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Development and validation of an MRI‑based radiomic nomogram to distinguish between good and poor responders in patients with locally advanced rectal cancer undergoing neoadjuvant chemoradiotherapy

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Abstract

Purpose In the clinical management of patients with locally advanced rectal cancer (LARC), the early identifcation of poor and good responders after neoadjuvant chemoradiotherapy (N-CRT) is essential. Therefore, we developed and validated predictive models including MRI fndings from the structured report template, clinical and radiomics parameters to differentiate between poor and good responders in patients with locally advanced rectal cancer who underwent neoadjuvant chemoradiotherapy.

Methods Preoperative multiparametric MRI from 183 patients with locally advanced rectal cancer (122 in the training cohort, 61 in the validation cohort) was included in this retrospective study. After preprocessing, radiomic features were extracted and two methods of feature selection was applied to reduce the number of radiomics features. Logistic regression (LR) and random forest (RF) machine learning classifers were trained to identify good responders from poor responders. Multivariable logistic regression analysis was used to incorporate the radiomic signature and clinical risk factors into a nomogram. Classifer performance was evaluated using the area under the curve (AUC), accuracy, sensitivity, specifcity, positive predictive value (PPV), and negative predictive value (NPV).

Results For the diferentiation of poor and good responders, the radiomics model with an LR classifer achieved AUCs of 0.869 and 0.842 for the training and validation cohorts, respectively. The nomogram showed the highest reproducibility and prognostic ability in the training and validation cohorts, with AUCs of 0.923 (95% confdence interval, 0.872–0.975) and 0.898 (0.819–0.978), respectively. Additionally, the nomogram achieved signifcant risk stratifcation of patients in respect to progression free survival (PFS).

Conclusions The nomogram accurately diferentiated good and poor responders in patients with LARC undergoing N-CRT, and showed signifcant performance for predicting PFS.

Keywords Rectal cancer · Radiomics · Neoadjuvant chemoradiotherapy · Response

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Abbreviations

Introduction

Colorectal cancer ranks as the third most frequent malignancy worldwide, and 30%–50% of colorectal cancer occurs in the rectum [\[1,](#page-9-0) [2\]](#page-9-1). Currently, neoadjuvant chemoradiotherapy (N-CRT) followed by total mesorectal excision (TME) is considered the recommended treatment for locally advanced rectal cancer (LARC) [\[3](#page-9-2), [4](#page-9-3)], with N-CRT playing an important role in the tumor treatment. However, the therapeutic outcomes following N-CRT for LARC vary considerably, ranging from no tumor regression to intermediate regression, and even pathological complete response (pCR) $[5-8]$ $[5-8]$ $[5-8]$.

Early detection of poor responders and good responders to N-CRT plays an important role in the choice of appropriate therapeutic strategies. If poor responders could be precisely detected before TME, more appropriate treatment strategies such as timely surgery and extensive surgery could be good choices for poor responders, to avoid inefective use of high radiation doses or high doses of chemotherapy drugs $[9-11]$ $[9-11]$ $[9-11]$ $[9-11]$. However, the accurate identifcation of good and poor responders to N-CRT currently relies on surgical specimens, and therefore results in a substantial time delay. Thus, early identifcation of good and poor responders is highly important for determining therapeutic strategies.

By extracting high-dimensional data from medical imaging, radiomics may reveal hard-to-visualize information that is closely associated with tumor heterogeneity $[12-15]$ $[12-15]$. Recent advances in radiomics have shown that it can be useful in tumor prognosis and therapy guidance $[16]$ $[16]$, and previous articles have demonstrated that MRI radiomics features can be used to predict pCR to N-CRT in patients with LARC [[17–](#page-9-11)[19](#page-9-12)]. To the best of our knowledge, few articles have reported on the use of radiomics to predict good and poor responders after N-CRT, and the role of radiomics feature analysis in the prediction of good responders and poor responders has not yet been established.

Therefore, the purpose of our study was to generate MRIbased radiomics models for the preoperative prediction of poor and good responders to N-CRT in patients with LARC.

Materials and methods

Patient population

Our institutional review board approved this retrospective study and waived the requirement for informed patient consent. The picture archiving and communication system of our institution was searched for consecutive patients who underwent rectal MRI between March 2014 and May 2019. The inclusion criteria for this study were: (a) rectal adenocarcinoma confrmed by pathological examination; (2) stage T3/T4 LARC; (3) no evidence of distant metastasis; (4) underwent standard N-CRT. The exclusion criteria were: (1) incomplete N-CRT for any reason; (2) incomplete MR imaging; (3) no postoperative pathological results. The patient selection process is summarized in Supplementary item S1.

Neoadjuvant‑CRT

All patients underwent radiation therapy with a 3D-conformational multiple feld technique with a total dose of 45 Gy (daily fraction of 1.8 Gy, delivered 5 days a week for 5 weeks). The chemotherapy regimen was as follows: during radiation therapy days, intravenous injection of 60 mg/m² oxaliplatin weekly, and daily oral administration of 825 mg/ m² capecitabine.

Reference standard

The reference standard for the response to N-CRT was based on the histopathologic reports for the surgically resected specimens. All histopathologic analysis was evaluated by two dedicated gastrointestinal pathologists with 9 and 15 years of experience, who were blind to the clinical and MRI fndings. The histopathological analysis of the resected specimens included the N-CRT response according to the tumor response grading (TRG) proposed by Mandard et al. [[20\]](#page-9-13). The criteria for the TRG are illustrated in Supplementary item S2. The enrolled patients were divided into two groups according to the TRG: good responders (pTRG1–2) and poor responders (pTRG3–5).

MRI protocol

The majority (66.7%, 122 of 183) of the rectal MRI examinations were acquired on a Signa 3.0-T MRI scanner (GE Medical Systems, Milwaukee, USA) in the Southern District of our hospital and were used as a training cohort, while the remaining patients (33.3%, 61 of 183) were scanned on a Signa HDX 3.0-T MRI scanner (GE Medical) in the West District of our hospital, and were used as a validation cohort. The MRI protocol included axial T2-weighted imaging (T2WI), difusion-weighted imaging (DWI; from which apparent diffusion coefficient [ADC] maps were generated), and multiphase contrast-enhanced T1-weighted imaging (CE-T1WI) obtained with four timeframes: one pre-contrast $(L1)$ and three post-contrast, at 15 s $(L2)$, 60 s $(L3)$, and 120 s (L4). For the CE-T1WI, 90–100 mL of the gadolinium-based contrast agent dimeglumine gadopentetate (Magnevist; Schering Diagnostics AG, Berlin, Germany) was administered intravenously at a rate of 2.5 mL/s through a high-pressure injector (Optistar LE, LiebelFlarisheim Company, OH, USA). The MRI acquisitions and parameters are summarized in Supplementary item S3.

Image segmentation and radiomic feature extraction

Two radiologists with 7 and 15 years of abdominal imaging experience who were blinded to the patients' pathological outcomes delineated the entire volume of interest (VOI) around the tumor in a slice-by-slice manner. T2WI, ADC maps, and the L2 timeframe of the CE-T1WI were used for VOI segmentation. Freely available open-source software (3D-Slicer, version 3.4.2,<https://www.slicer.org/>) was used for the imaging segmentation and feature extraction. Resampling to a voxel size of $1 \times 1 \times 1$ mm and Gaussian filtering with sigma values of 0.5, 1.0, and 1.5 were performed with 3D-Slicer. All extracted radiomics features are shown in Supplementary item S4.

Intra‑observer and inter‑observer agreement

Thirty samples were randomly chosen from the T2WI, ADC maps, and CE-T1WI acquired on the two MRI scanners, and the intra-observer and inter-observer agreements for the radiomics features extracted by the two radiologists were measured. To evaluate intra-observer reproducibility, radiologist 1 performed VOI delineations twice within 1 week. To evaluate inter-observer reproducibility, radiologist 2 independently delineated the VOIs once following the same procedure, and the resulting radiomics features extracted from the VOIs of radiologist 2 were compared with the radiomics features extracted by radiologist 1. Radiologist 1 performed all of the VOI delineations that were used to extract radiomics features.

Radiomics feature selection and dimensionality reduction

To avoid overftting and to select the most informative radiomics features for development of the predictive model, a radiomics feature selection process involving two main steps was performed. First, minimum redundancy maximum relevance feature selection (mRMR) was performed to eliminate redundant and irrelevant features. Second, the least absolute shrinkage and selection operator (LASSO) with tenfold cross-validation was applied to the remaining features for the regression of the high-dimensional data. A radiomics score (Rad-score) was then calculated for each patient in the training and validation cohorts using a linear combination of the selected radiomics features weighted by their respective coefficients.

MRI fndings including the structured report template, ADC values, clinical characteristics, and feature selection

Clinical data including sex, age, carcinoembryonic antigen (CEA), CA199, and CA125 were assessed. All MRI was reviewed by the same radiologists who delineated the VOIs. Decisions on MRI fndings, including the structured report template, were made by consensus. The two radiologists recorded the following: (1) T stage, (2) N stage, (3) circumferential resection margin (CRM), and (4) extramural vascular invasion (EMVI). The criteria for these MRI characteristics are listed in Supplementary item S5. The method used for ADC measurement is shown in Supplementary item S6.

Model building, machine learning classifers, and construction of the nomogram

To develop a clinical model, clinical factors for predicting the response to N-CRT, including MRI fndings from the structured report template, ADC value, sex, age, CEA, CA199, and CA125 were selected using univariate- and multivariate logistic regression. First, univariate logistic regression was performed on the clinical risk factors, and those predictive factors with a P value <0.05 were introduced into a multivariate logistic regression model with backwards step-wise selection and Akaike's information criterion as the stopping rule. Then, the features identifed in this multivariate regression were used to develop a clinical model. The imaging features selected by mRMR and LASSO were used to build a radiomics model. Random Forest and logistic regression classifers were applied in the clinical and radiomics models. The clinical factors selected by the univariate logistic regression and radiomic signature were used to build a nomogram for predicting the response to N-CRT. The workfow for imaging data processing and analysis is displayed in Fig. [1.](#page-3-0)

Follow‑up and survival analysis

Progression free survival (PFS) was defned as the interval from surgery to tumor progression, with tumor progression including local recurrence and/or metastasis or

Fig. 1 The workflow of imaging processing and data analysis

death. The enrolled patients were followed up by MRI every 6–12 months for the frst year after surgery, and then annually. Local recurrence or metastasis was confrmed by medical imaging and/or gastroscopic biopsy. Survival curves were plotted according to the Kaplan–Meier method with R software (version 3.4.2, <http://www.Rproject.org>), and the log-rank test was used to compare them.

Statistical analysis

All statistical analyses were performed with R software (version 3.4.2, [http://www.Rproject.org\)](http://www.Rproject.org). Continuous variables were analyzed by independent *t*-test or Mann–Whitney *U* tests. Categorical variables were analyzed by Fisher's exact test or the χ^2 test. The AUC of the ROC curve with 95% confdence intervals (CI) and a decision curve were used to assess the prediction of poor and good responders using the combined nomogram. The LASSO regression, mRMR, and ROC curve analyses were performed using the R packages of "glmnet", "mRMRe", and "pROC", respectively. The Random Forest classifer was built using the "randomForest" packages in R software. The agreement between the predicted risks and the actual results was evaluated using calibration curves and the Hosmer–Lemeshow test.

Results

The relevant characteristics of the training and validation cohorts are summarized in Table [1](#page-4-0). The overall distributions of age, sex, CEA, CA199, CA125, MR T stage, CRM, EMVI, and ADC values showed no signifcant diferences

between the two patient cohorts (*P*>0.05, respectively). The training set consisted of 55/122 (45.08%) good responders and 67/122 (54.92%) poor responders, whereas the validation set consisted of 28/61 (45.90%) good responders and 33/61 (54.10%) poor responders.

A total of 942 imaging features were extracted from the three modalities of T2WI, ADC mapping, and CE-T1WI. The inter-observer assessment showed a satisfactory agreement rate of 87.9% (mean ICC = 0.867, ranging from 0.001 to 0.985) for all 942 features, while the intra-observer agreement showed a satisfactory agreement rate of 95.6% (mean $ICC=0.922$, ranging from 0.005 to 0.997). Eighty-seven imaging features were excluded because of low intra- and inter-observer agreement (ICC < 0.75), and the remaining 855 imaging features were used for further analyses. From the remaining 855 features, 30 features were retained after the mRMR feature selection procedure, and these 30 retained features were then entered into the LASSO regression and were reduced to 13 potential predictors, including 2 features derived from ADC maps, 2 from T2WI, and 9 from CE-T1WI. The selected radiomics features and their coefficients are illustrated in Fig. [2](#page-5-0). The Rad-score of each patient in the training and validation cohorts was calculated using these 13 features (Fig. [3\)](#page-5-1). A radiomics model was constructed using the 13 features selected by mRMR and LASSO.

In the training cohort, good responders had signifcantly higher radiomics scores than poor responders $(P < 0.001)$; Fig. [4a](#page-6-0)), a fnding that was also confrmed in the validation cohort $(P < 0.001;$ Fig. [4b](#page-6-0)). In the training cohort, there was a signifcant diference in ADC values between the poor responders and good responders ($P=0.002$; Fig. [4c](#page-6-0)),

Table 1 Clinical and MRI data

CEA carcinoembryonic antigen, *CRM* circumferential resection margin, *EMVI* extramural vascular invasion

although this fnding was not confrmed in the validation cohort ($P=0.56$; Fig. [4](#page-6-0)d). The Rad-score achieved signifcantly better predictive capacity (AUCs of 0.869 in the training set and 0.842 in the validation set) than the ADC values (AUCs of 0.661 in the training set and 0.456 in the validation set).

The multivariate logistic regression analysis showed CRM, T stage, and ADC value to be independent predictors of a good or poor response (Table [2](#page-6-1)). A clinical model was

constructed incorporating CRM, T stage, and ADC value, and a nomogram was then constructed using CRM, T stage, ADC value, and the selected Radiomics features to diferentiate poor from good responders.

Table [3](#page-7-0) shows the prediction performance of the LR and RF classifers of the predictive models. The nomogram showed a strong prognostic ability in both cohorts, with AUCs of 0.923 (95% CI, 0.872–0.975) and 0.898 (0.819–978) in the training and validation sets, respectively (Fig. [5](#page-7-1)). The DeLong test indicated that there was no signifcant diference between the ROCs of the nomogram for the training and validation sets (P values = 0.884). The nomogram yielded the high accuracy (0.861), sensitivity (0.836) , and specificity (0.881) in both the training and validation cohorts (0.803, 0.714, 0.879, respectively). Moreover, the calibration of the nomogram showed a nonsignifcant Hosmer–Lemeshow test statistic in the training $(P=0.349;$ Fig. [6](#page-8-0)b) and validation sets $(P=0.538;$ Fig. [6c](#page-8-0)). The decision curve analysis illustrated in Fig. [6d](#page-8-0) shows that the nomogram was superior to the clinical factors when the threshold probability was within the range of 0.1–1.0.

For both the training and validation cohorts, the Kaplan–Meier curves of PFS for the prediction models are shown in Fig. [7](#page-8-1). The pathologic results (good responders vs. poor responders) signifcantly stratifed patients with respect to PFS in both the training and validation sets $(P = 0.00091)$ and $P=0.0039$, respectively). The nomogram achieved separation of the survival curves with *P* values of 0.0036 in the training set and 0.024 in the validation set.

Discussion

In this study, we investigated two machine learning algorithms for identifying good responders and poor responders in patients with LARC who underwent N-CRT. The nomogram model showed excellent discrimination and calibration for diferentiating the two cohorts, with AUCs of 0.923 in the training cohort and 0.898 in the validation cohort, and it achieved separation of survival curves in both training and validation sets, with *P* values of 0.0036 and 0.024, respectively.

Morphological information on MRI is widely used to evaluate the response to N-CRT. Cui et al. [[17\]](#page-9-11) built a model based on radiomics features to predict pCR in patients with LARC after they had undergone N-CRT, and showed that the T stage according to MRI was a positive predictive factor. Tang et al. [[21](#page-9-14)] reported that a nomogram using MRI fndings taken from a structured report template and clinical factors performed well in identifying poor responders after N-CRT, with AUCs of 0.823 on the training set and 0.820 on the validation set, and demonstrated that T stage according to the MRI structured report template was a signifcant

Fig. 3 Plots **a**, **b** show the radiomics Rad-score for each patient, while the heatmap shows the contributions of the selected features to the Rad-score

predictor. Our result is in accord with their fndings, although our nomogram showed better discrimination of good and poor responders in patients with LARC who underwent N-CRT, with AUCs of 0.923 on the training set and 0.898 on the validation set. Our nomogram also contained radiomics factors, which can provide nonvisual information on the underlying tumor heterogeneity [[22–](#page-9-15)[24](#page-9-16)]. Recent advances in radiomics have demonstrated that the approach has great potential for predicting tumor response [[25](#page-9-17)[–28\]](#page-9-18). Previous studies added imaging features extracted from DCE-MRI to radiomics analysis to identify pCR in LARC patients having undergone N-CRT, and obtained high AUCs [\[17](#page-9-11), [29\]](#page-9-19). DCE-MRI may provide comprehensive information with smaller image intervals and higher image contrast than T2-weighted imaging and difusion-weighted imaging. The addition of these radiomics predictive factors may further improve the predictive performance of our model.

After multiple logistic regression analysis, CRM, which was previously found to be an independent prognostic factor for local recurrence after surgery [[30,](#page-9-20) [31\]](#page-10-0), was also introduced into our nomogram. Owing to its high resolution for soft tissue, MRI is considered to be the most reliable imaging method for identifying potential CRM involvement [[32,](#page-10-1) [33](#page-10-2)], with Glynne-Jones et al. [\[34](#page-10-3)] fnding that CRM status could predict outcome after surgery following preoperative radiotherapy and chemoradiation, and Depypere et al. [[35\]](#page-10-4) demonstrating that CRM was correlated with the biological behavior of the tumor and therapy response after N-CRT. Studies have demonstrated that MRI-detected EMVI positivity is closely related to tumor recurrence after surgery in patients with LARC [\[36](#page-10-5), [37](#page-10-6)]. Chand et al. [[38](#page-10-7)] showed that detection of EMVI after N-CRT was prognostically signifcant, and was of independent prognostic signifcance for DFS. However, while Lee et al. [\[39](#page-10-8)] found that EMVI was

Fig. 4 Boxplots showing diferences between the good responders and poor responders. Plots **a**, **b** show the diference in Rad-score between the good responders and poor responders in the training and

Table 2 Univariate and multivariate logistic regression analysis of factors for prediction of a good or bad response

validation sets. Plots **c**, **d** show the diference in ADC values between the training and validation set

Factors	Univariate logistic regression		Multivariate logistic regression	
	OR (95% CI)	P value	OR (95% CI)	P value
CEA	$0.439(0.201 - 0.938)$	0.035		
MRI-T stage	$0.485(0.26 - 0.873)$	0.018	$0.154(0.052 - 0.39)$	< 0.001
MRI-CRM	$0.423(0.201 - 0.871)$	0.021	$0.204(0.057-0.635)$	0.009
ADC.	17.636 (3.431-103.986)	0.001	38.956 (2.642-804.916)	0.011
Sex	$0.774(0.374 - 1.591)$	0.487		
CA199	$2.222(1.081 - 4.651)$	0.031		
CA125	$0.263(0.12 - 0.559)$	0.001		
MRI-N stage	$0.346(0.197-0.558)$	< 0.001		
MRI-EMVI	$0.806(0.375 - 1.735)$	0.58		
Rad-score	$3.491(2.28 - 5.886)$	< 0.001	$3.597(2.132 - 6.95)$	< 0.001

the only signifcant factor correlating with patients' DFS in a univariate analysis, it was not signifcant in a multivariate analysis. Following the univariate and multivariate analysis, EMVI was not included in our nomogram. It may be that the lack of signifcance was related to the low number of EMVI-positive cases.

In previous studies, DWI and DWI-derived ADC values were used to access the response to N-CRT [\[40–](#page-10-9)[42](#page-10-10)], although the results remain controversial. Birlik and colleagues reported that the ADC values of good responders were signifcantly higher than those of poor responders [[43](#page-10-11)], but Cai et al. could not confrm this result [[44](#page-10-12)]. In our study, the diference in ADC values between good and poor responders varied between the training and validation sets. Our study showed a marked diference in ADC values between good and poor responders in the training set ($P = 0.002$), but not in the validation set ($P = 0.56$). The role of ADC values as an independent predictive factor for assessing the response to N-CRT therefore remains highly uncertain. Compared with the ADC values, the Rad-score

LR logistic regression, *RF* random forest, *PPV* positive predictive value, *NPV* negative predictive value

Fig. 5 Scatterplots of areas under the ROC curve (AUC) of classifers

model demonstrated more satisfactory results, with AUCs of 0.869 and 0.842 for predicting a good response in the training and validation sets. One possible explanation for the improved performance is that high-dimensional imaging features hold more detailed information on tumors, and that this information allows for more sensitive diferentiation between good responding and poor responding LARC patients.

The TRG system has been widely used to access the response to N-CRT in patients with LARC who underwent TME, and to stratify LARC patients after N-CRT according to DFS [\[45–](#page-10-13)[47\]](#page-10-14). In our study, we evaluated the relationship between TRG and prognosis, and found that patients with TRG 1–2 had longer PFS than poor responders with TRG 3–5, a fnding in accord with the results of Huh et al. [\[48](#page-10-15)]. There are few articles about using a nomogram to stratify LARC patients after N-CRT according to PFS. In our study, the nomogram also achieved separation of survival curves.

Machine learning based on radiomics was widely used to identify pCR patients with LARC after N-CRT. Horvat et al. [\[28](#page-9-18)] used RF classifer based on radiomics to predict pCR patients, with an AUC of 0.93. However, the validation group was missing in their study. In our study, RF classifer based on radiomics showed well classifcation performance for identifying good and poor responders with AUCs of 0.883 and 0.827 in the training and validation set, respectively. Moreover, nomogram is based on logistic regression analysis which is one of machine learning algorithms. Compared with other machine learning algorithms, the signifcant advantage of nomogram is visualization. This makes it easy to use.

Study limitations

Our study has some limitations. First, this was a retrospective study, and there is the potential for selection bias by not including patients on nonsurgical management. Second, the VOI segmentation was manually performed, and diferences in the extraction of imaging features may have occurred. Therefore, we performed a consistency check to control for variation in the variables. Third, this study used a dichotomous grading of good or poor responders, rather than the fve grades of the TRG; further studies are needed to provide a better generalization. Furthermore, the operation type, surgical approach, and treatments after surgery may signifcantly infuence the prognosis of LARC patients [\[33](#page-10-2)[–35](#page-10-4)], but as a preoperative predictive method, our nomogram involved only preoperative factors.

Conclusions

The nomogram combining multiparametric MRI-based radiomics features with CRM, T stage, and ADC values showed high performance in distinguishing between good responders and poor responders in patients with LARC who underwent N-CRT, and may be help in predicting PFS.

Fig. 6 The nomogram, its corresponding calibration curves for each dataset, and the decision curve analysis of the nomogram. Plots (**b**) and (**c**) present the calibration curves of the nomogram for the train-

ing and validation sets, respectively. Plot (**d**) presents the decision curve analysis for the nomogram

Fig. 7 Kaplan–Meier survival curves of patients in the training and validation sets, displaying patient stratifcation according to the pathology (**a**, **c**), nomogram model (**b**, **d**)

Compliance with ethical standards

Conflict of interest The authors declare that they have no conficts of interest in connection with this work.

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