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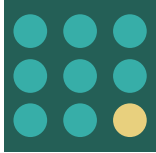
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Section

Pharmacogenetics



Editor-in-Chief

Prof. Dr. Enrico Mini
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Message from the Section Editor-in-Chief

The section of pharmacogenetics of the *Journal of Personalized Medicine* is open to receive high-quality research and review articles, as well as short communications on all aspects of pharmacogenetics (from gene to the clinic) for rapid publication. Interests are focused on the effects of genotype on the pharmacology of drugs in all therapeutic areas, leading to personalized treatments.

Key areas of coverage include:

- Effects of genetic variability on drug toxicity and efficacy;
- Identification and functional characterization of polymorphisms relevant to drug action;
- Integration of new developments in the genome project into clinical pharmacology, therapeutics, and medicine;
- Clinical implementation of pharmacogenetics;
- Identification of novel genomics targets for drug development;
- Companion diagnostics and drug development.
- The section combines articles from the entire range of biomedical research and science, including clinical pharmacology, clinical pharmacy, genetics, genomics, molecular biology, pharmacology and toxicology, biochemistry, epidemiology, and bioinformatics.

Selected Papers

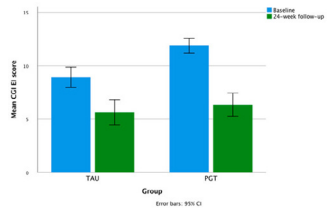
DOI:10.3390/jpm12020316

Pharmacogenomics-Guided Pharmacotherapy in Patients with Major Depressive Disorder or Bipolar Disorder Affected by Treatment-Resistant Depressive Episodes: A Long-Term Follow-Up Study



Authors: Antonio Del Casale, Leda Marina Pomes, Luca Bonanni, Federica Fiaschè, Clarissa Zocchi, Alessio Padovano, Ottavia De Luca, Gloria Angeletti, Roberto Brugnoli, Paolo Girardi, Robert Preissner, Marina Borro, Giovanna Gentile, Maurizio Pompili and Maurizio Simmaco

Abstract: Treatment-resistant depression (TRD) reduces affected patients' quality of life and leads to important social health care costs. Pharmacogenomics-guided treatment (PGT) may be effective in the cure of TRD. The main aim of this study was to evaluate the clinical changes after PGT in patients with TRD (two or more recent failed psychopharmacological trials) affected by bipolar disorder (BD) or major depressive disorder (MDD) compared to a control group with treatment as usual (TAU). We based the PGT on assessing different gene polymorphisms involved in the pharmacodynamics and pharmacokinetics of drugs. We analyzed, with a repeated-measure ANOVA, the changes between the baseline and a 6 month follow-up of the efficacy index assessed through the Clinical Global Impression (CGI) scale, and depressive symptoms through the Hamilton Depression Rating Scale (HDRS). The PGT sample included 53 patients (26 BD and 27 MDD), and the TAU group included 52 patients (31 BD and 21 MDD)...



DOI:10.3390/jpm12050692

The Rise of Population Genomic Screening: Characteristics of Current Programs and the Need for Evidence Regarding Optimal Implementation



Authors: Kimberly S. Foss, Julianne M. O'Daniel, Jonathan S. Berg, Sabrina N. Powell, Rosemary Jean Cadigan, Kristine J. Kuczynski, Laura V. Milko, Katherine W. Saylor, Megan Roberts, Karen Weck and Gail E. Henderson

Abstract: Purpose: Advances in clinical genomic sequencing capabilities, including reduced costs and knowledge gains, have bolstered the consideration of genomic screening in healthy adult populations. Yet, little is known about the existing landscape of genomic screening programs in the United States. It can be difficult to find information on current implementation efforts and best practices, particularly in light of critical questions about equity, cost, and benefit. Methods: In 2020, we searched publicly available information on the Internet and the scientific literature to identify programs and collect information, including: setting, program funding, targeted population, test offered, and patient cost. Program representatives were contacted throughout 2020 and 2021 to clarify, update, and supplement the publicly available information. Results: Twelve programs were identified. Information was available on key program features, such as setting, genes tested, and target populations...



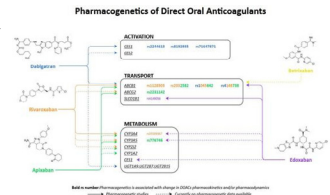
DOI:10.3390/jpm11010037

Pharmacogenetics of Direct Oral Anticoagulants: A Systematic Review



Authors: Johanna Raymond, Laurent Imbert, Thibault Cousin, Thomas Dufлот, Rémi Varin, Julien Wils and Fabien Lamoureux

Abstract: Dabigatran, rivaroxaban, apixaban, edoxaban, and betrixaban are direct oral anticoagulants (DOACs). Their inter-individual variability in pharmacodynamics and pharmacokinetics (transport and metabolism) is high, and could result from genetic polymorphisms. As recommended by the French Network of Pharmacogenetics (RNPGe), the management of some treatments in cardiovascular diseases (as antiplatelet agents, oral vitamin K antagonists, and statins) can rely on genetic testing in order to improve healthcare by reducing therapeutic resistance or toxicity.



This paper is a review of association studies between single nucleotide polymorphisms (SNPs) and systemic exposure variation of DOACs. Most of the results presented here have a lot to do with some SNPs of *CES1* (rs2244613, rs8192935, and rs71647871) and *ABCB1* (rs1128503, rs2032582, rs1045642, and rs4148738) genes, and dabigatran, rivaroxaban, and apixaban. Regarding edoxaban and betrixaban, as well as SNPs in the *CYP3A4* and *CYP3A5* genes, literature is scarce, and further studies are needed.

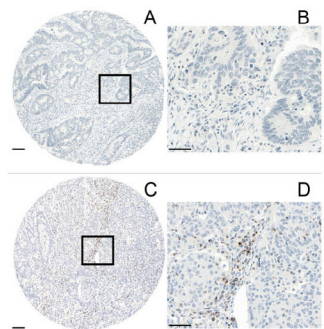
DOI:10.3390/jpm11080749

LAG-3 Expression Predicts Outcome in Stage II Colon Cancer



Authors: Gaëlle Rhyner Agocs, Naziheh Assarzadegan, Richard Kirsch, Heather Dawson, José A. Galván, Alessandro Lugli, Inti Zlobec and Martin D. Berger

Abstract: Introduction: LAG-3 is an inhibitory immune checkpoint molecule that suppresses T cell activation and inflammatory cytokine secretion. T cell density in the tumor microenvironment of colon cancer plays an important role in the host's immunosurveillance. We therefore hypothesized that LAG-3 expression on tumor-infiltrating lymphocytes (TILs) predicts outcome in patients with stage II colon cancer. Patients and Methods: Immunohistochemical staining for LAG-3 was performed on tissue microarrays (TMAs) of formalin-fixed paraffin-embedded tissue from 142 stage II colon cancer patients. LAG-3 expression was assessed in TILs within both the tumor front and tumor center and scored as either positive or negative. The primary endpoint was disease-free survival (DFS). Results: In patients diagnosed with stage II colon cancer, the presence of LAG-3 expression on TILs was significantly associated with better 5-year DFS (HR 0.34, 95% CI 0.14–0.80, $p = 0.009$). The effect on DFS was mainly due to LAG-3-positive TILs in the tumor front (HR 0.33, 95% CI 0.13–0.82, $p = 0.012$). Conclusion: Assessment of LAG-3 might help to predict outcomes in patients with stage II colon cancer and potentially identify those patients who might benefit from adjuvant chemotherapy. Therefore, LAG-3 may serve as a prognostic biomarker in stage II colon cancer.



Special Issues Open for Submission

Pharmacogenomics: Current Status and Future Perspectives

Guest Editor: Dr. Marta Miarons Font

Deadline: 5 February 2024



COVID-19 Medicines in Pharmacogenomics

Guest Editors: Dr. Satyavani Kalamurthi and Dr. Gurudeeban Selvaraj

Deadline: 20 February 2024



Drug-Drug-Gene Interactions and Adverse Drug Reactions

Guest Editor: Dr. Sarah Allegra

Deadline: 1 March 2024



Pharmacogenomics and Hypertension: Problems and Prospects

Guest Editors: Prof. Dr. Brian L. Rayner and Prof. Dr. Collet Dandara

Deadline: 25 March 2024



Pharmacogenomics of Drug Metabolism and Pharmacokinetics

Guest Editor: Dr. Subrata Deb

Deadline: 15 May 2024

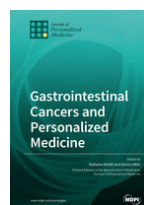


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Pharmacogenomics: From Basic Research to Clinical Implementation



Gastrointestinal Cancers and Personalized Medicine



Pharmacogenetics to Avoid Adverse Drug Reactions



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