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REVIEW

Radiogenomics in oncology: image-genome integration for personalized medicine

Radiogenómica en oncología: integración imagen-genoma para medicina personalizada

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ABSTRACT

Introduction: radiogenomics, which combines medical imaging data with genomic profiling, has emerged as a key tool in precision oncology. This noninvasive approach improves the diagnosis and prognosis of tumors such as lung, rectal, glioma, and breast cancer.
Objective: a systematic review (PRISMA 2020) was conducted of studies published between 2020 and 2025, extracted from PubMed, Scopus, Web of Science, ScienceDirect, and the Cochrane Library. Of 670 articles found, 21 met the inclusion criteria.
Method: this was a systematic review following the PRISMA 2020 guidelines. Original studies, reviews, and meta-analyses published in English or Spanish were included. Searches were conducted in PubMed, Scopus, Web of Science, ScienceDirect, and the Cochrane Library.
Results: of a total of 670 articles retrieved, 21 met the inclusion criteria. Most studies demonstrated a high predictive capacity of radiogenomic models to identify mutations such as EGFR and KRAS.
Conclusions: this study underscores the need to establish multicenter protocols and robust validations to ensure their clinical applicability and consolidate their role in personalized medicine.

Keywords: Radiogenomics; Image Interpretation; Magnetic Resonance Imaging; Precision Medicine; Biomarkers; Tumor; Artificial Intelligence; Oncology.

RESUMEN

Introducción: la radiogenómica, que combina datos de imagen médica con perfiles genómicos, se ha posicionado como herramienta clave en oncología de precisión. Este enfoque no invasivo mejora el diagnóstico y pronóstico de tumores como cáncer de pulmón, recto, gliomas y mama.
Objetivo: se realizó una revisión sistemática (PRISMA 2020) de estudios publicados entre 2020 y 2025, extraídos de PubMed, Scopus, Web of Science, ScienceDirect y Cochrane Library. De 670 artículos encontrados, 21 cumplieron los criterios de inclusión.
Método: se trata de una revisión sistemática siguiendo la guía PRISMA 2020. Se incluyeron estudios originales, revisiones y metaanálisis publicados en inglés o español. Las búsquedas se realizaron en PubMed, Scopus, Web of Science, ScienceDirect y Cochrane Library.
Resultados: de un total de 670 artículos recuperados, 21 cumplieron con los criterios de inclusión. La mayoría de los estudios demostraron una alta capacidad predictiva de modelos radiogenómicos para identificar mutaciones como EGFR y KRAS.
Conclusiones: este estudio subraya la necesidad de establecer protocolos multicéntricos y validaciones robustas para garantizar su aplicabilidad clínica y consolidar su rol en la medicina personalizada.

Palabras clave: Radiogenómica; Interpretación de Imágenes; Resonancia Magnética; Medicina de Precisión; Biomarcadores; Tumor; Inteligencia Artificial; Oncología.

INTRODUCTION

In the era of precision medicine, radiogenomics is emerging as a strategic tool in oncology, as it relates quantitative characteristics obtained from medical images to genomic profiles of the tumor. This approach allows for the description of intratumoral heterogeneity and the anticipation of molecular alterations, favoring the development of diagnostic and prognostic models with remarkable predictive power.[1,2] An example of this is the integration of tomography, resonance, and PET/CT data to predict mutations in genes such as EGFR, TP53, or KRAS, with areas under the curve (AUC) close to 0,80–0,90, supported by artificial intelligence techniques that increase prognostic stratification capacity.[3,4,5]

Despite these advances, the challenge of ensuring the reproducibility and clinical application of the models remains. Several reviews have pointed to wide methodological variability, ranging from image acquisition protocols to segmentation and feature selection.[6] Although there are validated models in neoplasms such as lung cancer or glioblastoma, few meet the criteria for multicenter standardization and reporting guidelines such as the Radiomics Quality Score (RQS), which aims to evaluate the methodological quality of radiomics and radiogenomics studies, or the Transparent Reporting of a Multivariable Prediction Model for Individual Prognosis or Diagnosis (TRIPOD), which establishes guidelines for the development and validation of predictive models.[7,8]

In this scenario, a gap becomes apparent: most previous reviews have focused on technical aspects or specific tumors, but there is a lack of an updated analysis that integrates the diagnostic and prognostic performance of recently published radiogenomic models, together with practical recommendations for their clinical standardization. This absence limits the possibility of translating the findings into medical practice.

The purpose of this article is precisely to critically review the evidence published between 2020 and 2025 on radiogenomic models in oncology, synthesize the findings in terms of diagnostic and prognostic performance, and propose technical recommendations that strengthen the reproducibility and clinical applicability of this approach. The aim is to contribute to the establishment of standardized protocols and to encourage collaborative research that promotes the integration of radiogenomics into personalized medicine.

METHOD

This study is a systematic review of the literature, developed in accordance with the PRISMA 2020 guidelines. Although international methodological guidelines were followed, the review could not be registered in PROSPERO, as this platform only accepts reviews with direct clinical outcomes in patients or animals, and the present study focuses on predictive radiogenomics models based on imaging and genomic data. The objective was to identify, evaluate, and synthesize the available scientific evidence on the integration of radiogenomics in personalized medicine-oriented oncology.

Inclusion and exclusion criteria

Original research articles published in English or Spanish between January 2020 and April 2025 were included, which evaluated the correlation between quantitative radiological characteristics and genomic profiles in cancer patients, as well as their application in diagnosis, prognosis, or prediction of therapeutic response. Case studies, conference abstracts, editorials, letters to the editor, narrative reviews, and systematic reviews were excluded, as the focus was on synthesizing primary evidence.

Sources of information and search strategy

The literature search was conducted between April and May 2025 in the PubMed, Scopus, Web of Science, and ScienceDirect databases. MeSH terms and related keywords were used, combined with Boolean operators. The complete search strategy was: (“radiogenomics” OR “radiogenomics” OR “radiogenómica” OR “radiomics” OR “radiómica”) AND (“oncology” OR “oncology” OR “oncología” OR “cancer” OR “tumor” OR “neoplasms”) AND (“personalized medicine” OR “precision medicine” OR “personalized medicine”) AND (“imaging” OR “medical imaging” OR “CT” OR “MRI” OR “PET”) AND (“genomics” OR “genómica” OR “mutation” OR “genetic profile”) AND (“machine learning” OR “deep learning” OR “artificial intelligence”). In addition, the reference lists of the selected articles were reviewed to identify relevant studies not retrieved in the initial search.

Study selection

The results were exported to Zotero, and duplicates were removed. The selection was carried out in two phases: reading of titles and abstracts by two independent reviewers, followed by full-text evaluation of potentially eligible studies. Discrepancies were resolved by consensus among the authors. Agreement between

reviewers was estimated using the Kappa coefficient.

Data extraction and synthesis

A standardized template was designed for data extraction, which included: author(s), year, country, type of cancer evaluated, sample size, imaging technique used, radiogenomic analysis methodology, software or tools applied, performance metrics (AUC, accuracy, sensitivity, specificity), main findings, reported clinical utility, and limitations.

The synthesis was performed in a structured narrative format, organizing the results around three axes: (i) diagnostic performance of radiogenomic models, (ii) prognostic and predictive value in therapeutic response, and (iii) methodological and technical aspects that condition their reproducibility.

Methodological quality assessment

The quality of the prediction model studies was assessed using the TRIPOD guideline, currently considered the standard for reporting and evaluating diagnostic and prognostic predictive models, and the ROBIS tool was used for previous systematic reviews.

A literature review was conducted following the predefined search strategy, and 21 articles were included. Screening was performed independently by two reviewers in two phases (title/abstract and full text) using a standardized form. Inter-rater agreement was quantified using Cohen's Kappa statistic, showing substantial agreement in the title/abstract phase and almost perfect agreement in the full-text reading, according to the Landis and Koch classification. Discrepancies were resolved by consensus, and when they persisted, by the opinion of a third, independent reviewer, although this was not necessary. Table 1 summarizes the records retrieved by the database and their refinement, table 2 shows the records after applying the inclusion and exclusion criteria, and the PRISMA 2020 diagram documents the complete selection flow.

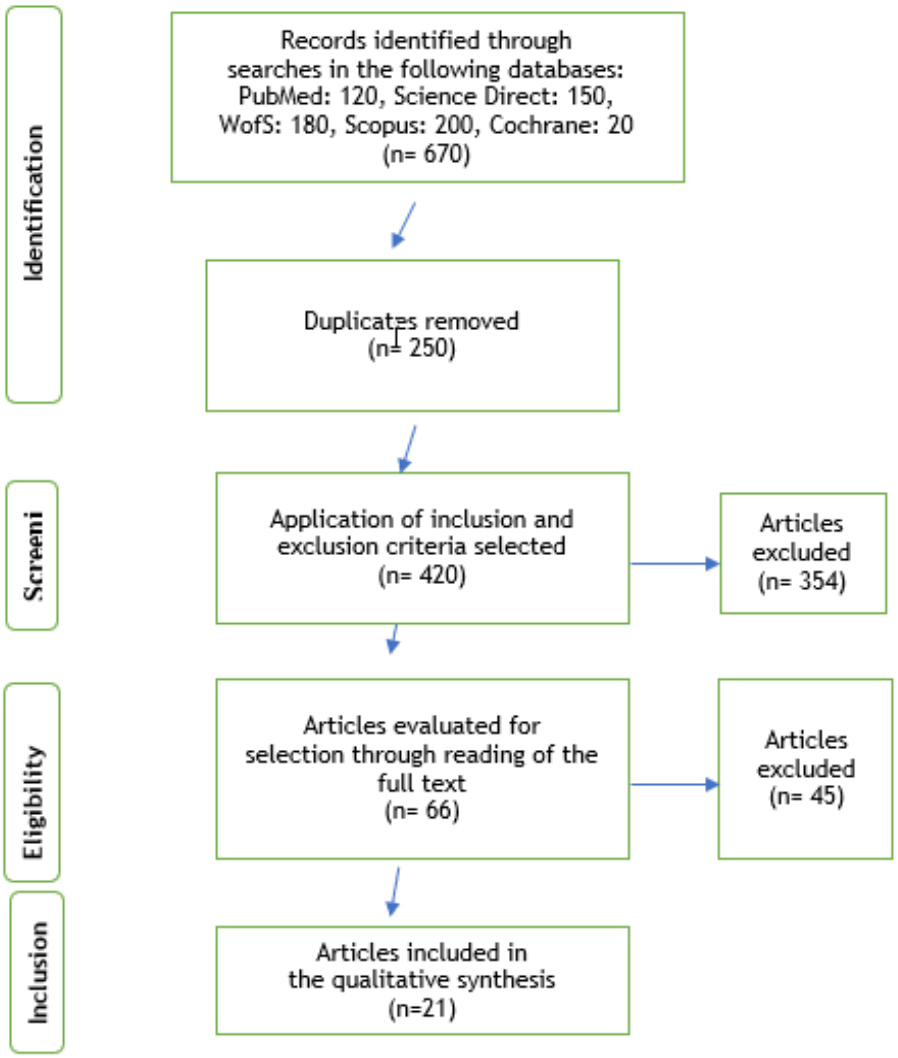


Figure 1. PRISMA study selection flow diagram

RESULTS

The search in five databases, from 2020 to 2025, retrieved 670 records. PubMed 120; Scopus 200; Web of Science 180; ScienceDirect 150; Cochrane 20. After removing 250 duplicates, 420 records were screened for title and abstract, of which 354 were excluded for not meeting the eligibility criteria. Sixty-six articles were evaluated in full text, and 45 were excluded for the following reasons: absence of radiomics–genomics integration (n=14), ineligible design (letters, editorials, or case series; n=11), non-oncological population (n=8), insufficient data or methodology (n=8), and overlap of cohorts (n=4). Consequently, 21 studies met the criteria and were included in the qualitative synthesis. The complete flow is shown in the PRISMA 2020 diagram (figure 1), and the reasons for full-text exclusion are detailed in table 2.

Table 1. Search strategy

Database	Documents retrieved	Duplicates removed	Unique records after deduplication	Excluded in screening (title/abstract)	Evaluated in full text	Included	Excluded at full text
PubMed	120	28	92	77	15	6	9
Scopus	200	90	110	85	25	7	18
Web of Science	180	80	100	87	13	3	10
ScienceDirect	150	50	100	91	9	3	6
Cochrane Library	20	2	18	14	4	2	2
TOTAL	670	250	420	354	66	21	45

Table 2 . Reasons for exclusion from full text (n=45)

Reason for exclusion	n	Operational criterion
Non-oncological population	8	Series on non-tumor pathology or animal models without clear translation to cancer.
Ineligible design (cases/letters/editorials)	11	Opinions, letters, case series without comparison/validation.
No explicit radiomics–genomics correlation	14	Radiomics-only or genomics-only studies without operational integration.
Insufficient data (incomplete metrics or methods)	8	No AUC/accuracy/CI; incomplete or irreproducible pipeline.
Duplicate cohort/overlap.	4	Same population reused without additional relevant analysis.
Total	4	

DISCUSSION

The results point to tangible clinical potential when the questions are clearly established, for example, inference of mutations or prognostic stratification in specific scenarios, and when working with well-curated datasets. The heterogeneity of designs, analytical pipelines, and methodological reports conditions the comparability and robustness of the conclusions.[9,10,11]

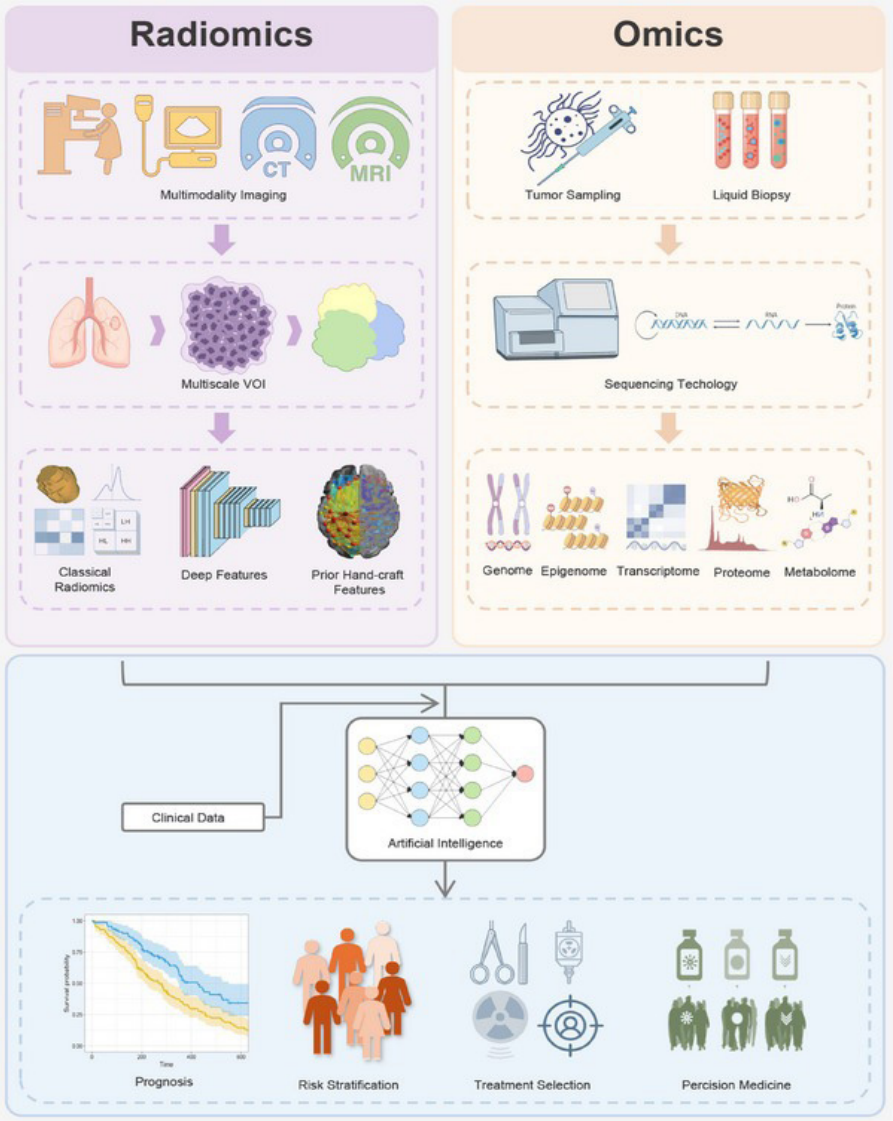
When examining studies by tumor location and imaging modality, a relatively consistent pattern is observed in lung cancer: CT-based models, with or without PET/CT, aimed at predicting point mutations and stratifying risk tend to report moderate to high performance. In neuro-oncology, multiparametric magnetic resonance imaging approaches have proven helpful for molecular classification and have shown more variable results when the objective is purely prognostic. In other, more common tumors such as breast, liver, and head and neck, the signal is more heterogeneous. There are reports with acceptable discriminatory capacity in specific tasks; however, the frequency of external validations is lower, and the dispersion of metrics is greater. The most commonly reported performance measures have been area under the curve (AUC), accuracy, and sensitivity/specificity.[1,2,3,15]

A cross-sectional reading of these metrics suggests that performance improves when radiogenomic descriptors are combined with simple, easily accessible clinical variables such as age, stage, or treatment, as opposed to the image alone. Even so, the inter-study variation resulting from preprocessing, segmentation, selection, and stability of functions and validation strategies currently prevents us from affirming the consistent superiority of one technique or modality over another beyond specific examinations, such as chest CT for epidermal growth receptor or multiparametric MRI for molecular signatures in gliomas.[16,17]

Clinical extrapolation remains very limited. The area under the curve is high, but these values cannot be sustained without calibration or external validation, whether geographical or temporal. According to RQS,

segmentation and clinical justification are usually well described, but external validation, stability testing, impact/cost assessment, and code/data availability are lacking. With TRIPOD, there are repeated gaps in sample size, missing data, calibration, and reclassification, and little reporting of temporal/geographic validations. In PROBAST, biases due to participant selection, non-standardized predictors (equipment dependence), and analyses with risk of overfitting predominate.[10] Where there was harmonization and standardization of image flow and functions, performance was more stable; when calibration was lacking and there was only internal validation, high metrics with little generalization appeared. This is in line with already known barriers: small samples, heterogeneity of pipelines, lack of pre-registration, and lack of reproducible code.

In practice, radiogenomics complements, but does not replace, biopsy: it helps prioritize molecular testing, anticipate alterations, and stratify treatment. To move forward, it is necessary to standardize the acquisition/extraction of results, continue using TRIPOD, evaluate bias with PROBAST, and incorporate external validation, calibration, and clinical utility.[11,12] In addition, code and functionality dictionaries should be shared and harmonization applied in order to improve reproducibility. Its clinical adoption requires multicenter validation, explicit calibration, pipeline harmonization, and transparent reporting.



Sourse: information obtained from He et al.[14]

Figure 2. Schematic diagram illustrating the integration of radiomics with omics data for precision cancer care

The first step is to collect data, including images and biological samples. From these resources, various dimensions of radiomic characteristics and molecular signatures of cancers are extracted and refined. Finally, radiomic and omic data are interconnected and integrated using advanced artificial intelligence algorithms to build accurate clinical prediction models.

Beyond its diagnostic potential, radiogenomics allows the construction of spatial and contextual maps that relate tumor biology to its microenvironment, opening up new perspectives for more precise therapeutic

interventions. In line with this, radiomics enables the extraction of quantitative information from medical images and the linking of this information to molecular profiles, thereby improving diagnosis and personalized medicine. These advanced techniques transform images into clinically relevant data, optimizing tumor characterization, therapeutic prediction, and the monitoring of oncological diseases without the need for invasive interventions.[18]

Despite all the benefits, its large-scale implementation in clinical practice still requires overcoming barriers related to system interoperability and external validation of the models developed, among other challenges, such as the need for standardization in the acquisition and processing of medical images, since technical variability between equipment and protocols can affect the reproducibility of findings.[13] Likewise, the validation of predictive models in diverse populations and heterogeneous clinical contexts is essential to ensure their universal applicability and avoid biases that limit their use. From an ethical perspective, dilemmas arise regarding the privacy of biomedical data and the protection of patients' genetic identities, especially when large-scale image and genomic information databases are integrated. The adoption of advanced technologies poses the risk of deepening inequalities in access to personalized health services, which requires clear policies to ensure equity and distributive justice in their implementation.[14,19,20,21]

Table 3. Review articles

Article name	Publication date and authors	Methodology and objective	Conclusions and recommendations
The era of radiogenomics in precision medicine: an emerging approach to support diagnosis, treatment decisions, and prognostication in oncology	2020 - Shui et al.[1]	Developed using a narrative approach with the aim of synthesizing the integration of radiomic and genomic data in the context of precision oncology. The methodology included the collection and preprocessing of medical images and molecular profiles, the segmentation of tumor regions, and the extraction of quantitative features through radiomics techniques. Subsequently, machine learning algorithms were applied to construct predictive models for diagnosis, prognosis, and personalized therapeutic selection.	Radiogenomics is positioned as an inevitable consequence of precision medicine, offering significant advantages over conventional methods, such as cost reduction, access to comprehensive tumor information beyond the limitations of biopsies, and higher spatial resolution to capture tumor heterogeneity. The automated generation of quantitative data from medical images, combined with clinical and genomic profiles in open databases, consolidates radiogenomics as a solid link between tumor phenotype and genotype, facilitating the creation of predictive and prognostic models with clinical potential.
Radiogenomics in rectal cancer: an emerging approach for personalized medicine.	2023 - O'Sullivan et al.[15]	Study developed through a systematic review based on the PRISMA 2020 guidelines, with the aim of analyzing contemporary applications of radiogenomics in the management of rectal cancer. The methodology included a structured search of scientific databases.	Radiogenomics shows high potential in predicting therapeutic response in rectal cancer by combining structural image information with molecular characteristics of the tumor. This integration allows for improved patient stratification and optimized clinical decisions, such as the selection of neoadjuvant therapies or the identification of candidates for less invasive treatments. However, its clinical applicability is limited by the lack of external validation of existing models and methodological heterogeneity between studies. The promise of radiogenomics as a non-invasive tool, which can be considered a "virtual biopsy," requires overcoming significant challenges related to workflow standardization , inter-institutional reproducibility, and data quality. The absence of uniform protocols for image acquisition and tumor segmentation compromises the comparability of results, highlighting the need for collaborative, multicenter initiatives to strengthen the evidence base and facilitate its incorporation into routine oncology practice.

PET radiogenomics and imaging phenotypes: current knowledge and future perspectives in cancer diagnosis	2025 - Filippi et al.[4]	The study was designed as a systematic review, developed under the PRISMA guidelines, with the aim of synthesizing the current evidence on the application of PET-based radiogenomics in oncology. An exhaustive search was conducted in databases such as PubMed, Scopus, and Web of Science, including publications up to October 31, 2024. Original studies integrating radiomic and genomic analysis in human populations were selected, and variables related to tumor type, radiopharmaceutical used, segmentation methods, statistical strategies applied, and clinical outcomes evaluated were extracted. The methodological quality of each study was assessed using the Radiomics Quality Score (RQS 2.0) scale, considering criteria such as external validation, data reproducibility, transparency in methodology, and multicenter design, which allowed for a critical evaluation of the scientific rigor of the included studies.	The combination of radiomic data obtained by PET with genomic information has shown significant potential for improving tumor characterization, particularly in terms of predicting specific mutations such as EGFR or KRAS. This approach allows for a more accurate assessment of the tumor's biological profile, thus contributing to the personalization of treatment. It is important to consider the limited methodological quality of many of the studies included, marked by a lack of external validation, the use of retrospective designs, and poor standardization of workflows. This situation compromises the reproducibility of the findings and hinders their clinical application, underscoring the urgent need for prospective, multicenter studies with rigorously structured methodological protocols.
Integrating radiogenomics and machine learning in musculoskeletal oncology care	2025 - Kumar et al.[5]	Advanced computational methodology to integrate medical imaging data and genomic profiles in the context of musculoskeletal oncology. Radiomic variables were extracted from different imaging techniques and combined with transcriptomic, epigenetic, and mutational data to create a multimodal profile. To handle the high dimensionality of the data, reduction techniques such as LASSO and PCA were applied, and then regression and classification models were used to construct predictors of tumor molecular characteristics. Multimodal fusion enabled the generation of "virtual biopsies" using artificial intelligence, with the aim of detecting key mutations and guiding therapeutic decisions.	The integration of radiomic and genomic data using artificial intelligence tools represents a promising strategy for improving the diagnosis and molecular characterization of musculoskeletal tumors. This approach allows the prediction of relevant genetic alterations without the need for invasive procedures, promoting safer and more efficient personalized medicine. Despite the demonstrated potential of the multimodal models developed, their clinical implementation still faces significant challenges, such as workflow standardization, the need for robust databases, and external validation in large cohorts. Therefore, it is concluded that future research should focus on improving reproducibility and developing collaborative protocols to facilitate their adoption in oncology medical practice.
Radiogenomics: bridging the gap between imaging and genomics	2024 - Vivacqua et al.[16]	The study was designed as a comprehensive narrative review to analyze the current state of radiogenomics in the context of precision oncology. Relevant scientific information was compiled by combining the analysis of high-resolution medical images and genomic data derived from tumor profiles. A methodological framework was described that includes the high quantitative extraction of image features (radiomics) using artificial intelligence techniques, together with systematic integration with omic data such as genetic, transcriptomic, and proteomic sequences. Specific clinical applications in solid tumors (such as breast, lung, and glioma) were then identified, and technical advances, current challenges, and potential areas for future research were evaluated.	Radiogenomics is establishing itself as a key tool for precision medicine, enabling non-invasive correlation between tumor phenotypic characteristics visible in medical images and underlying molecular alterations. This approach facilitates the prediction of genomic profiles relevant to diagnosis, prognosis, and therapeutic selection, contributing to more personalized and efficient decision-making in oncology. Despite its transformative potential, the clinical implementation of radiogenomics still faces significant limitations, such as the lack of standardization in image acquisition and processing, the scarcity of prospective multicenter studies, and the need for external validation of predictive models.

The prognostic value of radiogenomics using CT in patients with lung cancer: a systematic review	2024 - Jiang et al.[3]	The study was conducted as a systematic review according to PRISMA guidelines and was pre-registered in PROSPERO (CRD42023472571). A comprehensive search was conducted in key databases such as PubMed, Embase, Web of Science, and Cochrane Library, up to May 13, 2024, using predefined inclusion criteria to identify research combining radiomics and genomics in prognostic models for lung cancer. Methodological quality was assessed using the radiomics quality score (RQS) and the PROBAST tool for risk of bias. Finally, the AUC and C-index values of the radiogenomic models were analyzed and compared with those of the unimodal models, highlighting the superior performance of the former.	The combination of radiomic features extracted from computed tomography (CT) with genomic data significantly improves the predictive capacity of prognostic models in lung cancer patients, outperforming unimodal approaches. This integration allows for a more accurate assessment of tumor behavior, favoring risk stratification and personalized clinical decision-making. Despite the potential value of radiogenomic models, their clinical applicability is still limited by the low methodological quality of several studies, heterogeneity in segmentation and data extraction methods, and limited external validation. These findings underscore the need for prospective, standardized, multicenter studies to more robustly translate this emerging approach into clinical practice.
Imaging genomics of cancer: a bibliometric analysis and review	2025 - Gou et al.[13]	Systematic review with bibliometric analysis, focusing on the field of radiogenomics applied to cancer. A structured search was conducted in the PubMed, Embase, and Web of Science databases up to July 2024, using controlled terms and combinations such as “radiogenomics” and “cancer.” The selection of studies was performed independently by two researchers, applying inclusion criteria that restricted the articles to original research in humans, published in English, and using radiogenomics methodologies. Subsequently, a detailed data extraction was carried ou , and finally a bibliometric analysis was integrated using the Bibliometrix and VOSviewer packages, which allowed mapping publication trends, collaboration networks, and citation patterns in the area.	Research in oncological radiogenomics has grown exponentially over the last decade, revealing a consolidated interest in integrating medical imaging characteristics with genomic data to improve the diagnosis, prognosis, and therapeutic personalization of cancer. Despite methodological advances in the use of artificial intelligence and radiomics tools to extract complex features from medical images, the heterogeneity of the approaches used and the lack of standardization of workflows represent an obstacle to the consolidation of radiogenomics as a clinical tool. It is concluded that future research should focus on the multicenter validation of predictive models , database interoperability, and the development of consistent methodological frameworks that allow radiogenomic knowledge to be effectively translated into the healthcare setting.
Correlation between NF1 genotype and imaging phenotype on whole-body MRI: NF1 radiogenomics	2020 - Lui et al.[21]	Twenty-nine patients diagnosed with neurofibromatosis type 1 (NF1) and germline mutations previously identified by targeted next-generation sequencing were selected. Based on previous whole-body magnetic resonance imaging (WBMRI) studies, 218 neurofibromas (97 discrete and 121 plexiform) were analyzed using a coronal STIR sequence. Each tumor was segmented individually, and 59 image features were extracted using a proprietary volumetric analysis platform (3DQI). A radiomic heatmap was constructed to explore associations between image features and mutation domains/types, both at the tumor level and per patient. Linear mixed-effects models and one-way analysis of variance (ANOVA) were applied to compare the similarity of radiomic profiles within and between different genetic mutation groups.	This preliminary study shows a significant correlation between germline mutations in the NF1 gene and patterns of radiomic features of neurofibromas assessed by whole-body magnetic resonance imaging. The findings support the existence of a radiogenomic link between the NF1 genotype and the imaging phenotype, reinforcing the potential of radiogenomics as a non-invasive tool for molecular characterization in neurofibromatosis type 1.

The integration of radiological and genomic data promises to transform contemporary oncology by enabling more precise, dynamic medicine tailored to each patient's individual characteristics. Radiogenomics is expected to play a crucial role in clinical decision-making, from initial diagnosis to the selection of targeted therapies and monitoring of therapeutic response, with the potential to improve clinical outcomes and patients' quality of life.[1] In addition, radiogenomics could contribute to the discovery of new prognostic and predictive biomarkers, driving translational research and encouraging the design of more efficient and personalized clinical trials. In the long term, the incorporation of this discipline into digital health platforms and its linkage with other omics, such as transcriptomics and proteomics, could consolidate a comprehensive approach to tumor biology that transcends the current limits of cancer diagnosis and treatment.[20] This scenario, although promising, requires sustained investment and commitment to research, technological infrastructure, and the training of professionals capable of interpreting and integrating the complexity of the multidimensional data that radiogenomics provides.

CONCLUSION

The synthesis of the 21 studies shows consistent signals in two specific scenarios: lung cancer with CT to infer mutations, especially with EGFR/KRAS, and gliomas with multiparametric MRI for molecular classification, with quantified performance ranging from moderate to high in internal validations and variable results in other locations. The integration of imaging with clinical variables tends to outperform unimodal models, but clinical extrapolation is limited by poor external validation, lack of calibration, and workflow heterogeneity.

Overall methodological quality remains low to moderate: RQS scores are affected by the absence of external validation and stability analysis; TRIPOD scores show persistent gaps in sample size, handling of missing data, and calibration reporting; and, according to PROBAST, the risk of bias is concentrated in participant selection, definition of predictors, and analysis with potential overfitting. This highlights precise operational needs for translation based on harmonizing, acquiring, segmenting, and standardizing functionality.

Radiogenomics, in its current state, complements, rather than replaces, biopsy, where molecular testing is prioritized, anticipating alterations of therapeutic interest and supporting stratification in defined contexts. To consolidate its clinical adoption, a prospective, multicenter agenda is required, with the publication of code and functionality dictionaries, harmonization procedures, and interoperable repositories, so that the observed performance translates into real, reproducible utility in oncology practice.

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CONFLICT OF INTEREST

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