



# Pharmacogenetic Variants: Genetic Differences Shaping Medication Response and Safety

Hannah Wilson\*

Department of Pharmacogenetics, University of Manchester, Manchester, UK

## DESCRIPTION

Pharmacogenetic variants are differences in Deoxyribonucleic Acid (DNA) that can influence how an individual responds to a medicine. These genetic differences may affect drug metabolism, transport, receptor activity, immune recognition, or other biological processes involved in medication action. As a result, patients receiving the same medicine and dose can experience different therapeutic effects or adverse reactions. Understanding pharmacogenetic variants provides useful information for medication selection and dose adjustment when appropriate clinical guidance is available. Human genetic variation includes single-nucleotide variants, insertions, deletions, copy-number differences and larger structural changes. Some variants have little measurable biological effect, while others alter the amount or function of a protein. When the affected protein participates in drug metabolism or pharmacological activity, the genetic difference may influence medication response.

Drug-metabolizing enzymes are among the most important areas of pharmacogenetics. Cytochrome P450 enzymes participate in the metabolism of many medicines. Genes such as *Cytochrome P450 2D6*, *CYP2C19* and *CYP2C9* contain variants that can alter enzyme activity. Depending on the specific medicine, reduced enzyme activity can result in slower drug elimination or reduced conversion of a prodrug into its active form. Increased enzyme activity can produce a different response by changing the rate of drug processing. *CYP2D6* contains numerous genetic variants, producing considerable differences in enzyme activity among individuals. Some people have very low *CYP2D6* activity, while others have normal or increased activity. Medicines metabolized through this pathway can therefore produce different concentrations or effects depending on the patient's genetic profile. Clinical interpretation depends on the specific medicine because the same metabolic phenotype can have different consequences for different drugs.

*CYP2C19* is another clinically relevant pharmacogenetic pathway. Variants affecting this enzyme can influence the

metabolism of several medicines, including selected antiplatelet agents and acid-reducing drugs. In some cases, reduced enzyme activity can decrease the conversion of a prodrug into its active form. Genetic information can help clinicians consider alternative treatments when validated prescribing recommendations are available. *CYP2C9* variants can influence the metabolism of medicines such as warfarin and certain other therapeutic agents. Warfarin response is also influenced by Vitamin K Epoxide Reductase Complex Subunit 1 (*VKORC1*) variation, which affects sensitivity to the medicine. Genetic information may therefore contribute to dose selection, although clinical factors such as age, diet, liver function, other medicines and vitamin K intake also have substantial effects.

Drug transporter genes represent another important group of pharmacogenetic factors. Transport proteins control the movement of medicines across cell membranes and influence absorption, distribution and elimination. Genetic variation can alter transporter expression or activity, changing the amount of medicine reaching particular tissues. This may influence both therapeutic activity and unwanted effects. Genetic variants can also affect drug targets. Medicines often act through receptors, enzymes, ion channels, or signaling proteins. A change in the gene encoding one of these targets may modify protein structure, expression, or activity. Such changes can alter how strongly a medicine interacts with its target and may contribute to differences in treatment response.

Immune-related genes are important in the prediction of selected adverse drug reactions. Certain human leukocyte antigen variants are associated with increased susceptibility to serious immune-mediated reactions caused by particular medicines. Genetic testing before treatment can identify individuals carrying specific variants when clinical guidelines recommend screening. In suitable cases, avoiding the associated medicine can reduce the risk of a severe reaction. Pharmacogenetic variants are also relevant to oncology. Tumor cells can contain genetic alterations that influence the activity of receptors, enzymes, signaling pathways and other molecular

**Correspondence to:** Hannah Wilson, Department of Pharmacogenetics, University of Manchester, Manchester, UK, E-mail: hannah.wilson@pharmgen.uk

**Received:** 29-Aug-2025, Manuscript No. JPP-25-32620; **Editor assigned:** 01-Sept-2025, PreQC No. JPP-25-32620 (PQ); **Reviewed:** 15-Sept-2025, QC No. JPP-25-32620; **Revised:** 22-Sept-2025, Manuscript No. JPP-25-32620 (R); **Published:** 29-Sept-2025, DOI: 10.35248/2153-0645.25.16.144

**Citation:** Wilson H (2025). Pharmacogenetic Variants: Genetic Differences Shaping Medication Response and Safety. J Pharmacogenom Pharmacoproteomics. 16:144.

**Copyright:** © 2025 Wilson H. 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.

targets. Testing tumor DNA can identify changes associated with sensitivity or reduced response to particular medicines. Unlike inherited variants, tumor-specific alterations may occur only within cancer cells and can change during disease progression.

Laboratory methods for identifying pharmacogenetic variants include targeted genotyping, polymerase chain reaction, microarray analysis and DNA sequencing. Targeted tests examine selected variants associated with particular medicines. Broader sequencing methods can examine multiple genes and identify a larger range of genetic changes. The appropriate

testing approach depends on the medicine, clinical purpose, laboratory facilities and available interpretation resources. The interpretation of pharmacogenetic variants requires more than simply identifying a DNA change. A variant may have different clinical significance depending on the gene, allele, medication and biological pathway involved. Some variants have well-established effects, while others have uncertain or limited evidence. Clinical databases and pharmacogenomic guidelines can assist healthcare professionals in translating genetic findings into appropriate medication decisions.