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THE ROLE OF BIOMARKERS IN ASSESSING TOXICITY: ADVANCES IN TOXICOGENOMICS AND PERSONALIZED MEDICINE

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Abstract
Biomarkers play an increasingly critical role in modern toxicity assessment by enabling early detection of adverse biological effects and improving mechanistic understanding of toxic responses. Advances in toxicogenomics, high-throughput transcriptomics, and computational modeling have accelerated the development of predictive biomarkers that support precision toxicology and personalized medicine. This systematic literature review was conducted in accordance with PRISMA 2020 guidelines to synthesize empirical evidence on biomarker-based toxicity assessment, with particular emphasis on toxicogenomics innovations and individualized risk prediction. A comprehensive search of Google Scholar, DOAJ, and ScienceDirect identified 210 records published between 2015 and 2025. Following duplicate removal, screening, and eligibility assessment, 14 peer-reviewed empirical studies were included in the final qualitative synthesis. The findings indicate that transcriptomics-based biomarkers remain the dominant platform for toxicity prediction, particularly for drug-induced liver injury and mechanistic chemical profiling. Artificial intelligence and machine learning approaches were also prominent, enhancing biomarker discovery, multi-organ toxicity prediction, and carcinogenic risk assessment. Emerging evidence further highlights the growing importance of epigenetic and exposomic biomarkers for monitoring real-world environmental exposures and supporting personalized toxicity evaluation. Overall, the review demonstrates a clear transition toward genomic biomarker frameworks, reduced reliance on animal testing, and integration of multi-omics and AI technologies in next-generation risk assessment. These developments underscore the evolution of toxicity assessment toward more predictive, mechanistic, and individualized paradigms, with biomarker innovation central to the future of precision toxicology.

Keywords: Biomarkers, toxicogenomics, transcriptomics, personalized medicine, predictive toxicology

1. Introduction

Development of toxicogenomics is one of the most revolutionary changes in the study of biomarkers. Toxicogenomics is an amalgamation of toxicology and genomics as well as high-throughput molecular profiling technologies to gain an insight on how toxic exposures can modulate gene expression and cellular pathways. Toxicogenomics is useful in mechanistic understanding of the toxicity pathways by analyzing global transcriptomic alterations and also in the identification of predictive genomic biomarkers. The method has made it possible to detect toxicity earlier, interpret mechanistically, and assess chemical risks better (Liu et al., 2019). Toxicogenomics is already becoming one of the primary elements of the next-generation risk assessment, providing more correct and human-relevant virtual alternatives to traditional animal-based testing (Qin et al., 2016). Developments in the field of transcriptomics and high-throughput screening systems have added further impetus to the use of toxicogenomics in safety pharmacology and regulatory toxicology. One of the most significant fields in which toxicogenomics has expressed significant utility is the drug-induced liver injury (DILI) that is among the most significant causative agents of drug withdrawal and clinical trial failure. Toxicogenomic profiling has given new mechanistic insights into liver toxicity and enhanced the early detection of hepatotoxic risk (Lauschke, 2021). Also, recent studies have extended toxicogenomics past organ-specific toxicity to integrative transcriptomics, which is applied to assess multi-organ toxicity. Indicatively, models of generative artificial intelligence have been suggested to interpolate organ-specific transcriptomic reactions, which allow predicting the full spectrum of toxicity in biological systems (Li et al., 2024). According to such innovations, the growing intersection of toxicogenomics and computational biology and artificial intelligence in predictive toxicology is apparent.

Another significant change in the toxicity evaluation is the integration of the toxicogenomics and personalized medicine. Personalized medicine focuses on the treatment plans which are individualized and depend on genetic vulnerability, molecular patterns and the history of environmental exposures. Precision toxicology is also based on the same principle but individual toxicity risks are predicted by reference to biomarkers instead of individual population averages. Innovations in the field of genome are also continuing to open the path to more personalized care, such as enhanced adverse drug reactions prediction (Saki, 2024). Moreover, the idea of the exposome, which refers to the aggregation of genome-environment interactions, has strengthened the necessity of genetic-environmental interactions to be incorporated into toxicity assessment systems (Niedzwiecki et al., 2019). Integrations of multi-omics biomarkers and translational exposomics are now being seen as key to the comprehension of complex toxicity reactions and the future of individual risk prediction. Nevertheless, much work is done in the field despite such improvements. The discovery and validation of biomarkers has not been consistent in the literature and regulation in practice is usually slow. Even though there is a drastic increase in the number of toxicogenomics methods, there is still no unified body of evidence that consolidates the interplay between biomarkers, toxicogenomics, and personalized medicine to enhance prediction of toxicity. The recent literature has also emphasized the role of the strong toxicogenomics approach to tackle toxicity and carcinogenicity, especially in liver risk testing (Pandiri et al., 2023). Additionally, the new computational resources, including hierarchical biomarker discovery models, are potentially useful, but need to be systematically tested in different toxicity scenarios (Rana et al., 2025). Thus, it is necessary to systematize the existing empirical evidence to clarify the current advances, define trends and outline the research priorities in the future.

Objectives of the study:

1. To identify and synthesize empirical evidence on key biomarker types and toxicogenomics approaches used in modern toxicity assessment.
2. To examine emerging trends and challenges in integrating biomarker-based toxicogenomics with personalized medicine for predictive and precision toxicology.

2. Methodology

2.1 Study Design

This was a systematic literature review study that was carried out following the PRISMA 2020 guidelines. The purpose of the review was to bring together empirical studies in the application of biomarkers in measuring toxicity especially with recent developments in toxicogenomics and personalized medicine. The research was systematic to make the methodology rigorous and reproducible. The articles used in the review were published between 2015 and 2025 to accommodate the current developments in the subject matter. The methodology was systematic, which made it possible to identify, screen and synthesize the relevant studies to minimize selection bias and facilitate a high level of reliability of the conclusions made based on the evidence base.

2.2 Eligibility Criteria

The pre-defined criteria of eligibility was used to allow consistency and objectivity in the study selection process. The authors searched peer-reviewed empirical articles published between 2015 and 2025 which discussed the use of biomarkers in toxicity evaluation with particular interest in toxicogenomics and personalized medicine. Quantitative and qualitative studies were taken into consideration. Non-peer reviewed studies, those with no empirical results and those with serious methodological weaknesses were eliminated. This strategy also made sure that quality and relevant studies only added to the final synthesis to boost validity of the findings of the review in the biomarkers and toxicity context.

2.3 Information Sources

The relevant studies were collected with the help of three major scholarly databases: Google Scholar, DOAJ and Science Direct. These databases were selected due to their broad-based toxicology, genomics and biomedical data. Besides search through electronic databases, a manual search through the relevant articles was done to determine whether there were any other studies in the databases. Such multi-source methodology enhanced the completeness of the search and reduced the chances of loss of important studies on biomarkers and toxicity test.

2.4 Search Strategy

A search strategy was worked out on the basis of Boolean operators and keywords to help to find the relevant studies included in the review. The search query was: (“biomarkers" OR toxigenomics OR genomic biomarkers or predictive biomarkers) AND toxicity (or toxicity assessment or drug toxicity) AND personalized medicine (or precision medicine) AND 2015 (or 2025).

2.5 Study Selection

It was done according to the PRISMA guidelines, and the selection of studies was carried out to provide transparency and methodological rigor. In the first stage, a total of 210 records were located after extensive search of database and checking of reference files. After the screening and eligibility assessment process, only studies which corresponded to the set inclusion criteria were retained. Finally, a final synthesis was done on 14 studies. This is why this structured selection methodology was important to make sure that the studies that were included were relevant and gave valuable information on the role of biomarkers in toxicity and toxicogenomics towards a high quality and reliable review of the scientific literature that exists.

2.6 Data Extraction

To have uniformity in studies, data extraction was done through a framework that was standardized. Data was obtained about the study features, types of biomarkers, toxicity effects, and methodology. Other information about sample sizes, population characteristics, and use of biomarkers in personalized medicine and toxicogenomics was also noted. The systematic nature of this extraction process made it possible to systematically compare the results across studies and it made sure that the

synthesis was performed with reliable and consistent data, errors in the extraction process were also reduced to a minimum.

2.7 Risk of Bias Assessment

Risk of bias was evaluated against the quality of the included studies with a structured tool designed to fit the research designs, such as Joanna Briggs Institute (JBI) Critical Appraisal Checklist and Critical Appraisal Skills Programme (CASP) tool. The risk of bias was assessed in such important areas like selection bias, performance bias, detection bias, and attrition bias. A study was classified as presented with low, high or unclear risk of bias in each domain. Articles with great methodological flaws were filtered out at the eligibility stage so that only top-quality evidence would be used in the final analysis. Such a strict evaluation enhanced the validity of the results and reduced the influence of the substandard researches on the overall review.

2.8 Data Synthesis

The synthesis of the findings of the included studies was carried out with the help of a narrative synthesis. Since the designs of the studies, the biomarkers and the toxicity outcomes were heterogeneous, the studies were thematically classified into the type of biomarkers and the type of toxicity endpoints. The synthesis was made in comparing the results of various types of biomarkers and in determining the similar tendencies and differences in the outcomes. The synthesis also dealt with the importance of toxicogenomics in personalized medicine.

3. Results

3.1 Study Selection outcomes

All the results of the study selection were made in a systematic way, following the PRISMA 2020 guidelines to guarantee transparency and rigor. A thorough search in Google Scholar, DOAJ and ScienceDirect found 200 records but an extra 10 studies were accessed by manual reference searching and as such, 210 records were obtained. Following the elimination of 20 duplicate articles, there were 190 unique studies to screen the title and abstracts. In this screening phase, 160 records were filtered out due to it not being relevant to biomarker-based toxicity, non-empirical, and it was not published within the years 2015-2025. Then, eligibility was evaluated on 30 full-text articles and 16 articles were excluded because of lack of empirical results, poor methodology, or lack of validated biomarker outcomes (Figure 1). Finally, 14 peer-reviewed empirical studies were found to fulfill all the inclusion criteria and were eligible in the ultimate qualitative synthesis.

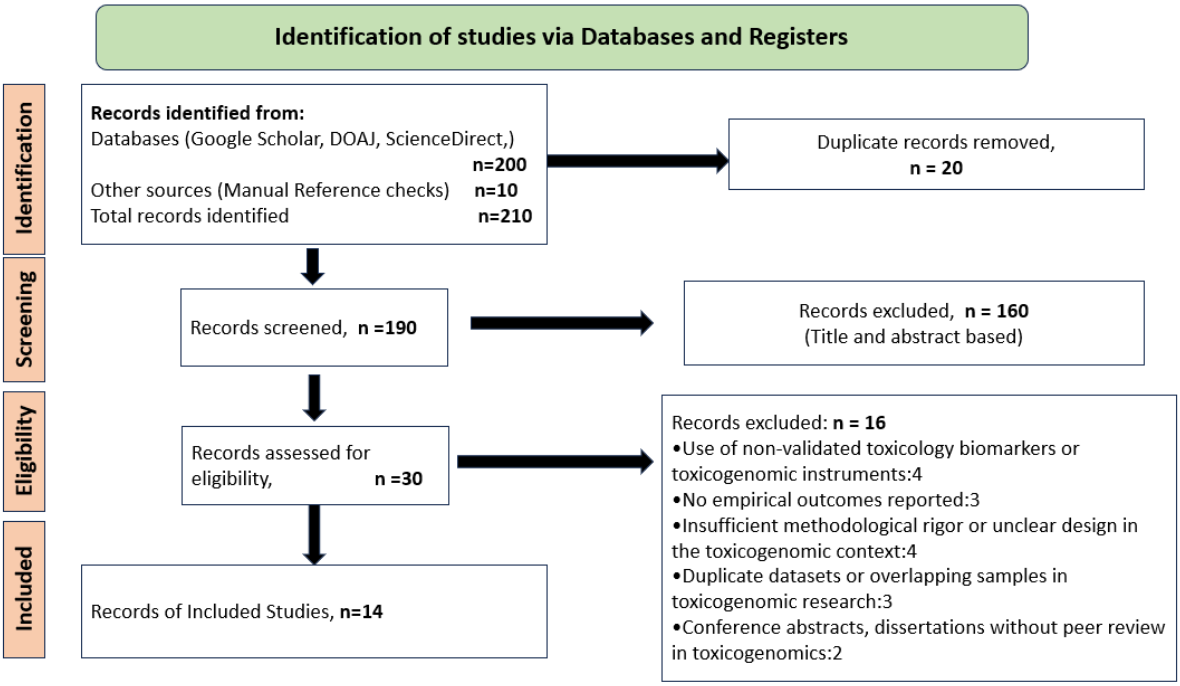


Figure 1. PRISMA chart

3.2 Characteristics of Included Studies

The systematic review encompassed 14 empirical studies that were peer-reviewed and published in 2015-2025, which emphasized the use of biomarker-based toxicity assessment, toxicogenomics, and personalized medicine (Table 1). The articles included were categorized on the basis of themes based on toxicity endpoints, biomarker type and methodological approach.

Table 1. Characteristics and Key Findings of Included Studies (n = 14)

Study (Author, Year)	Theme & Methodology Type	Biomarker Approach	Toxicity Endpoint	Key Findings
Bergen et al. (2025)	Toxicogenomics resource (Large-scale empirical dataset)	Transcriptomics atlas	DILI prediction	Improved DILI prediction using human toxicogenomics data.
Chen et al. (2024)	Exposure biomarkers (Population-based empirical study)	DNA methylation biomarkers	Industrial pollutant exposure	Reported methylation biomarkers linked to pollutant exposure.
Corton et al. (2022)	Regulatory genomic biomarkers (Collaborative empirical initiative)	Genomic biomarker framework	Tumorigenic potential	Established genomic biomarkers for carcinogenic risk assessment.
Harrill et al. (2024)	Mechanistic inference (High-throughput empirical study)	Transcriptomic signature screening	Chemical grouping	Classified chemicals through transcriptomic

				mechanistic signatures.
Li et al. (2015)	Genotoxicity biomarkers (Experimental in vitro study)	Toxicogenomic signature development	Genotoxicity in human cells	Developed an early transcriptomic genotoxicity signature.
Rahman et al. (2022)	AI biomarker discovery (Computational empirical ML study)	ML + toxicogenomics biomarkers	Regulatory endpoints	Predicted toxicity outcomes using ML-based biomarkers.
Rana et al. (2025)	Biomarker tool development (Computational modeling study)	Hierarchical discovery tool (ToxAssay)	Toxicogenomics screening	Introduced ToxAssay for efficient biomarker discovery.
Sakolish et al. (2025)	Kidney toxicity models (Comparative empirical in vitro study)	Proximal tubule cell models	Nephrotoxicity prediction	Identified optimal renal models for nephrotoxicity testing.
Sarigiannis et al. (2025)	Translational exposomics (Empirical integration study)	Genome–exposome biomarkers	Personalized toxicity risk	Supported personalized risk prediction via exposomics biomarkers.
Shin et al. (2025)	DILI phenotyping (High-throughput transcriptomics study)	Transcriptomics-based classification	Liver injury phenotypes	Distinguished liver injury subtypes using transcriptomics.
Singh et al. (2024)	AI carcinogenic risk prediction (Computational ML study)	Genomic instability biomarkers + AI	Carcinogenicity risk	Improved carcinogenicity prediction with AI biomarkers.
Singh et al. (2023)	Precision toxicology (Multi-omics computational study)	AI + OMICs integration	Personalized toxicogenomics	Advanced precision toxicity prediction through multi-omics AI.
Su et al. (2022)	Multi-organ prediction (Computational ML study)	Multi-label toxicogenomics model	Multi-organ pathology	Predicted multi-organ toxicity outcomes using ML models.
Zhang et al. (2015)	Systems pharmacology biomarkers (Translational framework study)	Biomarker-based safety assessment	Drug safety evaluation	Strengthened biomarker-based approaches for drug safety assessment.

3.3 Risk of Bias Assessment

Critical appraisal tools were used in determining the risk of bias JBI and CASP critical appraisal tools. In general, the majority of the studies reported low to moderate risk of bias with the higher levels of worries referring to the validation of computational models and exposure-related confounding (Table

Table 2. Thematic Risk of Bias Summary of Included Studies

Theme Category	Studies Included	Risk of Bias Level	Key Methodological Concern
High-throughput transcriptomics (DILI, mechanistic profiling)	Bergen (2025), Harrill (2024), Shin (2025)	Low	Strong datasets and reproducible pipelines
Genomic biomarker signature development	Li (2015), Corton (2022)	Low–Moderate	Requires broader validation for regulatory translation
AI/ML-based biomarker prediction models	Rahman (2022), Su (2022), Rana (2025), Singh (2023, 2024)	Moderate	Dataset heterogeneity and model generalizability
Epigenetic exposure biomarkers	Chen (2024)	Moderate	Potential confounding due to environmental variability
In vitro organ-specific toxicity models	Sakolish (2025)	Low–Moderate	Limited external validation across diverse populations
Exposomics and personalized medicine integration	Sarigiannis (2025)	Moderate	Complexity linking exposome biomarkers with clinical outcomes
Systems pharmacology safety frameworks	Zhang (2015)	Low	Conceptually robust but requires further empirical expansion

3.4 Transcriptomics-Based Biomarkers in Toxicity Assessment

In the studies covered, transcriptomics was the most used platform of biomarkers when it comes to toxicity. Gene expression profiling on a large scale was broadly used to discover mechanistic toxicity signatures and enhance adverse drug response prediction. Mass toxicogenomics resources facilitated the enhancement of drug induced liver injury (DILI) phenotype classification, which tracks the hepatotoxicity consequences that can be detected and stratified earlier (Bergen et al., 2025; Shin et al., 2025). Moreover, transcriptomic signature screening turned out to be helpful in terms of mechanistic inference and chemical grouping, proving to be applicable to the next-generation risk assessment strategies (Harrill et al., 2024). The establishment of basic work also proved that the optimized toxicogenomic signatures can be used with reasonable accuracy in the detection of the genotoxicity responses in the human in vitro systems (Li et al., 2015). Altogether, transcriptomics biomarkers are one of the pillars of predictive toxicology and precision safety assessment.

3.5 AI and Machine Learning for Predictive Biomarker Discovery

Table 3 outlines the key artificial intelligence and machine learning applications in the available studies. The evidence shows that there is an increasing use of computer models to discover toxicogenomics-derived biomarkers, multi-organ toxicity outcomes prediction, and carcinogenic risk assessment. These artificial intelligence-based solutions enhance the scalability and mechanistic interpretability and regulatory applicability of biomarker-based toxicity prediction and the development of precision toxicology.

Table 3. AI and Machine Learning Applications in Predictive Biomarker Discovery

Study (Author, Year)	AI/ML Approach Used	Biomarker Focus	Toxicity Prediction Outcome
Rahman et al. (2022)	Machine learning-based biomarker identification	Toxicogenomics-derived genomic biomarkers	Linked biomarkers with regulatory-relevant phenotypic toxicity endpoints
Su et al. (2022)	Multi-label learning model	Multi-organ toxicogenomics biomarkers	Predicted drug-induced pathology across multiple organs
Rana et al. (2025)	Hierarchical model-driven biomarker discovery tool (ToxAssay)	Transcriptomic biomarker discovery pipeline	Improved scalability and interpretability of toxicogenomics screening
Singh et al. (2024)	AI/ML-based carcinogenic risk prediction	Genomic instability biomarkers	Enhanced prediction of chemical-induced carcinogenic potential
Singh et al. (2023)	Integrative AI + multi-omics framework	OMICs-driven precision toxicology biomarkers	Advanced personalized toxicity prediction through omics integration
Harrill et al. (2024)	Transcriptomic signature-based computational grouping	High-throughput transcriptomic biomarkers	Supported mechanistic inference and chemical classification for toxicity assessment

3.6 Epigenetic, Exposomic, and Organ-Specific Biomarkers

In addition to the transcriptomics, the evidence also showed the significance of epigenetic and exposure-related biomarkers in toxicity monitoring. Signatures of DNA methylation were proposed as sensitive biomarkers in people exposed to various industrial pollutants and showed their value in real-life assessment of exposure toxicity (Chen et al., 2024). The particular part of the new biomarkers was the organ-specific development that could be observed in liver and kidney toxicity studies. The prediction of DILI using transcriptomics-based studies enhanced hepatotoxicity phenotyping (Bergen et al., 2025; Shin et al., 2025), and comparative proximal tubule in vitro models facilitated the enhanced nephrotoxicity testing platforms (Sakolish et al., 2025). Also, genome-environment interaction and personalized toxicity risk were connected, which supports the applicability of personalized medicine strategies, and translational exposomics frameworks (Sarigiannis et al., 2025).

3.7 Emerging Trends in Toxicogenomics and Personalized Toxicity Assessment

Table 4 identifies the significant developing trends within the included studies, such as the growth of human toxicogenomics resources, the rise in the use of AI-mediated biomarker discovery, and the growth in the adoption of genomic frameworks by regulation. The combination of exposomics, epigenetics, and organ-specific predictive models also exhibits the transition towards more tailored and even mechanistic toxicity testing.

Table 4. Emerging Trends in Toxicogenomics and Personalized Toxicity Assessment

Emerging Trend	Description	Supporting Included Studies
Large-scale human toxicogenomics resources	Human transcriptomic datasets improving toxicity prediction, especially DILI.	Bergen et al. (2025); Shin et al. (2025)

AI/ML-enabled biomarker discovery	Computational models enhancing biomarker identification and toxicity prediction.	Rahman et al. (2022); Su et al. (2022); Rana et al. (2025); Singh et al. (2024)
Regulatory transition toward genomic biomarkers	Genomic frameworks reducing reliance on animal carcinogenicity testing.	Corton et al. (2022); Zhang et al. (2015)
Exposomics and personalized medicine integration	Genome–exposome biomarkers supporting individualized toxicity risk assessment.	Sarigiannis et al. (2025); Chen et al. (2024)
Expansion to epigenetic biomarkers	DNA methylation signatures emerging as exposure and toxicity indicators.	Chen et al. (2024)
Organ-specific predictive toxicity modeling	Liver- and kidney-focused biomarker models improving targeted screening.	Sakolish et al. (2025); Bergen et al. (2025); Shin et al. (2025)

4. Discussion

The current systematic literature review summarized the empirical data concerning the use of biomarkers in the measurement of toxicity, especially the recent developments in toxicogenomics and personalized medicine. In general, these results indicate that toxicity assessment using biomarkers is changing by helping to detect adverse effects at an earlier stage, assess mechanistic knowledge better, and aid in a more predictive and personalized toxicity analysis. The thematic synthesis identifies transcriptomics as the new major platform of biomarkers, the fast convergence of artificial intelligence and machine learning in predictive toxicology, and the new role of epigenetics and exposomics in precision risk assessment.

One of the key conclusions of this review is the prevalence of biomarkers of transcriptomics in the contemporary toxicity assessment. The technology of high-throughput gene expression profiling has been a cornerstone technology in the identification of mechanistic toxicity signatures and prediction of adverse drug responses (Bergen et al., 2025; Harrill et al., 2024). Transcriptomic atlases and large-scale data have further assisted in the definition of drug induced liver injury (DILI) prediction and classification to aid in the previous detection of hepatotoxicity (Shin et al., 2025). The advances are in line with general progress in the modeling of toxicogenomics of regulatory risk assessment (Serra et al., 2020). Simultaneously, AI-based and machine learning-based computational methods have contributed greatly to the biomarker discovery. The toxicogenomics biomarkers have been modeled using machine learning systems to predict the regulatory-relevant toxicity endpoints and enhanced prediction capabilities across multi-organ systems (Rahman et al., 2022; Su et al., 2022). The models based on AI have also been effectively used in predicting carcinogenic risks using genomic instability biomarkers (Singh et al., 2024). In addition, omics-based screening platforms are scalable because hierarchical biomarker discovery tools like ToxAssay can be scaled (Rana et al., 2025). Lastly, the review underlines the increased applicability of epigenetic and exposomic biomarkers. DNA methylation patterns have appeared as delicate markers of environmental pollutant exposure that can be used to join the real-life toxicity evaluation process (Chen et al., 2024). It is also noted that the frameworks of translational exposomics highlight the necessity to incorporate genome-environmental interactions in the personalized toxicity risk prediction (Sarigiannis et al., 2025).

The theme findings highlight the importance of biomarkers in the development of organ-specific toxicity. DILI and liver toxicity are areas where toxicogenomics has been a priority area of study because of its clinical and regulatory interest. Massive transcriptomic datasets have enhanced the stratification of liver injury phenotypes mechanistically and enhanced accuracy in the assessment of hepatotoxicity (Bergen et al., 2025; Shin et al., 2025). These results are in line with the general acceptance of toxicogenomics as an important instrument of predicting early hepatotoxicity (Lauschke, 2021). Optimization of proximal tubule in vitro models also reflected nephrotoxicity, which established optimal renal systems in drug-induced kidney toxicity experiments (Sakolish et al.,

2025). This development of the organ-specific models is necessary to enhance predictive accuracy in a way that is not possible with the traditional toxicity endpoints. Moreover, genomic biomarker systems are gaining use in an attempt to aid the assessment of carcinogenicity risk and eliminate the use of rodent models (Corton et al., 2022). This change is associated with the rising demand of more mechanistic and human-relevant testing paradigms of toxicity (Turkez et al., 2017).

The articles presented demonstrate that there are a number of crucial new tendencies defining the current toxicity testing. To begin with, there is a definite proliferation of massive human toxicogenomics measurements, which will allow to predict the outcome of drug-induced toxicity more accurately (Bergen et al., 2025). Second, mechanistic toxicity prediction through AI is also developing at an impressive pace, and computational models enhance chemical taxonomies, predict risk of cancer, and bio-discover biomarkers (Rahman et al., 2022; Singh et al., 2024). Such tendencies follow the general systems biology strategies of combining multi-dimensional data to predict preclinical toxicity (Soy & Salwadkar, 2025). Third, the regulatory toxicology is gradually moving the traditional animal testing to the use of genomic biomarker-based systems. Joint efforts have shown that genomic markers could be used to predict tumorigenic potential, which can be used in the next-generation risk-level approaches (Corton et al., 2022; Zhang et al., 2015). The use of toxicogenomics is increasing worldwide, as well as in the assessment of the safety of intricate substances, including conventional medicines (Xueping et al., 2020).

One of the implications of the results is the increased integration of toxicogenomics and personalized medicine. Biomarkers can offer a chance to conduct a personalized safety assessment as it embodies genetic susceptibility, molecular pathway imbalances, and variability due to exposures. As discussed by exposomics models, genome-exposome integration facilitates the precision toxicology strategies that outgrow the population means prediction to the individualized risk prediction (Sarigiannis et al., 2025; Niedzwiecki et al., 2019). Besides, as transcriptomics prevails in use, metabolomics is becoming a genuinely translational instrument of precision medicine due to its ability to shed functional biochemical light on the mechanism of toxicity (Schmidt et al., 2021). Collectively, these trends suggest that the innovation of biomarkers is necessary to take the personalized toxicity prediction forward and enhance safety in the treatment.

The results of this review are consistent with the current toxicology studies that highlight the potential of omics technologies in the next generation risk assessment. Transcriptomics and toxicogenomics are also being seen as the basis of mechanistic toxicity modeling and regulatory translation (Serra et al., 2020; Qin et al., 2016). Moreover, the combination of AI and systems biology models is associated with the general trends in predictive toxicology and computational safety analysis (Soy & Salwadkar, 2025). Review findings also facilitate the continued changes towards the use of genomic biomarkers in the assessment of carcinogenicity and organ-specific toxicity (Pandiri et al., 2023). This review has a number of strengths. It also employed a PRISMA-based systematic approach, which guaranteed transparency and reproducibility. Recent developments in the field of toxicogenomics, AI-based biomarker discovery, and precision toxicology were reflected by the focus on the empirical studies published since 2015. Furthermore, thematic synthesis allowed the high-ranking incorporation of different types of biomarkers and toxicity endpoints into the evidence base that was incorporated.

The review is limited in spite of its contributions. The sample of selected studies was very low (n = 14) and it indicates strict eligibility criteria. There was a high level of heterogeneity in terms of study designs, biomarker platforms and toxicity outcomes, which made it impossible to conduct quantitative meta-analysis. Besides, unpredictability in validating biomarker methods and extrinsic generalizability might inhibit clinical and regulatory translations. To make regulation adoption more robust, future studies are advised to focus on a standardized approach to biomarker validation and cross-cohort studies of reproducibility. Increased focus should be put on clinical translation of toxicogenomics biomarkers, especially in the form of multi-omics data integration of transcriptomics, epigenetics, and metabolomics (Schmidt et al., 2021). Moreover, the further evolution of AI-based predictive models and systems biology will be necessary to improve the next-generation risk assessment and individual toxicity analysis (Rana et al., 2025; Soy & Salwadkar, 2025). Finally, the

biomarker innovation and regulatory science will help in the provision of safer therapeutics, less animal testing, and personalised forecast of toxicity.

5. Conclusion

This thematic literature review shows that biomarkers are rapidly changing the toxicity testing in that they allow for earlier, more mechanistic, and more predictive testing of negative biological impacts. Included work Toxicogenomics-based biomarkers, especially transcriptomics, appeared to be the platform of choice in signatures of toxicity and enhance risk prediction of key endpoints of drug-induced liver injury, nephrotoxicity, and carcinogenicity. Moreover, artificial intelligence and machine learning solutions were mentioned as key contributors to innovation, which improved biomarker discovery, chemical grouping, and prediction of multi-organ toxicity. New tools like epigenetic and exposomic biomarkers extend again the scope of the toxicity monitoring to real-life exposure situations and contribute to the personalized approach to assessing safety. The main value of this review is that it provides evidence of regulatory shifts toward genomic biomarker models that diminish the reliance on the traditional and animal-based testing and enhance next-generation risk assessment approaches. Such developments have significant practical implications, such as better drug safety screening, better mechanistic explanation of toxic responses, and greater assistance in predicting toxicity risks personally. Beyond these suggestions, the use of high-throughput omics biomarkers should be extended in the future, AI-enabled predictive models should be introduced into safety pharmacology, and tighter regulatory quality assurance of biomarker qualification and validation is necessary. Altogether, the current state of toxicity assessment is changing into a more predictive, mechanistic and personalized paradigm, and biomarker innovation is in the center of defining the future of precision toxicology.

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