Review Article
Pharmacogenomics – The New Trend for Personalized Medicine

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ABSTRACT
Pharmacogenetics and pharmacogenomics are two major emerging trends in medical sciences, which influence the success of drug development and therapeutics. In current times, though pharmacogenetic studies are being done extensively for research, its application for drug development needs to get started on a large scale. Pharmacogenetic studies can be used at various stages of drug development. The effect of drug target polymorphisms on drug response can be assessed and identified. In clinical studies, pharmacogenetic tests can be used for stratification of patients based on their genotype, which corresponds to their metabolizing capacity. This prevents the occurrence of severe adverse drug reactions and helps in better outcome of clinical trials. This can also reduce attrition of drug compounds. Recognition of inter-individual differences in drug response is an essential step towards optimizing therapy. Over the past decades, much evidence has emerged indicating that a substantial portion of variability in drug response is genetically determined, with age, nutrition, health status, environmental exposure, and concurrent therapy playing important contributory roles. To achieve individual drug therapy with a reasonably predictive outcome, one must further account for different patterns of drug response among geographically and ethnically distinct populations.

Introduction
Pharmacogenomics is the study of how genes affect a person’s response to drugs. This relatively new field combines pharmacology (the science of drugs) and genomics (the study of genes and their functions) to develop effective, safe medications and doses that will be tailored to a person’s genetic makeup.

Many drugs that are currently available are “one size fits all,” but they don’t work the same way for everyone. It can be difficult to predict who will benefit from a medication, who will not respond at all, and who will experience negative side effects (called adverse drug reactions).

How is pharmacogenomics affecting drug design, development and prescribing guidelines?
The Food and Drug Administration, which monitors the safety of all drugs in the United States, has included pharmacogenomic information on the labels of more than 150 medications. This information which can cover dosage guidance, possible side effects or differences in effectiveness for people with certain genomic variations can help doctors tailor their drug prescriptions for individual patients. Many Pharmaceutical companies are beginning to use pharmacogenomic knowledge to develop and market drugs for people with specific genetic profiles. Studying a drug only in those likely to benefit from it could speed up and streamline its development and greatly maximize its therapeutic benefit.[1]

Additionally, if scientists can identify the genetic basis for certain serious side effects, drugs could be prescribed only to people who are not at risk for them. As a result, potentially lifesaving medications, which otherwise might be taken off the market because they pose a risk for some people, could still be available to those who could benefit from them.

How is pharmacogenomics affecting medical treatment?
Currently, doctors base the majority of their drug prescriptions on clinical factors, such as a patient’s age, weight, sex, and liver and kidney function. For a small subset of drugs, researchers have identified genetic variations that influence...
how people respond. In these cases, doctors can use this information to select the best medication and identify people who need an unusually high or low dose.

**Figure 1: Drug Responses**

**How is pharmacogenomic information being used today?**

One current use of pharmacogenomics involves people infected with the human immunodeficiency virus (HIV). Before prescribing the antiviral drug abacavir (Ziagen), doctors now routinely test HIV-infected patients for a genetic variant that makes them more likely to have a bad reaction to the drug.

Another example is the breast cancer drug trastuzumab (Herceptin). This therapy works only for women whose tumors have a particular genetic profile that leads to overproduction of a protein called HER2. [2]

The U.S. Food and Drug Administration (FDA) also recommend genetic testing before giving the chemotherapy drug mercaptopurine (Purinethol) to patients with acute lymphoblastic leukaemia. Some people have a genetic variant that interferes with their ability to process the drug. This processing problem can cause severe side effects and increase risk of infection, unless the standard dose is adjusted according to the patient's genetic makeup.

The FDA also advises doctors to test colon cancer patients for certain genetic variants before administering irinotecan (Camptosar), which is part of a combination chemotherapy regimen.

The reasoning is that patients with one particular variant may not be able to clear the drug from their bodies as quickly as others, resulting in severe diarrhea and increased infection risk. Such patients may need to receive lower doses of the drug. [3]

**International Hap Map Project**

The goal of the International HapMap Project is to determine the common patterns of DNA sequence variation in the human genome and to make this information freely available in the public domain. An international consortium is developing a map of these patterns across the genome by determining the genotypes of one million or more sequence variants, their frequencies and the degree of association between them, in DNA samples from populations with ancestry from parts of Africa, Asia and Europe. The HapMap will allow the discovery of sequence variants that affect common disease, will facilitate development of diagnostic tools, and will enhance our ability to choose targets for therapeutic intervention. [4, 5]

The HapMap is a catalogue of common genetic variants that occur in human beings. It describes what these variants are, where they occur in our DNA, and how they are distributed among people within populations and among populations in different parts of the world. The International HapMap Project is not using the information in the HapMap to establish connections between particular genetic variants and diseases. Rather, the Project is designed to provide information that other researchers can use to link genetic variants to the risk for specific illnesses, which will lead to new methods of preventing, diagnosing, and treating disease. [5]

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Adenine, thymine, cytosine, and guanine, abbreviated A, T, C, and G. More than 6 billion of these chemical bases are strung together in 23 pairs of chromosomes, exist in a human cell. These genetic sequences contain such information that influences our physical traits, our likelihood of suffering from disease, and the responses of our bodies to substances that we encounter in the environment.

The genetic sequences of different people are remarkably similar. When the chromosomes of two humans are compared, their DNA sequences can be identical for hundreds of bases. But at about one in every 1,200 bases, on average, the sequences will differ. One person might have an A at that location, while another person has a G, or a person might have extra bases at a given location or a missing segment of DNA. Each distinct "spelling" of a chromosomal region is called an allele, and a collection of alleles in a person's chromosomes is known as a genotype. [7] Differences in individual bases are by far the most common type of genetic variation. These genetic differences are known as single nucleotide polymorphisms, or SNPs (pronounced "snips"). By identifying most of the approximately 10 million SNPs estimated to occur commonly in the human genome, the International HapMap Project is identifying the basis for a large fraction of the genetic diversity in the human species. [7]

For geneticists, SNPs act as markers to locate genes in DNA sequences. If a particular SNP is more common among people with hypertension, that SNP could be used as a pointer to locate and identify the gene involved in the disease. However, testing all of the 10 million common SNPs in a person's chromosomes would be extremely expensive. The development of the HapMap will enable geneticists to take advantage of how SNPs and other genetic variants are organized on chromosomes. Genetic variants that are near each other tend to be inherited together. For example, all of the people who have an A rather than a G at a particular location in a chromosome can have identical genetic variants at other SNPs in the chromosomal region surrounding the A. These regions of linked variants are known as haplotypes. [6]

Some Pharmacogenomic tests have been acknowledged for a long time and are accepted as routine tests; e.g. it has been known that those patients with glucose-6-phosphate dehydrogenase (G6PD) deficiency should avoid certain drugs because of the risk of haemolysis following their intake. The effect of a drug is traditionally assessed by clinical outcome, which includes laboratory tests and therapeutic drug monitoring (TDM). It has only been in the last 10–15 years that a number of pharmacogenomic tests have been available to supplement the traditional outcome measures and to aid with dose determination and choice of medication.

**Figure 2: International HapMap Project**

**Companion diagnostics**

Personalized medicine is an evolving field of medicine in which treatments are tailored to the individual patient. You may have a condition, for example, that is caused by a mutation in your genes. With advances in personalized medicine, you might be prescribed a medication that targets that specific mutation.

To learn which patients would benefit from a particular drug therapy or, conversely, which patients should not receive the medication, the Food and Drug Administration works with drug and device manufacturers that are developing certain tests called companion diagnostics.

A companion diagnostic is a medical device, often an in vitro device, which provides information that is essential for the safe and effective use of a corresponding drug or biological product. The test helps a health care professional determine
whether a particular therapeutic product’s benefits to patients will outweigh any potential serious side effects or risks. [8, 9]

Companion diagnostics can:
- identify patients who are most likely to benefit from a particular therapeutic product;
- identify patients likely to be at increased risk for serious side effects as a result of treatment with a particular therapeutic product; or
- monitor response to treatment with a particular therapeutic product for the purpose of adjusting treatment to achieve improved safety or effectiveness.

1000 Genomes Project
The 1000 Genomes Project is an ambitious effort to sequence the genomes of at least 1000 people to create the most detailed and medically useful catalogue to date of human genetic variation. Any two humans are more than 99 per cent the same at the genetic level: the small fraction of genetic material that varies among people can help to explain individual differences in susceptibility to disease, response to drugs or reaction to environmental factors. The 1000 Genomes Project therefore aims to produce an extremely detailed catalogue of human DNA variation that can be used in future studies of people with particular diseases. Across most of the human genome, the researchers taking part in this international collaboration are looking for variations that are present at a frequency of 1 per cent or more in the population; in genes, the goal is to find variations that are present in 0.5 per cent or less of the population. Producing a map at this resolution, which is unmatched by current resources, is likely to require sequencing of the genomes of at least 1000 people. The genomes of a diverse set of populations are being sequenced for the project. To preserve the anonymity of the people involved, the collection of samples follows a series of ethical guidelines and they are taken on the basis of informed consent. [17]

Some of the populations whose DNA is being sequenced in the 1000 Genomes Project include:
- Chinese in metropolitan Denver
- Gujarati Indians in Houston
- Han Chinese in Beijing
- Japanese in Tokyo
- Kayadtha in Calcutta, India
- Luhya in Webuye, Kenya
- Maasai in Kinyawa, Kenya
- Malawian in Blantyre, Malawi
- Toscani in Italy
- People of Mexican ancestry in Los Angeles
- People of African ancestry in the south-western United States.
- Puerto Rican in Puerto Rico
- Punjabi in Lahore, Pakistan
- Utah residents with ancestry from northern and western Europe
- Yoruba in Ibadan, Nigeria

The goal of the 1000 Genomes Project is to find most genetic variants that have frequencies of at least 1% in the populations studied. This goal can be attained by sequencing many individuals lightly. To sequence a person’s genome, many copies of the DNA are broken into short pieces and each piece is sequenced. The many copies of DNA mean that the DNA pieces are more or less randomly distributed across the genome. The pieces are then aligned to the reference sequence and joined together. [17]
Pharmacogenomics – Drug development-Today and Tomorrow
Drugs are tiny molecules that interact with proteins and other cellular molecules to change the way they work in the body.

By the time a new drug hits your pharmacist’s shelf it has likely gone through about 10 years of research and development.

In 2003, $33.2 billion was spent on pharmaceutical research and development. The cost of bringing just a single new drug to market was about $802 million.

Today’s drug development process is already seeing the first signs of change. Pharmacogenomics methods are gradually moving into practice. In fact, most Phase II and III clinical
drug trials now involve taking DNA samples of the participants. But we have a long way to go before the full potential of this new science is reached. [19]

Case Study
To develop a new drug that treats obesity - Using microarray technology, company scientists conduct gene expression studies and identify a gene that is overactive in a large percentage of obese patients. They characterize the protein this gene produces and discover that it is a receptor protein in nerve cells of the brain. They deduce that obese patients have too many of these receptors. This is the target.

Using computer models of the target protein, the team designs a drug to inhibit its function. Computer simulations of the drug in the brain reveal that the drug targets just the receptor types they are interested in.

The toxicologists test the drug in cell and animal models to measure DNA reactivity, liver and kidney toxicity and other factors. Potential effects of the drug on the environment are also evaluated.

The team evaluates the drug for large scale manufacture. In animal dosage studies it is determined that the computer predicted dosage will not be sufficient. The dosage is modified and the animal models respond to the drug. The drug is to be administered as a gel capsule and the dosage strength is set to 65 mg. [20] Investigational New Drug (IND) Application is filed with Food and Drug Administration (FDA).

An in depth description of drugs mechanism of action is provided. It is explained that the drug binds to and blocks a specific class of neural receptors overproduced in obese patients.

Phase I clinical trial with SNP analysis: 52 patients are enlisted in the phase I study of your new drug. Their SNP profile is obtained by taking a blood sample. You find that a small number of patients are unresponsive to the drug. Their SNP profile is associated with an unusually high production of an enzyme which breaks down the drug before it can do its job.

Phase II clinical trial: SNP profile pre-screening identifies patients who will not respond to the drug. 167 participants are recruited. The study determines that patients lose an average of 10 percent of their weight.

Phase III clinical trial: SNP profile pre-screening identifies patients who will not respond to the drug and those individuals are not recruited in the Phase III study. 645 participants are identified. The study confirms that patients lose 10 percent of their weight. However, it is discovered that most patients will regain that weight if taken off of the drug.

A New Drug Application (NDA) is to be filed with the FDA before the marketing of the drug is begun. All the genetic, molecular and clinical studies are to be included in the report.

Warfarin
The VKORC1 gene encodes the VKORC1 (Vitamin K epoxide reductase) protein, which is a key enzyme in the Vitamin K cycle. VKORC1 is a 163 amino acid integral membrane protein associated with the endoplasmic reticulum, and VKORC1 mRNA is broadly expressed in many different tissues.

VKORC1 is responsible for the conversion of Vitamin K-epoxide to Vitamin K, which is the rate-limiting step in the physiological process of Vitamin K recycling. The availability of reduced Vitamin K is of particular importance for several coagulation factor proteins that require it as a cofactor, including Factor VII, Factor IX, and Factor X.

Warfarin is a commonly prescribed oral anticoagulant used to prevent thromboembolic diseases in patients with deep vein thrombosis, atrial fibrillation, recurrent stroke or heart valve prosthesis. Warfarin, act as inhibitors of VKORC1, which physiologically leads to a reduced amount of Vitamin K available to serve as a cofactor for clotting protein. [11, 12]

Pharmacogenomics is helping doctors to provide patients with the right dose of warfarin.

Warfarin is an anti-coagulant, an agent that prevents blood clots forming. It works by interfering with vitamin K epoxide reductase, an enzyme involved in the blood clotting process. It is most commonly prescribed to people who:

- Have had a condition caused by a blood clot, such as deep vein thrombosis (DVT: blood clots in the legs) and pulmonary embolism (PE: blood clot in the lungs), or
- Are at risk of developing a blood clot, such as people with artificial heart valves.
Although now widely used, doctors have to be careful with providing the correct dose of warfarin to their patients. If the dose is too low it will have no effect, but if it’s too high the patient is at risk of bleeding.

Several factors affect the dose a patient needs, one of which is their genetic makeup. Many studies have focused on identifying the genetic factors influencing an individual’s response to warfarin. These studies have found that there are two types of genetic changes involved:

- Those affecting the breakdown of warfarin by enzymes in the liver. These are called the cytochrome P450 genes.
- Those involved in how the drug slows down blood clotting.

Because warfarin works by interfering with the enzyme vitamin K epoxide reductase, variations in the gene coding for this enzyme (VKORC1) can affect an individual’s sensitivity to Warfarin. [11, 12]

Despite knowing this, it is still difficult to apply this information in a clinical setting because not all of the factors affecting responses to warfarin have been identified. For example, age and weight also play a role.

At the moment, doctors rely on their clinical judgement and usually determine the correct dose of warfarin by starting at a very low dose and working up until the optimum dose is reached.

**Rheumatoid arthritis**

Azathioprine is an immunosuppressant, which means that it dampens the activity of the body’s immune system. It is used to help prevent rejection after organ transplant operations and also to treat a variety of inflammatory and autoimmune diseases such as rheumatoid arthritis.

In some individuals azathioprine is not activated in the body properly. As a consequence unconverted azathioprine builds up in their bone marrow, killing developing white blood cells and leaving the individual vulnerable to infection.

The conversion of azathioprine into its active form is catalysed by an enzyme called thiopurine S-methyltransferase (TPMT). Some variants of the gene encoding TPMT mean individuals cannot do this conversion, and this is when the unconverted azathioprine builds up in their bone marrow. [15]

Before being given the drug azathioprine, people with rheumatoid arthritis can now be tested to find out which variant of the TPMT gene they possess and whether azathioprine will be an effective treatment for them.

**TPMT- Thiopurine S-Methyltransferase**

![Figure 7: Rheumatoid Arthritis](image)
**Case Study**

Latrice is a 7 year old who has been diagnosed with Leukaemia, a type of cancer involving the bone marrow and blood cells.

Her doctor wants to start her chemotherapy as soon as possible. Purinethol is a common chemotherapy drug; it works by incorporating itself into rapidly dividing cancer cells and killing them. Purinethol was first used to treat leukaemia over 30 years ago.

While most patients benefited from the drug, doctors knew the treatment came with the risk of very severe, sometimes fatal side effects in certain patients. It wasn’t until the 1990’s that doctors began to understand why these patients responded so negatively to the drug.

The mystery was unravelled when scientists began looking at how the drug was broken down in the body. They discovered that the TPMT (thiopurine S-methyltransferase) enzyme is responsible for breaking down and inactivating the drug Purinethol. Further, they found that people vary in their TPMT enzyme activity level.

Because Purinethol is a toxic substance, it is important that it only remains in the body for a limited amount of time, affecting mainly cancer cells and not healthy cells. Therefore, before prescribing the drug, it is critical for doctors to know if a patient has enough TPMT enzymes to effectively inactivate Purinethol. If patients are unable to break down Purinethol, they will suffer toxic side effects.

89% of the children have the ability to fully breakdown the toxic anti-cancer drug, Purinethol. These children have the TMPT variation with full enzymatic activity. These children will not suffer severe side effects from Purinethol. 11% of children have a TPMT variation with partial activity, leading to less efficient breakdown of Purinethol.

These children will suffer severe side effects if given a full dose of the Purinethol treatment. However, they will benefit from a much lower dose. 0.33% of children have TPMT with insufficient enzymatic activity. As a consequence, Purinethol breakdown is lacking and the toxic substance is able to persist in the body. These children will suffer severe or fatal side effects if given any Purinethol.

Knowing which genetic variant of TPMT that Latrice has will influence her treatment tremendously. To determine the dosage of Purinethol that Latrice will need, her doctor takes a DNA sample from her blood and sends it to a Lab.

The lab runs a diagnostic test, based on SNP profiling, to determine which TPMT variation Latrice has. The doctor receives the test results, which show that Latrice has the partial TPMT activity variation. With this knowledge, he can confidently start Latrice on a reduced dosage of Purinethol.

Pharmacogenomic tests could also allow doctors to:

- Choose the right drug for a specific patient from an array of drug choices.
- Determine a patient’s risk for getting a particular disease and design a prevention strategy for that disease.
- Make accurate diagnoses, prescribe more efficient drug therapies, and avoid harmful side effects.

**How is it used?**

The tests for thiopurine methyltransferase (TPMT) enzyme activity or its underlying genetics are measured in people who are about to start treatment with a thiopurine drug. One or the other of these tests is used to identify individuals at risk of developing severe side effects from thiopurine therapy. Thiopurines such as azathioprine, mercaptopurine, and thioguanine are drugs that are prescribed for diseases such as acute, inflammatory bowel disease, and autoimmune disorders. They may also be prescribed for organ transplant recipients to help prevent organ rejection.

**When is it ordered?**

A doctor will typically order a TPMT enzyme activity test or genetic test before starting a patient on thiopurine drug treatment. Occasionally, a TPMT genotype test may be ordered when a person treated with thiopurine drug experiences side effects, such as a decreased WBC count.

**Phenotype test for TPMT**

- If someone has little to no detectable TPMT activity, they are at risk of developing severe side effects to thiopurine drugs. Usually the doctor will find an alternative drug treatment. Sometimes the doctor may prescribe a very small dose of the thiopurine.
- Low to intermediate TPMT activity also puts individuals at increased risk for toxicity. In this case, the doctor may reduce the dose of thiopurine drug given.
- If someone has normal TPMT activity, the doctor can treat the person with a standard dose of a thiopurine drug.[14, 16]

**Genotype test for TPMT**

- A genetic test to detect genetic variations in the TPMT gene will help determine TPMT activity and risk for side effects from low TPMT activity.
- Individuals with two "wild type" copies of the TPMT gene produce sufficient TPMT and have little risk of thiopurine toxicity. Most people fall into this category and can be treated with a standard dose.
- People who have one normal gene and one gene variation associated with decreased TPMT (heterozygous) may produce an intermediate amount
of TPMT. Approximately 30-60% of people who are heterozygous have severe side effects from standard doses of thiopurine. They will likely require reduced doses of the drug but may need to be given an alternative drug.

- People with two copies of a variant TPMT gene (homozygous) and who produce little to no TPMT have 100% likelihood of developing severe bone marrow toxicity (myelosuppression) when treated with conventional doses of thiopurine. They will likely be given an alternative drug.
- The genetic test usually detects the most common variants associated with TPMT deficiency. It is possible for a person to have a rare variant not detected by this test, who may subsequently experience serious side effects from treatment with a thiopurine drug. [14,16]

Cytochrome P450

Enzymes produced from the cytochrome P450 genes are involved in the formation (synthesis) and breakdown (metabolism) of various molecules and chemicals within cells. Cytochrome P450 enzymes play a role in the synthesis of many molecules including steroid hormones, certain fats (cholesterol and other fatty acids), and acids used to digest fats (bile acids). Additional cytochrome P450 enzymes metabolize external substances, such as medications that are ingested and internal substances, such as toxins that are formed within cells. There are approximately 60 CYP genes in humans. Cytochrome P450 enzymes are primarily found in liver cells but are also located in cells throughout the body. Within cells, cytochrome P450 enzymes are located in a structure involved in protein processing and transport (endoplasmic reticulum) and the energy-producing centres of cells (mitochondria). [13]

The enzymes found in mitochondria are generally involved in the synthesis and metabolism of internal substances, while enzymes in the endoplasmic reticulum usually metabolize external substances, primarily medications and environmental pollutants. Common variations (polymorphisms) in cytochrome P450 genes can affect the function of the enzymes. The effects of polymorphisms are most prominently seen in the breakdown of medications.

Depending on the gene and the polymorphism, drugs can be metabolized quickly or slowly. If a cytochrome P450 enzyme metabolizes a drug slowly, the drug stays active longer and less is needed to get the desired effect. A drug that is quickly metabolized is broken down sooner and a higher dose might be needed to be effective. Cytochrome P450 enzymes account for 70 percent to 80 percent of enzymes involved in drug metabolism.[13]

Each cytochrome P450 gene is named with CYP, indicating that it is part of the cytochrome P450 gene family. The gene is also given a number associated with a specific group within the gene family, a letter representing the gene's subfamily, and a number assigned to the specific gene within the subfamily. For example, the cytochrome P450 gene that is in group 27, subfamily A, gene 1 is written as CYP27A1.

Diseases caused by mutations in cytochrome P450 genes typically involve the build-up of substances in the body that are harmful in large amounts or that prevent other necessary molecules from being produced.

FDA, Pharmacogenomics and drug development

The FDA has provided certain guidelines for submission of pharmacogenetic test data by the pharmaceutical industries, as a part of drug development. As most of the pharmacogenetic test results are not well-established scientifically, such studies cannot be used by the FDA for regulatory decisions.

Guidelines have also been released pertaining to the time when a complete pharmacogenetic report is to be submitted and when an abbreviated report is to be submitted. Further, there are separate guidelines for submission of pharmacogenetic data for investigational new drug applications and unapproved and approved marketing applications.

As mentioned above, a well-established pharmacogenetic test is required as a valid biomarker for making regulatory decisions by the FDA. For a pharmacogenetic test to be accepted as a valid biomarker, the test should have a sound scientific framework and well established characteristics. [22, 23]

An example for a valid biomarker in pharmacogenetic tests would be those for drug metabolizing enzymes as a marker for drug efficacy and safety. Patients with variant alleles of the gene CYP2C9 and VKORC1 require lower doses of warfarin, as compared to patients with normal wild type alleles. This is a valid biomarker and pharmacogenetic data has been incorporated in the drug label for warfarin.

The FDA has made submission of a complete pharmacogenetic data report mandatory, if these results have been used for decision making in the animal study, to support the safety of the drug, or in clinical trials, for the selection of subjects, dose range or its modification. [24]

The complete data is also required in cases where the sponsor uses the pharmacogenetic test results to validate safety, efficacy, dosage selection and mechanism of action in the clinical trials. However, in cases where such pharmacogenetic test results are not being used by the sponsor to support the results of the trial, but the test is a valid biomarker for that drug, an abbreviated report of the pharmacogenetic test has to be submitted to the FDA.

Barriers to Pharmacogenomics progress

Pharmacogenomics is a developing research field that is still in its infancy. Several of the following barriers will have to be overcome before many pharmacogenomics benefits can be realized.

- Our limited knowledge of which genes are involved with each drug response. Since many genes are likely
to influence responses, obtaining the big picture on the impact of gene variations is highly time-consuming and complicated.

- Only one or two approved drugs may be available for treatment of a particular condition. If patients have gene variations that prevent them using these drugs, they may be left without any alternatives for treatment.
- Most pharmaceutical companies have been successful with their "one size fits all" approach to drug development. Since it costs hundreds of millions of dollars to bring a drug to market, these companies will be reluctant to develop alternative drugs that serve only a small portion of the population.
- Introducing multiple pharmacogenomic products to treat the same condition for different population subsets undoubtedly will complicate the process of prescribing and dispensing drugs. Physicians must execute an extra diagnostic step to determine which drug is best suited to each patient. To interpret the diagnostic accurately and recommend the best course of treatment for each patient, all prescribing physicians, regardless of specialty, will need a better understanding of genetics. [24]

Conflict of interest statement

We declare that we have no conflict of interest.

References


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