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2 Q1 **Potential Targets Analysis Reveals Dual PI3K/
3 mTOR Pathway Inhibition as a Promising
4 Q2 Therapeutic Strategy for Uterine
5 Q3 Leiomyosarcomas—An ENITEC Group Initiative**

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13 **Abstract**

14 **Purpose:** Uterine sarcomas are rare and heterogeneous tumors
15 characterized by an aggressive clinical behavior. Their high rates of
16 recurrence and mortality point to the urgent need for novel
17 targeted therapies and alternative treatment strategies. However,
18 no molecular prognostic or predictive biomarkers are available so
19 far to guide choice and modality of treatment.

20 **Experimental Design:** We investigated the expression of several
21 druggable targets (phospho-S6^{S240} ribosomal protein, PTEN,
22 PDGFR- α , ERBB2, and EGFR) in a large cohort of human uterine
23 sarcoma samples (288), including leiomyosarcomas, low-grade and
24 high-grade endometrial stromal sarcomas, undifferentiated uterine
25 sarcomas, and adenosarcomas, together with 15 smooth muscle
26 tumors of uncertain malignant potential (STUMP), 52 benign
27 uterine stromal tumors, and 41 normal uterine tissues. The potential
28 therapeutic value of the most promising target, p-S6^{S240}, was tested
29 in patient-derived xenograft (PDX) leiomyosarcoma models.
47

Results: In uterine sarcomas and STUMPs, S6^{S240} phos-
phorylation (reflecting mTOR pathway activation) was asso-
ciated with higher grade ($P = 0.001$) and recurrence ($P =$
0.019), as shown by logistic regression. In addition, p-S6^{S240}
correlated with shorter progression-free survival ($P = 0.034$).
Treatment with a dual PI3K/mTOR inhibitor significantly
reduced tumor growth in 4 of 5 leiomyosarcoma PDX models
(with tumor shrinkage in two models). Remarkably, the four
responding models showed basal p-S6^{S240} expression, where-
as the nonresponding model was scored as negative, suggest-
ing a role for p-S6^{S240} in response prediction to PI3K/mTOR
inhibition.

Conclusions: Dual PI3K/mTOR inhibition represents an effec-
tive therapeutic strategy in uterine leiomyosarcoma, and p-S6^{S240}
expression is a potential predictive biomarker for response to
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Translational Relevance

Uterine sarcomas are rare aggressive tumors characterized by high mortality rates and limited treatment options. Using an IHC screening approach, we aimed to investigate the expression of potential therapeutic targets in a large cohort of different human uterine sarcomas, encompassing all the main subtypes. We observed that p-S6^{S240}, reflecting mTOR pathway activity, is mainly expressed in high-grade sarcomas and that its presence correlates with shorter progression-free survival in leiomyosarcomas, the largest subgroup. Compounds targeting mTOR have shown limited success in leiomyosarcoma patients in clinical studies so far, possibly due to feedback-loop signaling activation. Here, we tested the efficacy of dual PI3K/mTOR inhibition on five different patient-derived leiomyosarcoma xenograft models. Our results provide preclinical evidence for the efficacy of dual PI3K/mTOR inhibition in uterine leiomyosarcoma patients and suggest that p-S6^{S240} could be considered as a predictive marker for response, opening new perspectives in terms of patients' treatment and stratification strategies.

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Introduction

Uterine sarcoma is the general term referring to a heterogeneous group of rare neoplasms with diverse histologic features, that together account for 3.4% of all uterine corpus malignancies (1). Although rare, they entail substantial morbidity and mortality, with frequent recurrences and distant metastases, even after hysterectomy (2). Leiomyosarcoma is the most frequently diagnosed and a very aggressive subtype, accounting for 60% of all uterine sarcomas (1). Low-grade endometrial stromal sarcomas (LGESS) account for 20% of uterine sarcomas, and they usually follow a less aggressive disease course compared with leiomyosarcoma, with a more indolent growth and delayed recurrences (2). The remaining 20% of uterine sarcomas comprise high-grade ESS (HGESS), undifferentiated uterine sarcoma (UUS), and adenocarcinomas. Smooth muscle tumors of uncertain malignant potential (STUMP) also arise from the myometrium, and represent a very rare entity that cannot be diagnosed as benign or malignant (3). Uterine sarcoma subtypes with HG histology are generally the most aggressive and are associated with poor prognosis. Adjuvant treatment is decided on the basis of the histologic subtype, but in general is scarce and of limited benefit, underlining the urgent need for new treatment options (2, 4).

During the past decade, our knowledge on the molecular aspects of sarcomas has expanded thanks to the advent of next-generation sequencing methods, which allowed biomarker identification and categorization into molecular and prognostic subgroups (5, 6). However, although efforts have been taken to identify therapeutic targets in sarcomas of the uterus, little

Note: Supplementary data for this article are available at Clinical Cancer Research Online (<http://clincancerres.aacrjournals.org/>).

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consensus has been attained so far on their expression prevalence, mainly because of the limited sized sample sets available, variations in detection protocols, and different cutoffs for positivity. In this study, we present the results of an immunohistochemical screening of relevant targets performed on one of the largest human uterine sarcoma sample sets published so far. Through collaboration within the European Network of Individualized Treatment in Endometrial Cancer (ENITEC), we collected more than 300 human uterine sarcoma samples and corresponding clinical data, being able to perform disease course analysis and investigate correlations between potential targets and clinical parameters. For targets analysis, we selected phosphorylated S6 ribosomal protein (p-S6^{S240}), the tumor suppressor and PI3K pathway inhibitor PTEN, platelet-derived growth factor receptor- α (PDGFR- α), erb-b2 receptor tyrosine kinase 2 (ERBB2/HER-2), and EGFR. Phosphorylated S6 is an important downstream player in the mTOR pathway, and PTEN inhibits the PI3K pathway upstream. PI3K/mTOR signaling has been implicated in leiomyosarcoma, confirmed by *in vitro* and *in vivo* studies (7, 8). PDGFR, ERBB2, and EGFR all have proven to be valuable targets in other cancer types. PDGFR, for example, is blocked by imatinib in gastrointestinal stromal tumors and dermatofibrosarcoma protuberans (9), whereas ERBB2 overexpression is tackled by the anti-ERBB2 antibodies trastuzumab and pertuzumab in breast cancer (10). Finally, EGFR is targeted by antibodies such as panitumumab in head and neck and colon cancer, and by tyrosine kinase inhibitors gefitinib and erlotinib in non-small cell lung cancer (11). To validate the results of such screening, we preclinically tested the most promising target in an *in vivo* context, using uterine sarcoma patient-derived xenograft (PDX) models. Of note, being established by implanting freshly isolated tumor fragments into immunocompromised mice, PDXs have proven high histologic and molecular similarity to the original tumor (12), together with high predictive value in terms of response to therapy (13).

Materials and Methods

Patient samples

After obtaining approval from the Medical Ethics Committee UZ/KU Leuven and Ethics Boards in collaborating centers, 303 archived formalin-fixed, paraffin-embedded sarcoma samples (6 of which are recurrences of included primary tumors), 52 benign uterine tumors, and 41 normal tissues were collected from 19 European hospitals, 13 of which are associated to ENITEC. A total of 307 unique tumor samples (malignant and benign), along with clinical data, were collected through ENITEC, with the following collaborating centers: UZ Leuven, Belgium ($n = 100$), Vall d'Hebron University Hospital, Barcelona, Spain ($n = 37$), MUMC Maastricht, Maastricht, the Netherlands ($n = 35$), Charles University in Prague—1st Faculty of Medicine, Prague, Czech Republic ($n = 23$), Turku University Hospital, Turku, Finland ($n = 23$), University Hospital Graz, Graz, Austria ($n = 23$), Haukeland University Hospital, Bergen, Norway ($n = 22$), Provincial

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132	Hospitals in Gdynia - Oncology Center, Gdynia, Poland ($n = 11$),	193
133	Radboud UMC, Nijmegen, the Netherlands ($n = 7$), University	194
134	Hospital Bonn, Bonn, Germany ($n = 7$), UMC Utrecht, Utrecht,	195
135	the Netherlands ($n = 7$), University Hospitals Köln, Köln, Ger-	196
136	many ($n = 6$), and Karolinska University Hospitals, Stockholm,	197
137	Sweden ($n = 6$). Remaining tumor samples were contributed by	198
138	MST Enschede (Enschede, the Netherlands), ZGT Almelo and	199
139	Hengelo and SKB Winterswijk, the Netherlands ($n = 26$), St. Jean,	200
140	Ste. Anna-St. Remi and St. Etienne, Brussels, Belgium ($n = 11$),	201
141	Yperman, Ieper, Belgium ($n = 2$), AZ Turnhout, Belgium ($n = 1$),	202
142	Mariaziekenhuis, Overpelt, Belgium ($n = 1$), and Imelda Hospi-	203
143	tal, Bonheiden, Belgium ($n = 1$). The sample set included 157	
144	leiomyosarcomas (4 recurrent matching to primary leiomyosar-	
145	coma), 68 LGESSs, 26 UUSs, 15 HGESSs (2 recurrent matching to	
146	primary LGESS), 17 adenosarcomas, 15 STUMPs, 5 HG uterine	
147	sarcomas, not otherwise specified (HG uSAR NOS), 44 leiomyo-	
148	mas, 8 endometrial stromal nodules (ESN), 23 healthy myomet-	
149	rial specimens, and 18 healthy endometrial samples. Of all	
150	collected tissue blocks, 6,5% was obtained from surgeries before	
151	2000, 62,5% was obtained between 2000 and 2010, and 31%	
152	dated from 2010 or later. Patient follow-up ranged from 1 month	
153	to 30 years. In addition to the external classification of tumors,	
154	carried out in the center of origin by the local pathologist, all cases	
155	were reviewed and reclassified in a blinded manner by the	
156	dedicated central pathologist P. Moerman, uterine tumors expert,	
157	according to the WHO 2014 classification (14). Cases with	
158	discordant diagnoses were excluded, and only cases where con-	
159	cordance was reached by the two independent pathologists were	
160	included for the screening. For clinical data collection, the Inter-	
161	national Federation of Gynecologic Oncology 2009 system was	
162	applied for staging of all samples (see Supplementary Table S1 for	
163	clinical data and treatment modalities). HG cases were the fol-	
164	lowing: all leiomyosarcoma, HGESS and UUS, HG uSAR NOS,	
165	and adenosarcoma with sarcomatous overgrowth. LG cases were	
166	all LGESS and LG adenosarcoma.	
167	Immunohistochemical stainings	
168	Paraffin slides (4 μm) were heated for 3 to 4 hours at 55°C,	
169	deparaffinized in toluol, and rinsed in ethanol. Tissues were	
170	blocked for endogenous peroxidases by 30-minute incubation	
171	in 0.5% H_2O_2 (107209, Merck Millipore) in methanol. After	
172	washing in TBS, epitopes were retrieved as displayed in Supple-	
173	mentary Table S2, which summarizes details of the IHC methods.	
174	Tissues were cooled down slowly in TBS, except after enzymatic	
175	retrieval of EGFR, which was stopped by 5-minute incubation in	
176	cold (4°C) TBS. Upon extensive washing, tissues were blocked	
177	with 1% milk powder, 2% BSA (A4503, Sigma-Aldrich), and 0.1%	
178	Tween-80 (822187, Merck Millipore) in TBS before antibody	
179	incubation. Blocking solutions were removed and tissues were	
180	incubated with antibody solutions in TBS (Supplementary Table	
181	S2). The following primary antibodies were used: anti-phospho-	
182	S6 ^{S240} (M7300, Dako), anti-PTEN (clone 6H2.1, M3627, Dako),	
183	anti-PDGFR- α (C-20, sc-338, Santa Cruz Biotechnology), anti-	
184	ERBB2 (A0485, Dako), and anti-EGFR (clone 31G7, 280005,	
185	Zymed). Tissues were washed, blocked for 15 minutes (except	
186	for PTEN staining), and incubated with secondary antibodies or,	
187	for PTEN, with EnVision-HRP (K4001, Dako). After washing,	
188	slides for EGFR and phospho-S6 ^{S240} stainings were incubated	
189	with streptavidin-HRP (P0397, Dako) for 30 minutes and	
190	washed again. All antibodies were visualized by 10-minute incu-	
191	bation in 3,3'-diaminobenzidine (DAB, D5905, Sigma) +	
	0.015% H_2O_2 (107209, Merck Millipore) in the dark. Nuclei	193
	were stained with Mayer's hematoxylin, and tissues were dehy-	194
	drated in propanol, dipped in xylene, and mounted. Positive	195
	controls consisted of PDGFR-expressing ovarian carcinoma,	196
	PTEN-expressing normal endometrium, ERBB2-expressing breast	197
	carcinoma, EGFR-expressing tumor (grown in nude mice) from	198
	human HEC cells and S6-expressing endometrial carcinoma with	199
	S6 phosphorylation, confirmed by Western blot analysis. To	200
	ensure no staining was caused by a specific binding of second-	201
	ary/tertiary molecules, control slides without addition of primary	202
	antibody were used.	203
	Evaluation and scoring of immunohistochemical stainings	204
	All stainings were evaluated semiquantitatively, using a scoring	205
	system (Supplementary Table S3) that takes into account both the	206
	staining intensity (0 = absent, 1 = weak, 2 = moderate, and 3 =	207
	strong) and the percentage of stained cells (0 = absent, 1 = less	208
	than 1%, 2 = 1%–10%, 3 = 11%–33%, 4 = 34%–66%, and 5 =	209
	67%–100%; ref. 15). Both scores were added to obtain a maxi-	210
	mum score of 8. Stainings were evaluated only in the cellular	211
	component where expression was expected. Tissues were consid-	212
	ered positive at a cut-off score of 6, corresponding to strong	213
	positivity in $\geq 11\%$ of cells, moderate positivity in $\geq 34\%$ of cells,	214
	or weak staining in $\geq 67\%$ of cells. This cutoff was deemed	215
	clinically relevant for therapeutic applications, as a targeted ther-	216
	apy would most likely be effective when a sufficient number of	217
	cells express the target. For ERBB2, this coincides with the gen-	218
	erally applied scoring system approved by the FDA (16). Tissues	219
	were evaluated by the observer (T. Cuppens) and in randomly	220
	selected cases (25%) additionally by a second observer (A. Coose-	221
	mans). For these specific cases, a concordance of $>90\%$ was	222
	reached between scorings by the two independent researchers.	223
	Photographs of representative cases were taken using the Axios-	224
	kop microscope (MRc5, Zeiss) and the ZEN 2.0 software.	225
	Establishment and validation of PDX models	226
	Animal experiments were approved by the Animal Ethics	227
	Committee of KU Leuven (Leuven, Belgium). Mouse xenograft	228
	models were established in collaboration with the Trace Platform	229
	(UZ/KU Leuven). Small fragments of tumor tissue (3-3-3 mm),	230
	obtained during necessary surgery or biopsy upon informed	231
	consent, were implanted interscapularly in female NMRI nude	232
	mice of minimum 6 weeks old (Taconic) and expanded in several	233
	generations.	234
	Treatment of PDX models	235
	Mice were randomized according to tumor volume (when	236
	tumor volumes reached 200–250 mm^3) and treated for 19 to	237
	22 days (5–9 mice/group for BEZ235- and placebo-treated groups,	238
	3–7 mice for trabectedin-treated groups). Some mice in the	239
	trabectedin groups were excluded due to signs of toxicity around	240
	the tail vein. BEZ235 (Novartis, through Selleckchem, S1009) was	241
	prepared in 10% N-methyl-2-pyrrolidone (sc-237581, Santa Cruz	242
	Biotechnology)/90% polyethylene glycol (90878, Sigma) and	243
	administered orally, daily, in a dose of 40 mg/kg. Placebo-treated	244
	mice received the same volume of vehicle as the BEZ235-treated	245
	group. Trabectedin (Yondelis) was acquired from the UZ Leuven	246
	Hospital Pharmacy, aliquoted in DMSO (102952, Merck Milli-	247
	pore), and diluted in saline. It was administered intravenously	248
	(0.15 mg/kg; tail vein), once weekly. Tumor volumes were mea-	249
	sured with a caliper twice weekly (calculated using the following	250

253 formula: length \times width \times depth $\times \pi/6$), and mice body weights
 254 were monitored. Treatment was discontinued after 3 weeks or
 255 when the tumor reached a volume of 2,000 mm³. After sacrifice,
 256 all tumors were stained and scored for p-S6^{S240} level as before.
 257 Significant weight loss was defined as a loss of 15% of the body
 258 weight recorded at the beginning of the treatment.

259 Statistical analyses

260 IBM SPSS Statistics 20 was used for all statistical analyses
 261 except for the *in vivo* treatment experiments. Age and tumor size
 262 were considered continuous variables, whereas all other vari-
 263 ables were categorical. The χ^2 test was used to compare staining
 264 results (portion of positive samples) between histologic sub-
 265 groups. To determine potential associations between stainings
 266 and clinical variables (e.g., stage, age, tumor size) for primary
 267 versus recurrent tumors and LG versus HG histologies, univari-
 268 ate analyses were first carried out using χ^2 tests for categorical
 269 variables. Next, logistic regression was performed including
 270 only one variable for continuous and categorical variables, to
 271 permit direct comparison with multivariate logistic regression
 272 analysis, including all variables that showed a significant cor-
 273 relation in univariate analysis. Univariate survival analyses
 274 were carried out using the Kaplan–Meier method/log-rank test.
 275 In the *in vivo* treatment experiments, tumor volumes of different
 276 treatment groups were compared over time using two-way
 277 repeated measures ANOVA in GraphPad.

278 Results

279 HG uterine sarcomas are characterized by aggressive clinical 280 behavior and poor prognosis

281 We collected and analyzed the following patient samples:
 282 leiomyosarcoma ($n = 153$), LGESS ($n = 68$), UUS ($n = 26$),
 283 HGESS ($n = 13$), STUMP ($n = 15$), adenocarcinoma ($n = 17$), and
 284 HG uSAR NOS ($n = 5$), which could not be categorized in any
 285 conventional tumor group. Leiomyosarcoma, HGESS, UUS, and
 286 HG uSAR NOS are HG tumors. Of 17 adenocarcinoma patients, 4
 287 were diagnosed with an HG variant (with sarcomatous over-
 288 growth). The remaining adenocarcinoma were considered LG, as
 289 well as the LGESS. No grade was assigned to STUMP cases. The
 290 most important clinical data summarized per histologic subtype
 291 are shown in Supplementary Table S1. Information on disease-
 292 specific survival (DSS) and progression-free survival (PFS) was
 293 available for 242 and 210 patients, respectively. First, we pooled
 294 all patients with HG and LG tumors and compared their survival,
 295 confirming that HG tumors are clinically more aggressive (Sup-
 296 plementary Fig. S1A and S1B, both $P < 0.001$). For LG patients, the
 297 5-year DSS and PFS rates were 86% and 64%, respectively,
 298 whereas for HG patients, after 5 years only 33% were alive and
 299 18% showed no progression. Next, we determined survival rates
 300 for all separate subtypes (Supplementary Fig. S1C and S1D). The
 301 5-year DSS rate was 0% to 22% in UUS patients, around 30% in
 302 HGESS patients, and 35% in leiomyosarcoma patients, contrast-
 303 ing with 85% in LGESS patients. Concurrently, the 5-year PFS rate
 304 was 0% to 10% in UUS patients, 0% to 29% in HGESS patients,
 305 18% in leiomyosarcoma patients, and 63% in LGESS patients. Of
 306 note, patients diagnosed with STUMP had a significantly better
 307 PFS compared with patients diagnosed with leiomyosarcoma
 308 (median PFS = 41 months in STUMP and 17 months in lei-
 309 myosarcoma, $P = 0.023$), although the difference in DSS was not
 310 significant (median DSS = 52 months in STUMP and 35 months

in leiomyosarcoma, $P = 0.086$), probably due to the low number
 of STUMP patients. For adenocarcinoma patients, the 5-year sur-
 vival estimation was not feasible due to the smaller sample set,
 with fewer events. The 3 HG adenocarcinoma patients with avail-
 able follow-up data died of disease within 26 months (100%). Of
 the patients with LG adenocarcinoma, only 1 of 11 (9%) patients
 died of disease (after 25 months), and the follow-up time of other
 patients was between 19 and 119 months.

Overall, patient subgroups with HG tumors are characterized
 by a substantially worse prognosis, and the largest subgroup of
 uterine sarcoma presented in our study, as in the general popu-
 lation, is leiomyosarcoma.

The PI3K/mTOR pathway and PDGFR- α are potential targets in different uterine sarcoma subtypes

On the basis of available literature data and therapeutic poten-
 tial (i.e., for which therapeutic agents are available and active in
 other cancer types), we investigated in our cohort of human
 uterine sarcoma samples the expression of the following drug-
 gable molecular targets: phospho-S6^{S240}, PTEN, PDGFR- α ,
 ERBB2, and EGFR. Their expression levels were determined in a
 total of 396 samples, including malignant tumors (leiomyosar-
 coma, LGESS, HGESS, UUS, adenocarcinoma, and HG uSAR NOS),
 tumors of uncertain malignancy (STUMP), benign tumors (lei-
 myoma and ESN), and normal myometrium and endometrium.
 Expression data for the five selected proteins are summarized
 in Table 1, per histologic subgroup, and for pooled HG and LG
 samples. Representative images for the stainings and a detailed
 description of the adopted scoring system are shown in Supple-
 mentary Fig. S2 and Supplementary Table S3, respectively. Tissues
 were considered positive at a score of 6 or higher, corresponding to
 weak staining in $\geq 67\%$ of cells, moderate staining in $\geq 34\%$ of
 cells, or strong staining in $\geq 10\%$ of cells. Considering all uterine
 sarcomas and STUMP cases together, p-S6^{S240} was scored positive
 in 26% of samples. Loss of PTEN expression was seen in 34% of
 cases, with up to 50% loss in UUS samples. The most frequently
 expressed protein was PDGFR- α (82%), while ERBB2 and EGFR
 were detected in 5% and 9% of cases, respectively. EGFR was
 almost exclusively detected in the stromal component of adeno-
 carcinoma: 31% of LG adenocarcinoma and 75% of HG adenocar-
 cinoma expressed EGFR. Remarkably, ERBB2 was mainly expressed
 in the epithelial component of adenocarcinoma: 58% of LG ade-
 nocarcinoma and 100% of HG adenocarcinoma showed ERBB2
 expression. Although this component is considered benign, it
 showed more frequent ERBB2 expression compared with normal
 endometrial epithelial cells ($P = 0.001$ for LG and $P < 0.001$ for
 HG, as determined by χ^2 test).

Taken together, our data show that PDGFR- α is a potential
 target in all uterine sarcoma subtypes, PI3K/mTOR targeting is an
 option in 26% of cases, mainly leiomyosarcoma, HGESS and
 UUS, and ERBB2/EGFR seem to be targetable in a minority of
 cases, mostly adenocarcinoma. Recently, pazopanib, a multikinase
 inhibitor also targeting PDGFR, was approved for treatment of
 leiomyosarcoma after a successful randomized phase III trial (the
 PALETTE study; ref. 17), confirming the potential predictive value
 of such a histologic scoring system.

In addition, we assessed cyclin D1 expression and the presence
 of t(10;17)(q22;p13) rearrangement, leading to the fusion gene
 YMHAE/NUTM2A/B, in HGESS and UUS cases because these
 alterations have been linked to HGESS and as the 14-3-3 onco-
 protein, resulting from the translocation, has been suggested as a

Table 1. Expression of therapeutic targets in uterine sarcomas, benign tumors, and normal tissues

	p-S6 ^{S240}		PTEN		PDGFR-α		ERBB2		EGFR	
	Prim	Rec	Prim	Rec	Prim	Rec	Prim	Rec	Prim	Rec
All sarcomas + STUMP	60/261 (23%)	15/36 (42%)	160/249 (64%)	27/34 (79%)	219/261 (84%)	25/36 (69%)	9/264 (3%)	5/37 (14%)	22/261 (8%)	5/37 (14%)
Prim + Rec	77/299 (26%)		188/285 (66%)		245/299 (82%)		14/303 (5%)		27/300 (9%)	
Pooled HG	50/177 (28%)	14/26 (54%)	111/173 (64%)	20/24 (83%)	156/177 (88%)	19/25 (76%)	6/179 (3%)	2/26 (8%)	12/177 (7%)	2/26 (8%)
LMS	32/131 (24%)	11/22 (50%)	91/129 (71%)	17/21 (81%)	118/133 (89%)	18/21 (86%)	2/133 (2%)	2/22 (9%)	6/132 (5%)	1/22 (5%)
Prim meta	2/2 (100%)		1/2 (50%)		1/2 (50%)		0/2 (0%)		0/2 (0%)	
HGESS	3/13 (23%)	2/2 (100%)	7/13 (54%)	1/1 (100%)	12/13 (92%)	0/2 (0%)	3/13 (23%)	0/2 (0%)	1/13 (8%)	0/2 (0%)
UUS	14/25 (56%)	0/1 (0%)	11/23 (48%)	1/1 (100%)	19/23 (83%)	0/1 (0%)	0/25 (0%)	0/1 (0%)	1/24 (4%)	0/1 (0%)
HG AS stroma	0/4 (0%)		2/4 (50%)		3/4 (75%)		1/4 (25%)		3/4 (75%)	
HG AS epithelium	0/2 (0%)		1/1 (100%)		1/2 (50%)		2/2 (100%)		0/1 (0%)	
HG USAR NOS	1/4 (25%)	1/1 (100%)	0/4 (0%)	1/1 (100%)	4/4 (100%)	1/1 (100%)	0/4 (0%)	0/1 (0%)	1/4 (25%)	1/1 (100%)
Pooled LG	6/69 (9%)	1/10 (10%)	37/61 (61%)	7/10 (70%)	54/69 (78%)	6/11 (55%)	3/70 (4%)	3/11 (27%)	9/69 (13%)	3/11 (27%)
LGESS	4/57 (7%)	0/9 (0%)	32/51 (63%)	6/9 (67%)	45/57 (79%)	5/10 (50%)	3/58 (5%)	2/10 (20%)	6/57 (11%)	2/10 (20%)
LG AS stroma	2/12 (17%)	1/1 (100%)	5/10 (50%)	1/1 (100%)	9/12 (75%)	1/1 (100%)	0/12 (0%)	1/1 (100%)	3/12 (25%)	1/1 (100%)
LG AS epithelium	1/11 (9%)		3/10 (30%)		10/12 (83%)		7/12 (58%)		1/12 (8%)	
STUMP	4/15 (27%)		12/15 (80%)		9/15 (60%)		0/15 (0%)		1/15 (7%)	
Benign tumors										
Leiomyoma	1/43 (2%)		18/26 (69%)		10/26 (43%)		0/42 (0%)		0/44 (0%)	
Endometrial stromal nodule	0/8 (0%)		2/6 (33%)		3/8 (38%)		0/8 (0%)		0/8 (0%)	
Normal tissues										
Myometrium	1/21 (5%)		9/16 (56%)		4/23 (17%)		0/23 (0%)		0/23 (0%)	
Endometrium stroma	1/17 (6%)		4/12 (33%)		11/16 (69%)		0/18 (0%)		2/18 (11%)	
Endometrium epithelium	4/17 (24%)		4/12 (33%)		11/16 (69%)		1/18 (0%)		0/17 (0%)	

NOTE: Displayed are numbers and proportions (%) of positive cases. The two primary metastatic leiomyosarcoma cases are excluded from the pooled analyses that are divided according to primary or recurrent tumors. Epithelial components of adenocarcinoma cases are not considered as separate samples and are therefore not included in the pooled samples. STUMP cases do not have a grading system and are displayed as a separate category.

Abbreviations: AS, adenocarcinoma; Prim, primary; Prim meta, primary metastasis; Rec, recurrent.

Table 2. Logistic regression: predictors of HG versus LG histology

Variable	N	Univariate OR (95% CI)	P	Multivariate OR (95% CI)	P
p-S6 ^{S240}					
Negative	120	1			
Positive	44	5.385 (1.803-16.082)	0.003	7.242 (2.294-22.866)	0.001
Tumor size	164	1.176 (1.076-1.286)	<0.001	1.158 (1.056-1.270)	0.002
Age	164	1.034 (1.008-1.061)	0.010	1.027 (0.998-1.057)	0.064

NOTE: Logistic regression with "LG histology" as a reference. OR > 1 and $P < 0.05$ indicate a statistically significant correlation of the variable with HG histology. Abbreviation: CI, confidence interval.

therapeutic target (18–20). We confirmed that cyclin D1 was expressed more in HGESS (7/15; 47%) than in UUS (4/25; 16%), as shown by the χ^2 test ($P = 0.035$). Likewise, previous studies have reported 8 of 14 and 7 of 18 cyclin D1-positive HGESS cases (18, 21). Of 12 interpretable HGESS and 19 UUS cases, only 2 HGESS cases showed the t(10;17) translocation (one was confirmed by RT-PCR; the other case had no available RNA) and both had very strong (>90% positive nuclei) cyclin D1 staining, confirming the findings by Lee and colleagues (ref. 22; see Supplementary Methods and Supplementary Fig. S3). Our results are in line with previous studies that detected the translocation with FISH, where 4 of 14 and 4 of 16 cases were positive (18, 21). Although the portion of translocation-positive cases is higher in other studies (7/12 and 5/8), this may be explained by variability between methods, as exemplified by Micci and colleagues (20, 23). Cyclin D1 expression did not correlate with DSS, PFS, or any of the five investigated proteins.

P-S6^{S240} expression correlates with recurrent and HG tumors and with shorter PFS

To identify links between protein expression and tumor characteristics, we checked for correlations with tumor grade and primary versus recurrent tumors. Remarkably, p-S6^{S240} was observed more frequently in HG tumors (66/205; 32%) than in LG tumors (7/79; 9%; $P = 0.004$) and was also detected more frequently in recurrent tumors (15/36; 42%) than in primary tumors (60/261; 23%; $P = 0.016$), as calculated by χ^2 test. Also, ERBB2 was expressed more frequently in recurrent tumors (5/37; 14%) than in primary tumors (9/264; 3%; $P = 0.006$). Subsequently, logistic regression analyses (correcting for other factors correlated with grade and recurrence) showed that p-S6^{S240} was independently associated with both histologic aggressiveness ($P = 0.001$; Table 2) and recurrence ($P = 0.019$; Table 3), whereas ERBB2 was associated only with recurrence ($P = 0.011$). Together, these findings suggest that mTOR pathway activation may be associated with disease progression in uterine sarcomas. Because leiomyosarcomas represent the largest uterine sarcoma subgroup, and are generally HG, we further focused our analyses on this subgroup. In leiomyosarcoma, phosphorylation of S6^{S240} was detected in 29% of cases, significantly more frequently than in LM

($P < 0.001$; χ^2 test) and healthy myometrium ($P = 0.018$). P-S6^{S240} was the only variable that was more often detected in recurrent leiomyosarcoma (11/22; 50%) than in primary leiomyosarcoma (32/131; 24%; $P = 0.014$; χ^2 test); hence, multivariate analysis was irrelevant. Of note, two primary metastatic leiomyosarcomas were included in the analysis and both showed p-S6^{S240} positivity. To assess the potential prognostic value of the investigated proteins, we carried out survival analyses in uterine sarcoma subgroups. Interestingly, p-S6^{S240} positivity correlated with shorter PFS in leiomyosarcoma patients ($P = 0.034$) and showed a trend toward shorter DSS in univariate analysis (Fig. 1A and B). Loss of PTEN, which negatively regulates PI3K signaling, correlated with shorter DSS ($P = 0.039$) in leiomyosarcoma patients, but not with PFS (Fig. 1C and D). Multivariate analysis was not feasible due to the small sample size obtained after filtering out cases with missing data.

Taken together, our data suggest that p-S6^{S240} correlates with HG and recurrent uterine sarcomas, an observation that was also confirmed in leiomyosarcoma cases, the largest uterine sarcoma subgroup. In addition, p-S6 and PTEN may have prognostic value in leiomyosarcoma patients.

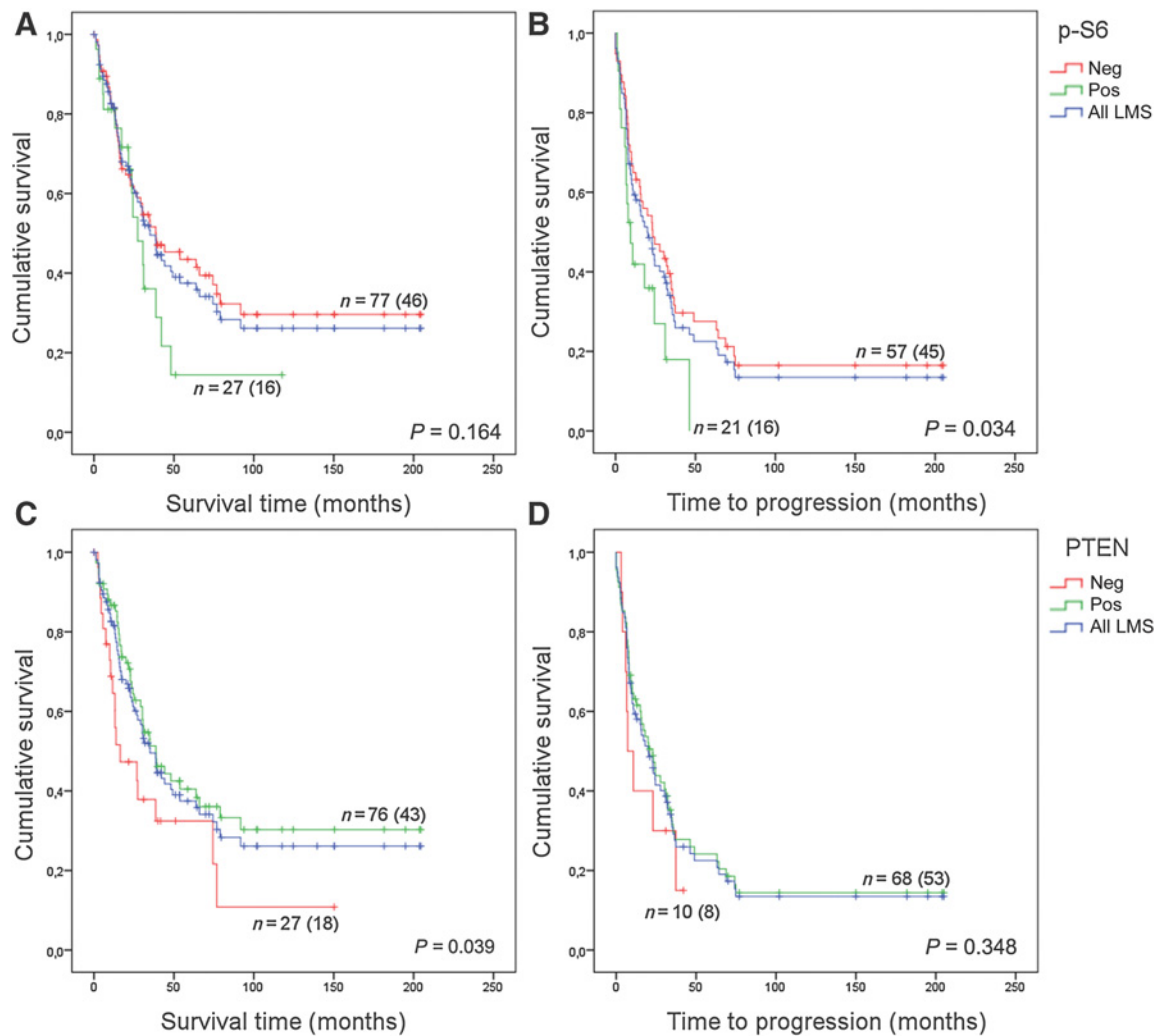
Dual inhibition of mTOR and PI3K reduces tumor growth in p-S6^{S240}-positive leiomyosarcoma PDX models

The finding that p-S6^{S240} positivity is correlated with HG and recurrent uterine sarcomas suggests that mTOR pathway activation may play a central role in uterine sarcoma progression. To validate this observation, we decided to test the efficacy of mTOR pathway inhibition in clinically relevant PDX models of uterine leiomyosarcoma. Despite previous clinical trials with mTOR-targeting agents for treatment of leiomyosarcoma patients, so far, none of the tested compounds (e.g., ridaforolimus, temsirolimus) have been approved for leiomyosarcoma by the FDA (7). It has been suggested that the lack of clinical effect could be due to the feedback activation of AKT as a consequence of mTOR complex 1 (mTORC1) inhibition, which can sustain tumor growth through mTOR complex 2 (mTORC2) signaling (24, 25). For this reason, we selected a dual PI3K/mTOR inhibitor, BEZ235, also able to block mTORC2. Five PDX models were derived from uterine leiomyosarcoma of different patients, from which the clinical

Table 3. Logistic regression: predictors of recurrent versus primary tumor samples

Variable	N	Univariate OR (95% CI)	P	Multivariate OR (95% CI)	P
p-S6 ^{S240}					
Negative	222	1			
Positive	75	2.393 (1.162-4.929)	0.018	2.408 (1.156-5.016)	0.019
ERBB2					
Negative	283	1			
Positive	14	4.516 (1.423-14.336)	0.011	4.567 (1.406-14.827)	0.011

NOTE: Logistic regression with "primary tumors" as a reference. OR > 1 and $P < 0.05$ indicate a statistically significant correlation of the variable with recurrent samples. Abbreviation: CI, confidence interval.

**Figure 1.**

Survival of leiomyosarcoma patients according to p-S6^{S240} and PTEN expression. **A–D**, Kaplan-Meier survival curves showing DSS (**A** and **C**) and PFS (**B** and **D**) of leiomyosarcoma patients. **A** and **B**, The log-rank test with corresponding *P* values applies to the p-S6^{S240}-negative (red) and p-S6^{S240}-positive (green) curves. Blue curves (all leiomyosarcomas) are depicted as comparison. The number of patients in the analyses is indicated next to the curve with number of events between brackets. **C** and **D**, The log-rank test applies to the PTEN-negative (red) and PTEN-positive (green) curves.

Q13

455 characteristics are shown in Supplementary Table S4. Each model
 456 was treated for 3 weeks with BEZ235, placebo, and trabectedin
 457 (Yondelis), an alkylating chemotherapeutic agent approved for
 458 leiomyosarcoma treatment after failure of anthracyclines. We
 459 chose trabectedin as a chemotherapy control as it is the youngest,
 460 most recently approved chemotherapy. Its antiproliferative prop-
 461 erties rely on multiple mechanisms, including the inhibition of
 462 transactivated transcription and the interaction with DNA repair
 463 proteins (26). Of five treated leiomyosarcoma models, four
 464 showed response to dual PI3K/mTOR inhibition (Fig. 2). Whereas
 465 the tumor volume was stabilized in EMC029, tumor growth was
 466 slowed down in EMC050. Furthermore, tumor shrinkage was
 467 observed in EMC036 (21% reduction, compared with placebo)
 468 and EMC041 (35% reduction, compared with placebo). No
 469 response to BEZ235 was noted in EMC031, a recurrent, pretreated
 470 leiomyosarcoma. Response to trabectedin was noted in four
 471 models, while EMC029 showed a trend (nonsignificant) toward

473 response after 8 days. No mice in any arms of the treatment
 474 experiments showed significant weight loss (data not shown).

475 Interestingly, the four responding models showed in their
 476 placebo-treated tumors expression of p-S6^{S240}, with mean scores
 477 between 6,3 and 7,8 (see Table 4 for mean scores; representative
 478 images are shown in Fig. 2), whereas all BEZ235-treated tumors
 479 were scored as negative. In the nonresponding model (EMC031),
 480 p-S6^{S240} staining in placebo-treated tumors was scored as nega-
 481 tive, with a mean score of 5,1. These findings suggest that p-S6^{S240}
 482 expression can be used to predict response to PI3K/mTOR block-
 483 age in leiomyosarcoma.

484 To extend our testing of dual PI3K/mTOR inhibition beyond
 485 BEZ235, EMC041 was additionally treated with a combination of
 486 the mTORC1/2 inhibitor TAK-228 and the PI3K α inhibitor alpe-
 487 lisib. The combination of TAK-228 and alpelisib was as effective as
 488 BEZ235 in inhibiting tumor growth (no significant difference
 489 between both treatment groups), supporting in general our

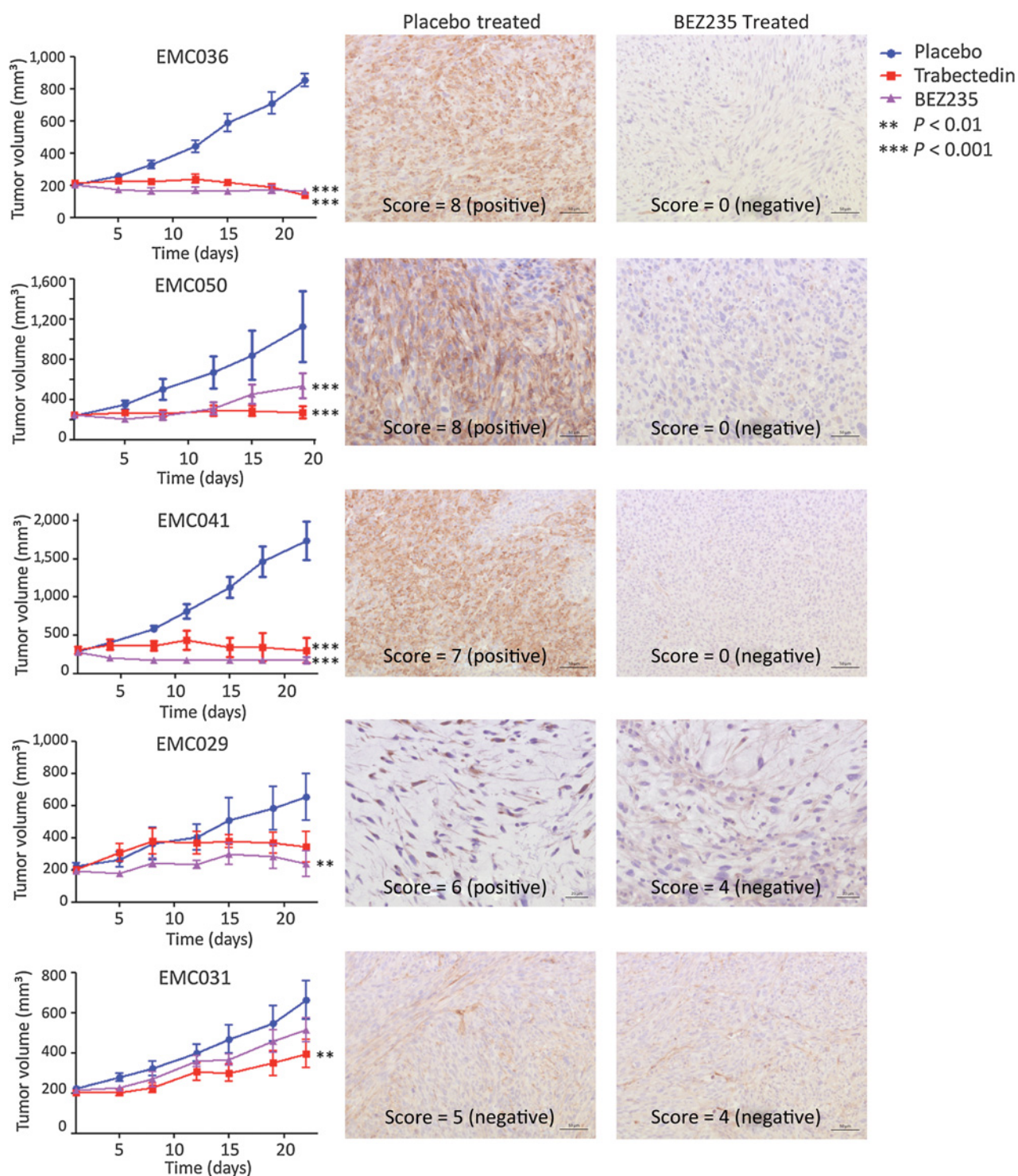


Figure 2.

In vivo dual inhibition of mTOR and PI3K by BEZ235 in uterine leiomyosarcoma PDX models. Mice were treated with BEZ235, trabectedin (as a chemotherapy control), or placebo. Tumor volumes were measured twice weekly, and growth curves of treated mice were compared with placebo-treated mice using two-way repeated measures ANOVA. Data points and error bars represent mean values and SEM. Significant effects (compared with placebo) are indicated with ** and ***. Tumor growth curves are depicted with p-S6^{S240} stainings and scores of representative tumors of each model (left, placebo-treated tumor; right, BEZ235-treated tumor). Pictures were taken at $\times 20$ magnification (scale bar, 50 μm) and at $\times 40$ magnification for EMC029 (scale bar, 20 μm). A larger magnification was used for EMC029 to increase visibility as the cells show a small amount of cytoplasm. Numbers of mice for placebo, trabectedin, and BEZ235-treated groups are respectively: EMC036: $n = 6, 6, 5$; EMC050: $n = 6, 7, 6$; EMC041: $n = 6, 3, 6$; EMC029: $n = 5, 4, 5$; EMC031: 7, 7, 9.

Table 4. Response of PDX models to BEZ235 with p-S6^{S240} scores

Model	Response to BEZ235	p-S6 ^{S240} mean score placebo-treated tumors	p-S6 ^{S240} status placebo-treated tumors
EMCO36	Decrease in tumor volume	7,8	Positive
EMCO50	Decrease in tumor growth	7,7	Positive
EMCO41	Decrease in tumor volume	7,0	Positive
EMCO29	Stable tumor volume	6,3	Positive
EMCO31	No response	5,1	Negative

NOTE: Five PDX models were treated with BEZ235, trabectedin, and placebo. Placebo-treated tumors were scored for p-S6^{S240} level. For each model, the mean scores of all placebo-treated tumors are depicted.

492 approach of dual PI3K/mTOR inhibition in leiomyosarcoma
493 (Supplementary Methods; Supplementary Fig. S4).

494 Thus, four of five uterine leiomyosarcoma models, which were
495 p-S6^{S240} positive, responded to dual PI3K/mTOR inhibition,
496 which can represent a new therapeutic option for leiomyosarcoma
497 patients with p-S6^{S240}-positive tumors.

498 Discussion

499 We analyzed a large cohort of samples from uterine sarcoma
500 patients for the expression of selected druggable therapeutic
501 targets, to determine the subgroups for which specific targeted
502 agents would be the most potentially effective.

503 Here, we show that PDGFR- α is expressed in the majority of
504 samples, in all sarcoma subtypes. Importantly, after initiation of
505 this study, pazopanib, targeting PDGFR, KIT, FGFR, and VEGFR,
506 was approved for the treatment of leiomyosarcoma patients after a
507 successful placebo-controlled phase III trial (17). Another recent
508 phase II trial showed the addition of PDGFR- α inhibitor olar-
509 atumab to doxorubicin is beneficial in soft tissue sarcoma patients
510 (including leiomyosarcoma; ref. 27). Our results confirm that
511 PDGFR- α is frequently expressed in uterine leiomyosarcoma, but
512 also other uterine sarcoma types show expression in at least 75%
513 of cases, suggesting that pazopanib/olaratumab should also be
514 tested in other uterine sarcoma subtypes. Of note, 2 LGES
515 patients have been reported to show response to imatinib in case
516 reports, encouraging further studies (28, 29). Although one case
517 expressed KIT (PDGFR status unknown), the other case showed
518 no KIT expression or activating mutation, but was strongly posi-
519 tive for PDGFR, suggesting imatinib acted through PDGFR in the
520 latter case. Indeed, because KIT is not mutated in uterine sarcomas
521 (6), imatinib may exert its effect by PDGFR blocking in uterine
522 sarcomas (9).

523 ERBB2 and EGFR, although being important targets in other
524 cancer types, have not been studied frequently in uterine sarcomas
525 (7). An exception is the study by Movva and colleagues (6),
526 describing that ERBB2 is rarely overexpressed in leiomyosarcoma
527 and ESS. In our sample set, ERBB2 and EGFR were rarely detected,
528 except in adenosarcoma. ERBB2 was expressed in the epithelial
529 component in 58% of LG adenosarcoma and in 100% of HG
530 adenosarcoma cases. Contrarily, EGFR expression in adenosar-
531 coma was seen in a minority of epithelial cells, whereas it was
532 expressed in the stromal component in 31% of LG adenosarcoma
533 and in 75% of HG adenosarcoma cases. This stromal-epithelial
534 distribution of EGFR and ERBB2 in adenosarcoma is in line with
535 their expression pattern in carcinosarcomas (30-32). Only two
536 other studies reported on the expression of EGFR (2/6 positive
537 cases) and ERBB2 (0/6 and 0/10 positive cases) in adenosarcoma,
538 but without evaluating the epithelial component (30, 32). In
539 addition, we show that in uterine sarcomas, ERBB2 is more

frequently detected in recurrent samples than in primary tumors,
541 suggesting that ERBB2 may play a role in sarcoma progression.
542

543 The PI3K/mTOR pathway has been implicated in the patho-
544 genesis of leiomyosarcoma, and preclinical studies have shown
545 effect of mTOR-targeting agents (7, 8). A negative regulator of
546 PI3K/mTOR signaling, PTEN, is frequently deleted in leiomyo-
547 sarcoma (6, 33). In our cohort, absence or low expression of PTEN
548 was noted in 28% of leiomyosarcoma samples. This is concordant
549 with earlier findings, showing decreased expression of PTEN in
550 20% to 38% of leiomyosarcoma cases (6, 34). Another study
551 reported PTEN loss by IHC in only 7% of uterine leiomyosarcoma
552 (35). This discrepancy is likely due to the use of different
553 scoring systems. In leiomyosarcoma patients, we showed that
554 PTEN loss correlates with shorter DSS. PTEN loss has been
555 shown previously to have prognostic value in other gynecologic
556 cancer types (36, 37). Next to its prognostic role, loss of PTEN
557 may also guide therapy decisions. Indeed, PTEN-deficient
558 tumors may be more sensitive to PARP inhibitors, due to
559 PTEN's role in genomic integrity, with PTEN loss leading to
560 defects in homologous recombination (38).

561 Downstream to mTOR signaling, S6 kinases (S6K) are activated
562 through phosphorylation. A well-known target of S6K is the S6
563 ribosomal protein, a component of the 40S ribosomal protein.
564 Here, we used the phosphorylated form of S6 as a read-out for S6K
565 activity, and thus mTOR pathway activation (39). The S6 protein
566 can be phosphorylated at serines 235/236 and 240/244. Pende
567 and colleagues (40) have described phosphorylation at S235/236
568 even when mTOR-activated kinases S6K1 and 2 are knocked out.
569 In this situation, phosphorylation at S240/244 was obliterated,
570 suggesting that mTOR-activated S6K1/2s are the only kinases
571 responsible for phosphorylation at serines 240/244 in the S6
572 protein (40). Therefore, we chose to detect S6 phosphorylation at
573 serine 240 using a phospho-site-specific antibody. In our dataset,
574 29% of uterine leiomyosarcoma samples showed p-S6^{S240} posi-
575 tivity, significantly more than in benign lesions and normal
576 tissue. Similarly, Brewer Savannah and colleagues (35) reported
577 24% of uterine leiomyosarcoma to be strongly positive, and
578 Hernando and colleagues (41) found 44% of soft tissue leiomyo-
579 sarcoma samples to be p-S6^{S240} positive. Setsu and colleagues
580 (34) found 74,5% of soft tissue leiomyosarcoma samples to be
581 p-S6^{S235/236} positive. However, the latter report did not include
582 uterine lesions and used a lower cutoff for positivity.

583 In our study, p-S6^{S240} staining was observed more in HG and
584 recurrent tumors, suggesting that S6 phosphorylation might be an
585 event linked to disease progression. This finding is in line with the
586 previous report of Brewer Savannah and colleagues (35), who
587 observed higher levels of p-S6^{S235/236} in recurrent and metastatic
588 uterine leiomyosarcoma lesions. We are the first to report this
589 finding in a large cohort of 153 uterine leiomyosarcoma patients.
590 Furthermore, we show that p-S6^{S240} positivity correlates with

593 shorter PFS in leiomyosarcoma patients; hence, p-S6^{S240} could be
594 a prognostic marker in leiomyosarcoma patients.

595 MTOR inhibition showed modest effectiveness in preclinical
596 studies and in clinical trials on sarcomas, where leiomyosarcoma
597 patients (origin not specified) showed minor response to ridafor-
598 olimus and temsirolimus (7, 42, 43). Taking into account their
599 limited clinical effect, as well as the toxicities, the FDA has not
600 approved mTOR inhibitors for leiomyosarcoma patients so far.
601 This limited efficacy may be partly due to the absence of patient
602 selection, as no predictive markers are currently available. In
603 addition, these compounds only inhibit mTORC1, which may
604 lead to feedback activation of AKT and sustained signaling
605 through mTORC2 (25). New-generation inhibitors targeting also
606 mTORC2, as well as PI3K, have not been tested in gynecologic
607 sarcomas until very recently. SK-LMS-1, a vulvar leiomyosarcoma
608 cell line, has proven to be sensitive to BEZ235, the same dual
609 PI3K/mTOR inhibitor that we tested in our study (44). BEZ235
610 has also been shown to inhibit the proliferation of pazopanib-
611 resistant retroperitoneal undifferentiated pleomorphic sarcoma
612 (UPS) cells (45). However, in a genetically engineered mouse
613 model of UPS, BEZ235 inhibited tumor growth in only 3 of 9 mice
614 (46). BEZ235 inhibits various sarcoma cell lines, including rhab-
615 domyosarcoma, Ewing sarcoma, osteosarcoma, and chondrosar-
616 coma cells *in vitro*, although reported *in vivo* models show varying
617 response (47, 48).

618 In contrast with the cell line-based *in vivo* models, which
619 have been used in most studies on sarcomas, we have chosen to
620 establish PDX models, which better represent the original
621 tumor characteristics (13). Here, we show a strong response
622 of uterine leiomyosarcoma PDX models to BEZ235. Unfortu-
623 nately, after initiation of this study, BEZ235 development was
624 discontinued by Novartis, mainly due to toxicity (49).
625 BEZ235's clinical toxicity profile was unexpected because no
626 such adverse effects were observed in our preclinical tests or in
627 previous preclinical studies (47, 48). However, our results
628 provide preclinical evidence for the efficacy of dual PI3K/mTOR
629 inhibition in uterine leiomyosarcoma patients, supporting the
630 use of other (less toxic) dual PI3K/mTOR inhibitors like geda-
631 tolisib (Pfizer), as well as combinations of PI3K inhibitors (e.g.,
632 alpelisib by Novartis) and mTOR inhibitors (e.g., TAK-228 by
633 Takeda). Indeed, we here show that combined administration
634 of mTORC1/2 inhibitor TAK-228 and PI3K α inhibitor alpelisib
635 results in an equal tumor inhibition as obtained by BEZ235,
636 supporting our approach of dual PI3K/mTOR targeting in
637 leiomyosarcoma. Intriguingly, models showing p-S6^{S240}
638 expression responded better to PI3K/mTOR targeting, suggest-
639 ing that p-S6^{S240} could be used as a predictive marker for
640 response to PI3K/mTOR-directed agents. Iwenofu and collea-
641 gues (50) have previously suggested a role for p-S6^{S235/236} in
642 response prediction to ridaforolimus in sarcoma patients;
643 however, no uterine sarcomas were included in their study
644 (50). Taken together, our findings suggest that dual PI3K/
645 mTOR targeting might be an effective strategy in uterine
646 leiomyosarcoma.

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In conclusion, the expression of five therapeutically relevant
proteins was assessed in all uterine sarcoma subtypes, as well as in
benign uterine tumors and normal tissues. In a set of 303 uterine
sarcomas, we show that p-S6^{S240} expression identifies sarcomas
with a poor prognosis and predicts response to dual PI3K/mTOR
inhibition in PDX leiomyosarcoma models.

Disclosure of Potential Conflicts of Interest

Eva Wardelmann has received speakers bureau honoraria from Bayer,
Menarini, Nanobiotis, and Novartis and is a consultant/advisory board member
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disclosed by the other authors.

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