Evidence-Based Assessment and Prioritization of Candidate Genes (PTGS-2 and CYP2C9) Interacting with Celecoxib

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Background: Many pharmacogenetics and pharmacogenomics studies have been reported on response variation of non-steroidal anti-inflammatory drugs (NSAIDs) especially COX-2 inhibitors that may influence both efficacy and safety.

Among the different types of COX-2 inhibitors, Celecoxib is prescribed for acute pain, rheumatoid arthritis, ankylosing spondylitis, osteoarthritis, colorectal polyps, and familial adenomatous polyposis.

Objective: There is a huge amount of data available on genes interacting with celecoxib in terms of drug response, however, these studies are inconsistent.

To overcome this inconsistency, there is a dire need to integrate the available data and categorize genes interacting with celecoxib.

Methodology: We conducted the extraction of data from published articles (*n*=30511) with reference to celecoxib-gene interactions from online literature sources using semi-automated text mining approach.

Scoring algorithms were developed by assigning every gene a score depending on the available evidence according to Coriell Personalized Medicine Collaborative Pharmacogenomics Appraisal evidence scoring systems.

And we generated prioritized gene sets based on evidence scores.

Results: Twenty-seven genes with evidence were identified to be associated with the response of celecoxib from the literature search.

Seven genes were found to affect clinical outcomes of celecoxib, whereas, thirteen genes were found associated with pharmacodynamics and pharmacokinetics and seven genes were identified with potential clinical relevance.

Our analysis specified that celecoxib responds better in an individual with increased expression of *PTGS-2* and *CYP2C9* gene.

Conclusion: We utilized a semi-automated machine learning approach to extract genes from a wide-ranging corpus of scientific literature and we prioritized a set of twenty-eight genes based on the consistency and strength of evidence.

Furthermore, these identified genes should be used for validation and or replication in multiethnic cohorts and animal models to evaluate the response variation of celecoxib.