



Genotype–Drug Response: Connecting Genetic Variation with Differences in Medication Effects

Emily Anderson *

Department of Pharmacogenomic Medicine, University of Edinburgh, Edinburgh, UK

DESCRIPTION

Genotype-drug response describes the relationship between a person's genetic makeup and the way a medicine produces its effects. Individuals receiving the same medication and dose may experience different levels of benefit, unwanted reactions, or treatment failure. Genetic variation can influence drug metabolism, transport, receptor activity, immune recognition and cellular signaling. Understanding these relationships provides useful information for medication selection and dose adjustment in appropriate clinical settings. The human genome contains millions of genetic differences between individuals. Some variations have little biological effect, whereas others can change the amount or function of proteins involved in drug handling. Single-nucleotide variants, insertions, deletions, copy-number changes and other genomic alterations may affect enzymes, transporters, receptors and immune-related proteins. When such changes influence a medication-related pathway, they can contribute to differences in drug exposure or therapeutic response.

Drug metabolism is one of the most recognized areas of genotype-drug response. The liver contains several enzyme families that chemically modify medicines before elimination. Cytochrome P450 enzymes are especially important because they participate in the metabolism of many commonly used drugs. Variants in *Cytochrome P450 2D6*, *CYP2C19* and *CYP2C9* can produce differences in enzyme activity. Depending on the medicine, altered enzyme function can increase or decrease drug concentrations in the body. *CYP2D6* provides an example of extensive genetic diversity. Some individuals have reduced enzyme activity, while others have normal or increased activity. A medicine that is primarily cleared by *CYP2D6* may remain in the body for a longer period in individuals with low enzyme activity. In contrast, rapid metabolism may reduce drug exposure for selected medicines. The clinical effect depends on the particular medication and whether the enzyme converts the drug into an active or inactive form.

CYP2C19 variation can also affect medication response. This enzyme participates in the metabolism of several medicines, including selected antiplatelet agents and acid-reducing drugs. Certain genetic variants result in reduced enzyme activity, which may alter the amount of active medication available in the body. Pharmacogenomic information can assist treatment decisions when validated clinical recommendations are available. Drug transporters provide another connection between genotype and medication effects. Transport proteins control the movement of medicines across biological membranes. They influence intestinal absorption, movement into tissues, passage through cellular barriers and elimination through the liver or kidneys. Genetic differences in transporter genes can modify transporter activity and consequently affect the concentration of a medicine at its site of action.

Drug targets are also influenced by genetic variation. Medicines may act on receptors, enzymes, ion channels, or signaling proteins. A genetic change affecting one of these targets may alter its structure, abundance, or activity. As a result, the interaction between a medicine and its target can differ between individuals. This concept is particularly relevant in oncology, where molecular characteristics of tumor cells can influence sensitivity to specific therapeutic agents. Genetic factors can also contribute to adverse drug reactions. Certain variants in immune-related genes are associated with increased susceptibility to specific medication reactions. Human leukocyte antigen genes are notable examples because particular variants have been linked to serious immune-mediated responses to selected medicines. Genetic screening before treatment can help identify individuals at increased risk when an established clinical recommendation supports testing.

Warfarin illustrates how several genetic and clinical factors can influence dosing. Variants in Vitamin K Epoxide Reductase Complex Subunit 1 (*VKORC1*) can affect sensitivity to warfarin, while *CYP2C9* variants can alter its metabolism. Age, diet, liver function, other medicines and vitamin K intake also affect treatment response. Therefore, genotype information can

Correspondence to: Emily Anderson, Department of Pharmacogenomic Medicine, University of Edinburgh, Edinburgh, UK, E-mail: emily.anderson@pharmgen.uk

Received: 30-May-2025, Manuscript No. JPP-25-32593; **Editor assigned:** 02-Jun-2025, PreQC No. JPP-25-32593 (PQ); **Reviewed:** 16-Jun-2025, QC No. JPP-25-32593; **Revised:** 23-Jun-2025, Manuscript No. JPP-25-32593 (R); **Published:** 30-Jun-2025, DOI: 10.35248/2153-0645.25.16.139

Citation: Anderson E (2025). Genotype–Drug Response: Connecting Genetic Variation with Differences in Medication Effects. J Pharmacogenom Pharmacoproteomics. 16:139.

Copyright: © 2025 Anderson E. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution and reproduction in any medium, provided the original author and source are credited.

provide useful guidance but should be considered together with clinical characteristics and laboratory monitoring. Genotype-drug response relationships can involve prodrugs as well. A prodrug requires enzymatic conversion before producing its active pharmacological effect. If a genetic variant reduces the activity of the enzyme responsible for activation, the amount of active compound may decrease. This can lead to reduced treatment effectiveness. Conversely, increased enzymatic activity may alter the quantity of active metabolite produced.

Pharmacogenomic testing can identify clinically relevant genetic variants using targeted genotyping, sequencing, or other molecular methods. Targeted tests focus on selected variants

associated with specific medicines, while broader sequencing approaches can examine multiple genes. The appropriate method depends on the medicine, clinical purpose, laboratory resources and available interpretation guidelines. Genetic results must be interpreted carefully because the presence of a variant does not always predict a specific clinical outcome. Drug response is influenced by multiple factors, including age, organ function, nutrition, disease status, adherence, environmental exposure and interactions with other medicines. Genetic information therefore represents one component of medication assessment rather than an isolated predictor.