis of Mycobacterium tuberculosis polymorphisms reveals lineage-specific associations with drug resistance. BMC geno. 2019; 20(1):1-5.
- Libiseller-Egger J, Phelan J, Campino S, Mohareb F, Clark TG. Robust detection of point mutations involved in multidrug-resistant Mycobacterium tuberculosis in the presence of co-occurrent resistance markers Comp Biol. 2020; 16(12):e1008518.