



RNA-Based Drug Response: Molecular RNA Signatures and Their Influence on Therapeutic Outcomes

Isabella Morgan*

Department of Molecular Pharmacology, University of Cambridge, Cambridge, UK

DESCRIPTION

Ribonucleic Acid (RNA) based drug response describes the relationship between RNA molecules and the way biological systems react to pharmaceutical treatments. RNA participates in gene expression, protein production, cellular signaling and regulation of many physiological processes. Because medication can alter RNA activity while pre-existing RNA patterns can influence treatment effects, RNA provides valuable information about differences in therapeutic outcomes among individuals. Messenger RNA is one of the most important RNA classes involved in drug response. It carries information from DNA to ribosomes, where proteins are produced. Medicines can change the expression of genes associated with inflammation, metabolism, cell division, apoptosis, immune activity and signaling. Measuring changes in messenger RNA can therefore provide information about biological processes activated or suppressed after treatment.

RNA abundance differs between tissues and cell types. A medicine may produce a strong transcriptional response in one tissue while having a smaller effect in another. Liver cells, immune cells, neurons and tumor cells possess distinct RNA profiles because they perform different functions. Tissue-specific RNA information is therefore important when interpreting medication effects. MicroRNAs are another important group of regulatory RNA molecules. These short RNA molecules can bind to messenger RNA and influence its stability or translation. A single microRNA can affect multiple messenger RNAs, allowing it to participate in several biological pathways. Changes in microRNA levels may influence drug metabolism, inflammation, cell survival and signaling.

Long non-coding RNAs also contribute to medication response. These RNA molecules can regulate gene transcription, interact with proteins, influence chromatin organization and affect messenger RNA stability. Some long non-coding RNAs change in response to pharmaceutical exposure. Their expression patterns may therefore provide information about cellular

adaptation to treatment. Circular RNAs represent another RNA category with regulatory functions. Their closed molecular structure provides greater resistance to certain forms of degradation. Circular RNAs can interact with microRNAs, proteins and other RNA molecules. Changes in circular RNA expression have been associated with several biological processes, including cellular stress, inflammation, cancer development and treatment response.

RNA molecules can influence drug metabolism through regulation of metabolic enzymes. Cytochrome P450 enzymes, transport proteins and conjugating enzymes are controlled partly through gene expression. If RNA levels for these proteins increase or decrease, the capacity of a cell to process a medicine may also change. This can affect drug concentration and duration of exposure. RNA profiles can also reflect differences in drug targets. Receptors, enzymes, ion channels and signaling proteins are produced according to cellular gene-expression patterns. If the RNA encoding a particular target is present at a higher or lower level, the number of available protein molecules may change. Consequently, the response to a medicine acting on that target can differ between individuals or tissues.

In cancer therapy, RNA-based response patterns can provide information about tumor behavior. Cancer cells often display altered expression of genes involved in proliferation, DNA repair, immune signaling, metabolism and cell death. Treatment can modify these patterns, producing characteristic RNA changes. Comparing RNA profiles before and after medication exposure can help identify biological responses associated with treatment sensitivity or resistance. RNA information can also contribute to understanding immune responses to medicines. Cytokines, chemokines, receptors and other immune molecules are controlled through gene expression. Changes in their corresponding RNA levels can indicate activation or suppression of particular immune pathways. This is relevant to therapies that influence immune activity and to medicines associated with immune-mediated adverse effects.

Correspondence to: Isabella Morgan, Department of Molecular Pharmacology, University of Cambridge, Cambridge, UK, E-mail: isabella.morgan@rnapharm.uk

Received: 01-Dec-2025, Manuscript No. JPP-25-32651; **Editor assigned:** 03-Dec-2025, PreQC No. JPP-25-32651 (PQ); **Reviewed:** 17-Dec-2025, QC No. JPP-25-32651; **Revised:** 24-Dec-2025, Manuscript No. JPP-25-32651 (R); **Published:** 31-Dec-2025, DOI: 10.35248/2153-0645.25.16.162

Citation: Morgan I (2025). RNA-Based Drug Response: Molecular RNA Signatures and Their Influence on Therapeutic Outcomes. J Pharmacogenom Pharmacoproteomics. 16:162.

Copyright: © 2025 Morgan I. 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.

RNA sequencing technologies allow thousands of RNA molecules to be measured simultaneously. The resulting data can identify genes with increased or decreased expression and reveal groups of transcripts associated with particular biological processes. Computational analysis can classify RNA profiles and compare patterns between different treatment conditions. Single-cell RNA analysis provides information at the level of individual cells. A tissue may contain many cell populations with different responses to the same medicine. When RNA is measured from the entire tissue, signals from smaller populations can be obscured. Single-cell approaches can distinguish cellular subgroups and identify differences in their responses to treatment.

RNA modifications add another regulatory layer. Messenger RNA and other RNA molecules can contain chemical modifications that influence stability, translation, localization and processing. N6-methyladenosine is one widely recognized RNA modification. Enzymes that add, remove, or recognize such modifications can influence how RNA behaves inside cells. Variants in promoters, enhancers, untranslated regions and RNA-processing sites can alter transcript abundance or stability. A person carrying one genetic variant may produce more or less of a particular RNA molecule than another person. This can contribute to differences in protein levels and medication effects