Radiology

Bone Marrow and Tumor Radiomics at ¹⁸F-FDG PET/CT: Impact on Outcome Prediction in Non–Small Cell Lung Cancer

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Background: Primary tumor maximum standardized uptake value is a prognostic marker for non–small cell lung cancer. In the setting of malignancy, bone marrow activity from fluorine 18–fluorodeoxyglucose (FDG) PET may be informative for clinical risk stratification.

Purpose: To determine whether integrating FDG PET radiomic features of the primary tumor, tumor penumbra, and bone marrow identifies lung cancer disease-free survival more accurately than clinical features alone.

Materials and Methods: Patients were retrospectively analyzed from two distinct cohorts collected between 2008 and 2016. Each tumor, its surrounding penumbra, and bone marrow from the L3–L5 vertebral bodies was contoured on pretreatment FDG PET/CT images. There were 156 bone marrow and 512 tumor and penumbra radiomic features computed from the PET series. Randomized sparse Cox regression by least absolute shrinkage and selection operator identified features that predicted disease-free survival in the training cohort. Cox proportional hazards models were built and locked in the training cohort, then evaluated in an independent cohort for temporal validation.

Results: There were 227 patients analyzed; 136 for training (mean age, 69 years \pm 9 [standard deviation]; 101 men) and 91 for temporal validation (mean age, 72 years \pm 10; 91 men). The top clinical model included stage; adding tumor region features alone improved outcome prediction (log likelihood, -158 vs -152; P = .007). Adding bone marrow features continued to improve performance (log likelihood, -158 vs -145; P = .001). The top model integrated stage, two bone marrow texture features, one tumor with penumbra texture feature, and two penumbra texture features (concordance, 0.78; 95% confidence interval: 0.70, 0.85; P < .001). This fully integrated model was a predictor of poor outcome in the independent cohort (concordance, 0.72; 95% confidence interval: 0.64, 0.80; P < .001) and a binary score stratified patients into high and low risk of poor outcome (P < .001).

Conclusion: A model that includes pretreatment fluorine 18–fluorodeoxyglucose PET texture features from the primary tumor, tumor penumbra, and bone marrow predicts disease-free survival of patients with non–small cell lung cancer more accurately than clinical features alone.

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Fluorine 18–fluorodeoxyglucose (FDG) PET imaging is traditionally used for clinical staging, and tumor uptake has been shown to help predict recurrence in many solid cancers across a diverse set of studies (1–3). Other studies (4–7) investigated the clinical use of quantifying nontumor regions at FDG PET/CT to help predict cancer outcome. For example, bone marrow hypermetabolism is associated with a higher risk of mortality in lung cancer (6–8), and organs of the reticuloendothelial system (eg, spleen and liver) are associated with a higher risk of recurrence in breast cancer (4). To our knowledge, the underlying biologic mechanisms for these associations are not currently well defined, but putatively studied areas identify a systemic response to cancer where glucose metabolism plays a role.

Numerous studies (5,9–11) have shown that the development and maintenance of a systemic inflammatory response is associated with poorer outcomes in patients with cancer. Not surprisingly, blood correlates of this response, as measured by a complete blood cell count in the clinic, including platelets, white blood cells, and lymphocyte ratios, are also associated with cancer outcomes (12).

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Abbreviations

FDG = fluorodeoxyglucose, GLCM = gray-level co-occurrence matrix, LASSO = least absolute shrinkage and selection operator, MTV = metabolic tumor volume, NSCLC = non-small cell lung cancer

Summary

A model based on radiomic features extracted from fluorine 18–fluorodeoxyglucose PET/CT images in primary non–small cell lung cancer tumor, tumor penumbra, and bone marrow identified disease-free survival more accurately than clinical features alone.

Key Results

- A bone marrow and tumor region fluorine 18–fluorodeoxyglucose PET/CT radiomics model was better than the top-performing clinical model of stage for outcome prediction in non–small cell lung cancer (NSCLC; log likelihood, -158 vs -145; *P* = .001).
- A fully integrated clinical and radiomics model was a predictor of poor outcome in an independent data set for NSCLC (concordance, 0.72; *P* < .001).
- A validated dichotomous score stratified patients into high and low risk for poor outcome in NSCLC (5-year disease-free survival rates in the training and validation cohorts of 88.5% and 60.3%, respectively, in the low-risk group and 44.3% and 0%, respectively, in the high-risk group; *P* < .001).</p>

Conventional radiomic analysis aims to extract quantitative imaging markers and associate them with clinical outcomes (13). Radiomic features such as size, shape, intensity, and texture can describe an imaging phenotype that may indicate underlying biologic characteristics. Because bone marrow uptake at FDG PET/CT has been previously associated (6,7,14) with cancer outcome, we hypothesized that a radiomic analysis of the FDG PET activity in the bone marrow could identify a systemic response and thereby improve the prediction of lung cancer disease-free survival.

Radiomic studies (15) of lung cancer have focused on analyzing the tumor region with FDG PET and CT. Some studies have investigated the integration of basic clinical features such as type of non–small cell lung cancer (NSCLC), stage, or age for improving outcome prediction (16–18). We hypothesized that integrating primary tumor with tumor penumbra and bone marrow PET signal could define a more precise model for identifying poor lung cancer outcome. This could assist clinicians in stratifying patients at a higher risk of recurrence that may benefit from more aggressive adjuvant and personalized treatment options. The purpose of our study was to determine whether integrating FDG PET radiomic features of the primary tumor, tumor penumbra, and bone marrow identifies lung cancer disease-free survival more accurately than clinical features alone.

Materials and Methods

Patient Selection

This study was approved by our institutional review board and was Health Insurance Portability and Accountability Act compliant. Written informed consent was signed by all study participants before participation. No industry partners provided support for this study.

We retrospectively analyzed 291 patients with NSCLC from two prospectively acquired data sets (n = 145 and n = 146) (19). The first data set (training) consisted of consecutive patients with NSCLC referred for surgical resection from 2008 to 2012. This data set is publicly available in the Cancer Imaging Archive (20,21) and FDG PET in a subset of this population was previously investigated for tumor radiomics (n = 145), mutation status (n = 95), and oncogenomic alteration (n = 25) (19,22,23). The second data set (temporal validation) consisted of consecutive patients undergoing definitive therapy as part of an observational imaging marker study from 2010 to 2016. A subgroup of this data has evaluated FDG PET uptake for tumor radiomics (n = 146), genomic



Figure 1: Study flowchart shows all patients who were enrolled and all exclusions for the training and validation sets. The outcome was defined as recurrence for curable lung cancer (stage I–IIIA) and progression for incurable lung cancer (stage IIIB or IV). Patients who did not recur or progress were classified as disease free at the time of analysis. CBC = complete blood cell count.



Figure 2: Mapping the bone marrow in patients with non-small cell lung cancer for radiomics features. Axial, sagittal, and coronal cross-sections of L3, L4, and L5 vertebral body segmentations from a CT (top row), PET (middle row), and fused PET/CT (bottom row). Regions of interest on each image show the original manual thresholdbased segmentation (magenta), the 2-mm erosion (blue), and the 2-mm dilation (yellow). A = anterior, L = left, P = posterior, R = right.

alterations (n = 59), and circulating tumor cells (n = 30) (24,25).

For inclusion in our study, we required patients to have undergone an FDG PET/CT examination and had a complete blood cell count performed before treatment. Exclusion criteria resulted in 227 patients for analysis (Fig 1; training, 136 patients; validation, 91 patients).

We staged patients by using the American Joint Committee on Cancer seventh edition staging system (26). We used pathologic staging in the training data set and a combination of clinical and pathologic staging in the validation data set. Following treatment, patients were followed with standard clinical protocol. We evaluated disease-free survival to identify poor outcome, and time to event or last known follow-up was determined from the date of pretreatment FDG PET/CT imaging.

FDG PET/CT

FDG PET/CT was performed before definitive treatment by using one of four scanners (Allegro/Gemini TF PET/CT, Phillips Healthcare, Cleveland, Ohio; Biograph mCT, Siemens Healthcare, Erlangen, Germany; Discovery VCT, GE Healthcare, Waukesha, Wis; or Discovery LS PET/CT, GE Healthcare) at one of three local medical centers (Appendix E1 [online]). Glucose levels were checked before the patient underwent PET/ CT, and if they were elevated (>200 mg/dL) the patients were rescheduled.

Region-of-Interest Segmentation

All image postprocessing was performed by using commercially available software (MIM version 6.6; MIM Software, Cleveland, Ohio). All segmentations were performed by a postdoctoral scholar (S.A.M., with 7 years of image analysis experience after training) and verification was made by a board-certified physician in nuclear medicine (G.A.D., with 9 years of experience). All investigators were blinded to all clinical data and other imaging test results.

We used the manual three-dimensional spherical threshold tool to segment vertebral bodies with the CT portion of the PET/CT and transferred them onto the FDG PET image by using software (MIM version 6.6; MIM Software). We selected the

Table 1: Baseline Patient and Lesion Characteristics					
Parameter	Training Set $(n = 136)$	Validation Set (<i>n</i> = 91)	<i>P</i> Value		
Mean age (y)	69 ± 9	72 ± 10	.03		
Sex			.01		
Men	101 (74)	53 (58)			
Location			.33		
Upper lobe	85 (63)	51 (56)			
Lower lobe	51 (38)	40 (44)			
Type of NSCLC			.49		
Adenocarcinoma	107 (79)	68 (75)			
Nonadenocarcinoma*	29 (21)	23 (25)			
Smoking status			.14		
Current	30 (22)	13 (14)			
Former	85 (63)	56 (62)			
Never	21 (15)	22 (24)			
Cancer stage			.007		
0 [†]	4 (3)	0 (0)			
Ι	78 (57)	64 (70)			
II	29 (21)	7 (8)			
III	21 (15)	12 (13)			
IV	4 (3)	8 (9)			
Recurrence or progression			.10		
Yes	38 (28)	35 (38)			
No	98 (72)	56 (62)			
Blood variable [‡]					
WBC (1000/µL)	7.1 (3.3–76)	6.9 (2.9–13.8)	.91		
Hemoglobin (g/dL)	13.6 (5.0–18.3)	13.6 (7.9–16.8)	.66		
Platelets (1000/µL)	203 (76–582)	212 (93-407)	.47		

Note.—Unless otherwise indicated, data are number of patients and data in parentheses are percentages. Mean data are \pm standard deviation. NSCLC = non–small cell lung cancer, WBC = white blood cells.

* Includes squamous cell or non-small cell cancer not otherwise specified.

[†] Pathologic stage 0 disease is defined as a carcinoma in situ (TisN0M0) as per the

American Joint Committee on Cancer seventh edition staging system.

[‡] Data are median and data in parentheses are range.

L3–L5 vertebral bodies because they are the largest, are less sensitive to motion, and were previously explored to assess bone marrow uptake (6–8). To determine the impact of segmentation on radiomic features, we performed an automated two-dimensional dilation and erosion of 2 mm on each of the contours in the training data set to stimulate variability in segmentation (Fig 2).

The metabolic tumor volume (MTV) was segmented on the FDG PET images by using MIM (MIM Software) with the PET edge gradient-based semiautomatic segmentation tool (19). We defined and extracted the three-dimensional penumbra region, which bordered the MTV segmentation and extended 1 cm beyond it. Thus, three tumor regions were investigated: the MTV, the penumbra only, and the union of the MTV and penumbra regions. A previous study (19) reported the variability in MTV and penumbra segmentations.

Feature Extraction

We extracted radiomic features from the FDG PET images by using the Quantitative Image Feature Engine, implemented in the commercially available software (Matlab R2016Bl Mathworks, Natick, Mass) and available online (*https://github.com/riipl/3d_gifp*, commit 94c3d12) (27). Additional details on feature extraction are provided in Appendix E1 (online).

Feature Model Building and Selection

To determine the optimal features for predicting disease-free survival in the training data set, we built a generalized linear model with the least absolute shrinkage and selection operator (LASSO) by using the glmnet package on clinical features only (Appendix E1 [online]). We then added radiomic features to the baseline clinical model to assess model improvement by using LASSO. From these identified features, we built and compared univariable and multivariable Cox proportional hazard models in the training data set to identify the best-performing model. We locked and independently evaluated the top multivariable model in the temporal validation data set.

Statistical Analysis

We assessed demographic differences by using a Wilcoxon rank-sum test for continuous variables and χ^2 test for categorical variables. We applied *z* score transformation to all radiomic features before building the model. To determine robust features, we calculated intraclass correlation coefficients for each radiomic feature in the training cohort, and robust features with an intraclass correlation coefficient greater than 0.8 were selected for further analysis (28,29).

We used open-source software (R, version

3.4.3; R Project for Statistical Computing, Vienna, Austria) for feature selection, model building, and evaluation (30). The likelihood ratio P value was assessed to indicate a statistically significant result. We tabulated the Akaike information criterion and performed the likelihood ratio test to compare nested models. We used the concordance index to assess prognostic value and the Noether test to determine statistical significance. We also performed Kaplan-Meier analysis on the basis of risk scores generated from the locked multivariable model by dichotomizing groups into high and low risk on the basis of median risk prediction score determined in the training data set. Statistical significance was indicated by a P value less than .05.

Results

Patient Demographics

We analyzed a total of 227 patients, including 136 patients in the training cohort (mean age, 69 years \pm 9 [standard deviation]; 101 men) and 91 patients in the validation cohort (mean

Region of Interest	Total No. of Features $(n = 668)$		No. of Robust Features $(n = 586)$	
	Per Type	Per Region	Per Type	Per Region
Bone marrow		156		151
Intensity	12		12	
GLCM texture	144		139	
Tumor region				
MTV		200		154
Size	4		4	
Sphericity	1		1	
LVII shape	39		26	
Intensity	12		12	
GLCM texture	144		111	
Penumbra		156		127
Intensity	12		11	
GLCM texture	144		116	
MTV with penumbra		256		154
Intensity	12		12	
GLCM texture	144		142	

Note.—Data are number of features. Robust features refer to those with an intraclass correlation coefficient > 0.8. GCLM = gray-level co-occurrence matrix, MTV = metabolic tumor volume, LVII = local volume invariant integral.

Table 3: Cox Proportional Hazards Model Statistics for Univariable Features in the Training Cohort					
Feature Type	AIC	LR <i>P</i> Value	Hazard Ratio	Concordance*	
Clinical					
Stage	318.1	$< .001^{\dagger}$	1.93 (1.47, 2.53)	0.69 (0.60, 0.77)	
Age	337.2	.3	1.02 (0.98, 1.06)	0.58 (0.48, 0.67)	
Male patients	338.2	.8	1.09 (0.52, 2.29)	0.51 (0.45, 0.58)	
Never-smoker	337.5	.4	1.42 (0.66, 3.03)	0.52 (0.46, 0.58)	
Past smoker	335.6	.1	0.59 (0.31, 1.11)	0.55 (0.47, 0.63)	
Location in upper lung	338.2	.9	0.94 (0.49, 1.81)	0.52 (0.44, 0.59)	
Nonadenocarcinoma	338.2	>.99	1.01 (0.46, 2.20)	0.52 (0.45, 0.59)	
Blood variable					
WBC (1000/µL)	338.2	>.99	1.00 (0.96, 1.04)	0.57 (0.48, 0.67)	
Hemoglobin (g/dL)	336.0	.1	0.87 (0.73, 1.04)	0.54 (0.45, 0.64)	
Platelets (1000/µL)	334.8	.07	1.00 (1.00, 1.01)	0.60 (0.51, 0.69)	
Tumor					
MTV with penumbra GLCM energy MAD	327.3	$.001^{+}$	0.49 (0.29, 0.82)	0.65 (0.56, 0.73)	
Penumbra GLCM entropy IQR	331.5	$.01^{+}$	1.49 (1.12, 1.97)	0.59 (0.50, 0.69)	
Penumbra GLCM cluster shade maximum	328.4	$.002^{\dagger}$	1.59 (1.27, 1.98)	0.64 (0.55, 0.73)	
Bone marrow					
GLCM sum mean skewness	333.5	$.03^{\dagger}$	0.65 (0.42, 1.00)	0.58 (0.48, 0.67)	
GLCM cluster tendency skewness	334.1	$.04^{\dagger}$	1.47 (0.99, 2.18)	0.58 (0.50, 0.66)	

Note.—Data in parentheses are 95% confidence intervals. AIC = Akaike information criterion, GLCM = gray-level co-occurrence matrix, IQR = interquartile range, LR = likelihood ratio, MAD = mean absolute deviation, MTV = metabolic tumor volume, WBC = white blood cell.

* The probability that for a pair of randomly chosen samples the sample with the higher risk prediction will experience an event before the other sample.

[†] Statistically significant (P < .05).

age, 72 years \pm 10; 91 men). Patients in the training and validation cohorts were well matched for type of NSCLC (*P* = .49), smoking status (*P* = .14), and tumor location (*P* = .33) (Table 1). The training cohort was slightly younger (*P* = .03) and had a higher percentage of men (*P* = .01). There was also a difference in stage distribution across the data sets (P = .007), however, there was no difference in the proportion of patients who recurred or progressed (P = .10).

The median disease-free survival was 15 months (range, 1–95 months): 13 months (range, 2–95 months) in the training cohort

and 15 months (range, 1–58 months) in the validation cohort. The median follow-up time for censored patients without an event was 41 months (range, 1–113 months): 49 months (range, 1–113 months) in the training and 33 months (range, 1–74 months) in the validation cohort.

Imaging Feature Robustness

Despite the relatively large differences in bone segmentations with the expansion and contraction (Fig 2), bone marrow radiomic features were highly robust, and 96.8% (151 of 156) of features had an intraclass correlation coefficient greater than 0.8 (Table 2). The robustness of the MTV, penumbra, and MTV with penumbra features are shown in Table 2 (19).

Clinical Model for Identifying Outcome in NSCLC

From 11 clinical features analyzed (Table 3), stage was the only univariable predictor of poor outcome in the training data set (hazard ratio, 1.93 [95% confidence interval: 1.47, 2.53]; Akaike information criterion, 318.1; likelihood ratio, 20.2 [P < .001]). No other clinical variables or blood parameters were univariable predictors (Table 3; P > .05). When LASSO was used to select the best multivariable model, only one clinical feature (stage) was chosen ($\lambda = 0.0831$; cross-validation error rate, 10.3%).

Addition of FDG PET Tumor Region Radiomic Features

LASSO identified four features when tumor region radiomic features were integrated with clinical features ($\lambda = 0.0955$; cross-validation error rate, 10.4%): stage, one MTV with penumbra gray-level cooccurrence matrix (GLCM) texture feature (energy mean absolute deviation), and two penumbra GLCM texture features (entropy interquartile range and cluster shade maximum). All three imaging features were univariable predictors (all P < .01), and the MTV with penumbra texture feature was the best predictor with the lowest Akaike information criterion value of 327.3 (Table 3). Figure 3 demonstrates the qualitative meaning behind this GLCM energy texture feature with a hazard ra-

tio less than 1. Adding tumor region features to the clinical model of stage improved model performance (log likelihood, -152 vs -158, respectively; P = .007).



Figure 3: Clinical interpretation of texture features at fluorodeoxyglucose (FDG) PET. **A**, A homogeneous image and, **B**, a heterogeneous image are shown with their corresponding gray-level co-occurrence matrices (GLCMs) and texture values for an FDG PET image. GLCM examines the co-occurrence of intensity pairs between all neighboring pixels in an image. For example, **A**, there are many light pixels neighboring likewise light pixels, therefore there is a peak in the GLCM at lower pixel intensities. The energy radiomics feature calculates the sum of squares of the GLCM. Thus, because the texture in the image is more heterogeneous, the energy texture value is lower, **B**. This feature in the tumor with penumbra had a hazard ratio less than 1, indicating that greater heterogeneity at FDG PET imaging indicates a higher risk of poor outcome.

Table 4: Cox Proportional Hazards Model Statistics for the Top-performing Multivariable Model in the Training Cohort

Feature	Hazard Ratio	P Value
Clinical		
Stage	1.98 (1.45, 2.70)	$< .001^{*}$
Blood variable		
WBC (1000/µL)	0.99 (0.88, 1.11)	.81
Hemoglobin (g/dL)	0.99 (0.82, 1.20)	.93
Platelets (1000/µL)	1.00 (1.00, 1.01)	.93
Tumor		
MTV with penumbra GLCM energy MAD	0.69 (0.40, 1.19)	.18
Penumbra GLCM entropy IQR	1.35 (0.97, 1.86)	.07
Penumbra GLCM cluster shade maximum	1.17 (0.84, 1.63)	.36
Bone marrow		
GLCM sum mean skewness	0.52 (0.32, 0.84)	.008*
GLCM cluster tendency skewness	1.62 (1.02, 2.59)	.04*

Note.—Data in parentheses are 95% confidence intervals. GLCM = gray-level co-occurrence matrix, IQR = interquartile range, MAD = mean absolute deviation, MTV = metabolic tumor volume, WBC = white blood cells. * Statistically significant (P < .05).

Addition of FDG PET Bone Marrow Radiomic Features

When integrating bone marrow features with tumor, penumbra, and clinical features in the LASSO, it selected six features (λ

= 0.0955; cross-validation error rate, 10.4%): cancer stage, two bone marrow texture features, one MTV with penumbra texture feature, and two penumbra texture features. Both bone marrow features were univariable predictors (P < .04). The multivariable model that incorporated features selected by LASSO was a predictor of poor outcome (likelihood ratio, 45.8 [P < .001]; Akaike information criterion, 302.4) with a concordance of 0.78 (95% confidence interval: 0.70, 0.85). To account for any ab-



Figure 4: Radiomic imaging and clinical features are not well correlated. Pearson correlation coefficient heatmap for all features in the final radiomic model, including stage, blood variables, bone marrow, and tumor region radiomics. The color scheme that shows the degree of correlation is displayed on the right axis. GLCM = gray-level co-occurrence matrix, MTV = metabolic tumor volume, WBC = white blood cells.

normal blood counts, we added blood parameters as covariates when building the multivariable model and found no difference in model performance (likelihood ratio test P = .99; concordance, 078 [95% confidence interval: 0.70, 0.85]; likelihood ratio, 45.9 [P < .001]; Akaike information criterion, 308.4). Both before and after adjustment for blood parameters, stage (P< .001) and the two bone marrow radiomic features (P < .05) were significant variables in identifying outcome (Table 4).

Bone marrow imaging features demonstrated modest correlation with tumor imaging features, clinical variables, and blood parameters (Fig 4, all Pearson correlation < |0.35|; P > .04), suggesting that imaging features provide complementary information for outcome prediction. To confirm that this model performance was not an age-related phenomenon, we examined age as a covariate and found there was no impact on the model performance (log likelihood, -144 vs -145, respectively; P = .12).

We found that the fully integrated model outperformed the tumor features and clinical stage model (log likelihood, -145 vs -152, respectively; P = .02). This model also outperformed the model of stage alone (log likelihood, -145 vs -158, respectively; P = .001) and shows the added prognostic value of combining multiple regions of pretreatment FDG PET radiomic information for refining prognosis.

Fully Integrated Model Validation for Identifying Outcome in NSCLC

Next, we locked the coefficients and variables in the fully integrated model and evaluated the model by using our validation data set. We found that the model validated as a predictor of poor outcome (concordance, 0.72; 95% confidence interval: 0.64, 0.80; Noether P < .001). The fully integrated radiomic model separated patients into high and low risk of poor outcome (P < .001; Fig 5). The 5-year disease-free survival rates in the training and validations cohorts were, respectively, 88.5% and 60.3% in the low-risk group and 44.3% and 0% in the high-risk group. When comparing 5-year disease-free survival rates



Figure 5: A radiomics risk score stratifies patients with good versus poor outcome into two data sets. Kaplan-Meier curves for the fully integrated multivariable model that included stage, bone marrow radiomics, tumor radiomics, and blood variables in the, **A**, training cohort (n = 136; P < .001) and, **B**, validation cohort (n = 91; P < .001). Patients were stratified on the basis of the median risk value in the training cohort. The shaded regions represent the 95% confidence intervals. The 5-year disease-free survival in the training and validation cohorts were 88.5% and 60.3%, respectively, in the low-risk group and 44.3% and 0%, respectively, in the high-risk group. + = censored data.

of stage to the fully integrated radiomic model (Fig E1 [online]) we see lower disease-free survival rates in the training and validation cohorts in the low-risk group (78.2% and 42.6%, respectively). Figure 6 is an example of two patients from the validation data set whose outcomes were correctly predicted and had visibly different bone marrow uptake. We noticed that study participants with greater heterogeneous texture in the tumor, surrounding region, and bone marrow were likely to have a poor outcome.



Figure 6: A visual example of the value of bone marrow radiomics. A, B, Example sagittal CT (left), corresponding PET (middle), and fused PET/CT images (right) for two patients, on which the L3–L5 vertebral bodies are circled (magenta). The fully integrated model correctly predicted, A, the patient who was high risk and stage I with recurrence at 12-month follow-up and, B, the patient who was low risk and stage III without recurrence at 2.5-year follow-up. Qualitatively, patients who were high risk tended to have higher heterogeneous uptake in the bone marrow. Both PET images are shown with a window of 10 standardized uptake value units.

Discussion

Bone marrow uptake at fluorine 18–fluorodeoxyglucose (FDG) PET/CT was previously associated with cancer outcome (6,7,14). We proposed that a radiomic analysis of the FDG PET activity in the bone marrow could identify a systemic response and thereby improve the prediction of lung cancer outcome. We demonstrated that combining bone marrow features with cancer stage, tumor, and tumor penumbra radiomic features improves prognostic accuracy over stage alone (log likelihood, -145 vs -158; P = .001). This model was a predictor of poor outcome in an independent data set of patients with non–small cell lung cancer (NSCLC) (concordance, 0.72; P < .001) and demonstrated the ability to stratify patients into high and low risk for poor outcome (Kaplan-Meier P < .001).

In our study, we analyzed radiomic features within the bone marrow, integrated these features with clinically relevant data, adjusted for hematologic confounding variables (eg, anemia), and harnessed additional imaging data from the tumor and its penumbra to improve prognosis for patients with NSCLC. We also demonstrated that bone marrow radiomic features remain stable after expansion and contraction of the contours with high intraclass correlation coefficient values. This supports continued inquiries into semiautomatic or fully automatic segmentations of the vertebral body that would be beneficial to reduce the amount of processing time.

Textural analysis on FDG PET images identified GLCM features in the MTV with penumbra region to predict poor outcome. This suggests the importance of investigating features outside the tumor for improved prognostic models. Our findings are consistent with other radiomic studies that demonstrate the importance of peritumoral radiomic features at PET or CT for outcome prediction (19,31–33). These results are also consistent with previous studies (7,8) showing that a higher mean standardized uptake value in the bone marrow at diagnosis indicates poorer outcomes.

Previous work (34–36) has shown that FDG uptake in the bone marrow is associated with altered serum cytokine, C-reactive protein, and hematologic parameters. On the basis of our results and biologic plausibility, whole-body radiomics or deep learning with FDG PET examinations, which are performed routinely in the clinic from thigh to skull as so-called off-the-shelf PET/CT imaging data, may improve prognosis in NSCLC (4). Additionally, a next step of inquiry would be to integrate markers of systemic inflammation with this type of analysis.

Another strength of our study was including hematologic parameters for analysis. Because other studies have shown that hematologic parameters are associated with outcomes in cancer (12) and because hematologic derangements can affect bone marrow metabolism, we restricted our analysis to patients who had complete blood cell count counts available within 90 days of our study. Although none of these parameters were sta-

tistically significant univariable predictors of poor outcome, we were able to demonstrate that they did not affect the results of our analysis.

Our study had several limitations. We included patients enrolled largely from one medical center. The model was only investigated in a temporal validation cohort, and we did not perform any additional model tuning by using an external testing cohort. We also did not analyze patient diabetic status, body mass index, genetic markers, and specific pack-years of smoking history, which may impact bone marrow metabolism and outcome prediction. Future studies validating these results on larger and more diverse data sets is therefore warranted.

Investigation of these radiomic features by using other scanners and with additional external cohorts from other institutions is needed to assess the generalizability of our classifier in a realworld setting. We only evaluated first and second order GLCM texture features, but higher order features, such as wavelet, Law features, or deep learning, may improve predictive performance (15). Although we investigated three lumbar vertebrae per previous literature reports (6–8), the use of more or fewer vertebrae and/or other hematopoietic structures in the body may be useful. Also, because standardized uptake value quantitation can vary on the basis of a number of factors, normalization of standardized uptake value units to the blood pool may also be needed.

We found that a radiomics model that includes the clinical stage and image features from the bone marrow, tumor, and its surrounding region at pretreatment fluorine 18–fluorodeoxyglucose PET/CT identified patient outcome in non–small cell lung cancer better than stage alone. This model uses clinical and imaging data that can be collected for these patients and is ready for further validation. However, additional studies investigating the underlying biology responsible for these imaging phenotypes are needed.

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