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Pharmacogenomic Tools for Safer Chemotherapeutic Regimens

Hasan Davies*

Department of Pharmacy, Al-Zaytoonah University of Jordan, P.O. Box 130, Amman 11733, Jordan

Introduction

Chemotherapy remains a cornerstone of cancer treatment, playing a vital role in controlling tumor growth, preventing metastasis, and improving survival across a wide spectrum of malignancies. However, its therapeutic use is often limited by severe toxicity, unpredictable adverse effects, and interindividual variability in drug responses. For decades, oncologists have relied on weight-based dosing, standard regimens, and population-wide guidelines, which, although effective in some, can lead to life-threatening complications in others. The traditional "one-size-fits-all" approach to chemotherapy does not account for the genetic, metabolic, and physiological differences that exist among patients. he advent of pharmacogenomics-the study of how genetic variations affect individual responses to drugs-has ushered in a new era of personalized medicine in oncology. By identifying genomic variants in drug-metabolizing enzymes, transporters, and molecular targets, pharmacogenomic tools enable oncologists to predict treatment outcomes and tailor chemotherapy regimens to enhance efficacy while minimizing toxicity [1,2].

Description

Pre-treatment screening for DPYD variants is now included in EMA guidelines. Dose reduction or alternative therapies are recommended for patients with deficient DPYD function. Irinotecan, a topoisomerase I inhibitor used in colorectal and lung cancers, is metabolized by UGT1A1 into inactive SN-38 glucuronide. The UGT1A1 28 allele, a TA-repeat polymorphism in the promoter region, is associated with reduced enzyme expression. Genotyping can help personalize irinotecan dosing. The FDA recommends dose reduction in homozygous UGT1A1 patients to prevent hematological toxicity. Tamoxifen is a selective estrogen receptor modulator used in ER+ breast cancer. It is a prodrug metabolized into active endoxifen by CYP2D6. CYP2D6 genotyping informs whether tamoxifen will be effective or if alternative therapies like aromatase inhibitors should be considered. Methotrexate, a folate antagonist used in leukemia, lymphoma, osteosarcoma, and breast cancer, is influenced by MTHFR enzyme activity [3].

NGS platforms can simultaneously analyze multiple pharmacogenomic markers, enabling comprehensive risk profiling. Panels such as OncoPGx or Thermo Fisher's PharmacoScan provide actionable data across a broad spectrum of drugs. These arrays identify known pharmacogenetic variants costeffectively. SNP-based genotyping is used widely in clinical trials and academic research to stratify patient responses. Beyond static genotyping, transcriptomics and proteomics assess dynamic expression of drug-related enzymes and pathways, offering real-time insights into drug sensitivity and

*Address for Correspondence: Hasan Davies, Department of Pharmacy, Al-Zaytoonah University of Jordan, P.O. Box 130, Amman 11733, Jordan; E-mail: davieshasan@es.jo

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resistance. Al models can integrate genomic, clinical, and pharmacokinetic data to predict toxicity risks, recommend doses, and simulate treatment outcomes, improving decision-making in complex cancer cases [4].

Many comprehensive cancer centers have implemented preemptive PGx testing panels for patients initiating chemotherapy, supported by Clinical Decision Support Systems (CDSS) in electronic health records. Pharmacogenomic testing is increasingly being covered by insurance in regions where guidelines and evidence support clinical benefit, although cost-effectiveness studies continue to influence policy decisions. A 55-year-old male with metastatic colorectal cancer was scheduled for irinotecan-based FOLFIRI chemotherapy. UGT1A1 testing revealed a genotype. Based on guidelines, his dose was reduced by 30%, preventing severe neutropenia and allowing successful completion of 6 cycles. A 48-year-old woman on tamoxifen for ER+breast cancer experienced recurrence despite good adherence. Retrospective CYP2D6 genotyping identified her as a poor metabolizer. She was switched to an aromatase inhibitor, with better clinical control thereafter [5].

Conclusion

Pharmacogenomic tools represent a paradigm shift in oncology, enabling the transition from standardized chemotherapy protocols to individualized treatment regimens that optimize efficacy and minimize harm. By identifying genetic variants that influence drug metabolism, transport, and target interaction, clinicians can anticipate and prevent serious adverse effects, guide dosing decisions, and improve treatment adherence and outcomes. Despite current challenges in education, infrastructure, and policy, the momentum behind pharmacogenomics continues to grow. As genomic technologies become more accessible and integrated into clinical workflows, pharmacogenomic-guided chemotherapy will evolve from a promising innovation to a clinical necessity.

Acknowledgement

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Conflict of Interest

None.

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