CTNNB1 mutation analysis is a useful tool for the diagnosis of desmoid tumors: a study of 260 desmoid tumors and 191 potential morphologic mimics

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Desmoid tumors are benign monoclonal fibroblastic or myofibroblastic neoplasms, characterized by local invasiveness and high rates of recurrence. Desmoid tumors must be distinguished from benign fibroblastic and myofibroblastic lesions, as well as from low-grade sarcoma, which can appear histologically similar to desmoid tumors. This differential diagnosis can be very difficult, especially when diagnosis is based on a core needle biopsy. On the molecular level, most sporadic desmoid tumors are associated with mutations of the β -catenin gene (*CTNNB1*). A minority of desmoid tumors are associated with Gardner syndrome and mutations of the familial adenomatous polyposis gene. We identified the common *CTNNB1* mutations associated with sporadic desmoid tumors by direct sequencing: in (i) 260 cases of typical desmoid tumors; and (ii) in 191 cases of spindle cell lesions, which can morphologically ‘mimic’ desmoid tumors. Formalin-fixed paraffin-embedded tissues were obtained via core needle biopsy ($n = 150$) or open biopsy/surgical excision ($n = 301$). Only 16 cases (4%) were not analyzable (Bouin’s fixed tissue). *CTNNB1* mutations were observed in 223 of 254 (88%) of sporadic desmoid tumors. No *CTNNB1* mutations were detected in all other lesions ($n = 175$) studied. *CTNNB1* sequencing can be easily and reliably done using tissues obtained via core needle biopsy. Detection of *CTNNB1* mutations in formalin-fixed paraffin-embedded tissues among spindle cell lesions is proposed as a specific diagnostic tool for the diagnosis of desmoid tumors. This result has significant implications for patient care and management.

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Desmoid tumors are rare mesenchymal fibroblastic or myofibroblastic monoclonal neoplasms with an estimated incidence of two to four cases per million inhabitants per year.¹ They arise primarily in the extremities and the trunk wall, followed by the abdominal wall and the abdominal cavity.² Most cases develop sporadically in young adults, whereas a few cases occur with family backgrounds of adenomatous polyposis.³ Desmoid tumors are

low-grade tumors that are generally highly invasive and locally aggressive, but do not metastasize.^{4,5} However, the clinical course of desmoid tumors is unpredictable and some spontaneous regression has been observed. As a result, a ‘wait and see’ approach has been recently proposed.⁶

Histological diagnosis of a desmoid tumor, based on open biopsy or surgical excision, is usually straight forward. However, the universal use of core needle biopsies makes this diagnosis much more difficult. Several spindle cell lesions, such as low-grade sarcomas (particularly low-grade fibromyxoid sarcomas), or reactive lesions such as nodular fasciitis and scars, can appear similar to desmoid tumors. In the intra-abdominal cavity, desmoid tumors can quite often be mistaken for GIST.

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Tumorigenesis of sporadic desmoid tumors is linked to β -catenin stabilization involving β -catenin/WNT/TCF signaling.^{7,8} Several recent studies show that *CTNNB1* mutations are highly prevalent and were detected in 84 to 87% of all sporadic desmoid tumors. However, immunohistochemical detection of nuclear β -catenin is not a reliable test for distinguishing desmoid tumors from benign or malignant fibroblastic lesions.^{9–13}

In this study, we report the prevalence and spectra of *CTNNB1* mutations in a large cohort of sporadic desmoid tumors compared with a panel of lesions known to be histologically similar to or ‘mimic’ desmoid tumors, in order to evaluate the potential role of *CTNNB1* genotyping in the daily practice for positive and differential diagnosis of desmoid tumors.

Materials and methods

Case and Sample Selection

Ethical approval from the appropriate committees was obtained. Formalin-fixed, paraffin-embedded

specimens accrued between 2008 and 2011 were retrieved from Institut Bergonié’s pathology archives (Bordeaux, France). All tissue samples were obtained via core needle biopsy, open biopsy or surgical excision.

The study cohort included 260 cases of desmoid tumors and 191 non-desmoid spindle cell lesions. For the cohort of desmoid tumors, the following clinical data were collected: gender, age diagnosis, location (intra-abdominal, abdominal wall and extra-abdominal), size of tumor and cases of Gardner syndrome. The heterogeneous group of non-desmoid spindle cell lesions contained four main subgroups: sarcomas, benign fibroblastic tumors, reactive processes and sarcomatoid carcinomas (Table 1). The 12 cases of low-grade fibromyxoid sarcoma harbor the characteristic TLS (FUS) rearrangement (fluorescent *in situ* hybridization—FISH; data not shown). The 21 GIST present characteristic *KIT* mutations (exons 9, 11, 13 or 17) or *PDGFRA* mutations (exons 12, 14 or 18) (denaturing high-performance liquid chromatography and sequencing; data not shown). The 23 synovial sarcomas have a specific SS18 (SYT) gene rearrangement (FISH; data not shown).

For the purpose of this study, all cases were evaluated by routine hematoxylin and eosin-stained sections. All specimens were further screened and analyzed for histological controls by a pathologist specialized in soft tissue tumors (JMC) and only those with confirmed tissues adequate for analytic purposes were included. Moreover, paraffin blocks were sampled using a core needle in order to select only areas of tumor for DNA extraction.

CTNNB1 Sequencing

Following lysis of the 35 μ m tumor slices, nucleic acids were obtained using Qiagen column separation according to the manufacturer’s instructions (Qiagen, Hilden, Germany). Formalin-fixed paraffin-embedded tissues (422, 95%) and Bouin’s fixed tissues (20, 5%) were used for DNA extraction. From the 451 specimens (biopsies or resections), available DNA for sequencing was obtained in 435 cases (96%). DNA lymphocytes from 96 anonymous individuals were used as non-mutated controls. *CTNNB1* exon 3 was amplified using two primer couples (primer n°1 and primer n°2). Primer sequences are reported on Table 2. Briefly, approximately 50 ng of DNA was amplified with the thermal cycling profile of 95 °C for 5 min, then 40 cycles of 95 °C for 30 s, 62 °C for 45 s, 72 °C for 45 s, with a

Table 1 Description of the 191 spindle cell non-desmoid lesions

Subgroups	Samples analyzed	DNA extracted ^a
<i>Sarcoma</i>		
LGFMS	12	11
Low-grade sarcoma nos	8	8
GIST	21	21
Leiomyosarcoma	19	17
MPNST	14	11
Synovial sarcoma	23	17
<i>Reactive processes</i>		
Scar	34	34
Fasciitis/myositis	16	15
<i>Benign tumors</i>		
Fibroma	16	16
Superficial fibromatosis	2	2
Fibrothecoma	1	1
Perineurioma	1	1
Leiomyoma	1	1
Ossifying fibromyxoid tumor	1	1
Sarcomatoid carcinoma	22	19
Total number	191	175

Abbreviations: GIST, gastrointestinal stromal tumor; MPNST, malignant peripheral nerve sheath tumor; LGFMS, low-grade fibromyxoid sarcoma.

^aDNA extracted: samples which presented sufficient DNA extracted for *CTNNB1* exon 3 genotyping.

Table 2 Primer sequences

<i>CTNNB1</i> gene	Forward primer	Reverse primer
Primer n°1	5'-TCCAATCTACTAATGCTAATACTGTTTCGTA-3'	5'-AGGTATCCACATCCTCTTCCTCAG-3'
Primer n°2	5'-AACAGTCTTACCTGGACTCTGGAATC-3'	5'-CATTCTGACTTTCAGTAAGGCAATG-3'

final extension at 72 °C for 20 min. PCR products were sequenced using the same primers as for the PCR reaction with an automated cycle sequencing for both strands using the Big-Dye DyeDeoxy terminator cycle sequencing kit (Applied Biosystems, Foster City, CA, USA). Sequencing reactions were carried out on the ABI Prism 310 Genetic Analyzer (Applied Biosystems). As a reference for the β -catenin gene, NM 00109822091 aligned on a sequence of chromosome 3 (NCBI 36) was used.

Statistical Analysis

Data are summarized by frequency and percentages for categorical variables and by median and range for continuous variables. Differences between groups were assessed using χ^2 analyses or Fisher's exact test for qualitative variables, and the Kruskal–Wallis for continuous variables. For all statistical tests, differences were considered significant at the 5% level. Statistical analyses were performed using the STATA 11.0 software.

Results

Histopathology

Specimens obtained by open biopsy and surgical excision had the characteristic histological features of desmoid tumors:² poorly circumscribed monotonous proliferation of slender fibroblastic cells, long sweeping fascicles of bland, collagenous stroma, characteristic prominent vasculature and entrapped atrophic skeletal muscle fibers simulating giants cells at the periphery of the lesion. Specimens obtained by core needle biopsy presented morphological characteristics strongly suggestive of desmoid tumors but were often incomplete.

High Feasibility of Sequencing *CTNNB1* Mutations Using Formalin-Fixed Paraffin-Embedded Tissues and Core Needle Biopsies

Initially 451 lesions were included. Paraffin-embedded tissue was obtained via core needle biopsy ($n=150$; 33%) or open biopsy/surgical excision ($n=301$, 67%). A total of 431 specimens were fixed in formalin (95%) and 20 specimens were fixed in Bouin (5%). In all, 435 cases had sufficient DNA extracted for *CTNNB1* exon 3 genotyping. All desmoid tumors were analyzable and only 16 cases (4%) of spindle cell lesions were not analyzable (Bouin's fixed tissue); including 6 synovial sarcomas, 3 sarcomatoid carcinomas, 3 malignant peripheral nerve sheath tumors, 1 low-grade fibromyxoid sarcoma, 2 leiomyosarcomas and 1 fasciitis (Table 1). All of these specimens were obtained from surgical excision. As a result, for the cohort of 175 cases mimicking desmoid tumors, we had to recruit retrospective cases to complete the

Table 3 Characteristics of patients with a desmoid tumor according to the *CTNNB1* status

<i>CTNNB1</i> characteristics	Total (%)	Wild <i>CTNNB1</i> (exon 3) (%)	Mutated <i>CTNNB1</i> (exon 3) (%)	P-value*
<i>N</i>	254	31 (12)	223 (88)	
<i>Age</i>				0.3483
Median, years	41	39	42	
Range	1–88	8–85	1–88	
<i>Sex</i>				0.9082
Male	76 (30)	9 (12)	67 (88)	
Female	178 (70)	22 (12)	156 (88)	
<i>Tumor site</i>				0.5296
Abdominal cavity	59 (24)	5 (8)	54 (92)	
Abdominal wall	60 (24)	9 (15)	51 (85)	
Extra-abdominal	129 (52)	17 (13)	112 (87)	
Unknown	6	0	6	
<i>Tumor size</i>				0.2311
Median (mm)	45	30	46	
Range	5–260	12–200	5–260	
Unknown	111	14	97	
<i>Specimens</i>				0.3639
Core needle biopsy	65 (26)	10 (15)	55 (85)	
Open biopsy or surgical excision	189 (74)	21 (11)	168 (89)	

*P-value: differences were considered statistically significant when $P < 0.05$.

series. On the other hand, all cases recruited in daily practice contained high-quality analyzable DNA.

High Frequency of *CTNNB1* Mutations in Formalin-Fixed Paraffin-Embedded Tissues Specimens of Sporadic Desmoid Tumors

After excluding cases with a family history of familial adenomatous polyposis or Gardner syndrome ($n=6$, none with *CTNNB1* mutations), a collection of 254 sporadic desmoid tumors remained and was included in this analysis (Table 3). Of these, 178 were female (70%) and 76 were male (30%). Median age was 41 years and ranged from 1 to 88 years. The following locations were involved: 129 in extra-abdominal locations (52%), 59 in the abdominal cavity (24%), 60 in the abdominal wall (24%) and 6 of unknown site. The extra-abdominal desmoid tumors occurred: 59 in the limb (46%), 53 in trunk wall (41%) and 17 in the head and neck (13%). The size was known in 143 cases and ranged from 5 to 260 mm (median, 45 mm). A total of 65 specimens were obtained via core needle biopsy (26%) and 189 via open biopsy or surgical excision (74%). A mutation in exon 3 of the *CTNNB1* gene was identified in 223 (88%) of the 254 cases. The *CTNNB1* mutation spectra mostly included three point mutations in two codons (41 and 45) (Figure 1).

Figure 1 *CTNNB1* mutations detected in fibromatosis tumors. Typical heterozygous missense mutations found in exon 3 *CTNNB1* gene; (a) at codon 45 (S45F), (b) at codon 41 (T41A) and (c) at codon 45 (S45P).

Characteristics of Patients with Sporadic Desmoid Tumors by *CTNNB1* Genotype

A mutation in exon 3 of the *CTNNB1* gene was identified in 223 (88%) of the 254 cases. No mutations were detected in the DNA extracted from the lymphocytes of the 96 controls. All of the sequences were controlled in an independent experiment. The *CTNNB1* mutation spectra concerned mainly three point mutations in two codons (41 and 45): ACC to GCC in codon 41 (41A), resulting in the replacement of threonine by alanine, was identified in 132 cases (59%); TCC to TTT in codon 45 (45F), resulting in the replacement of serine by phenylalanine, was identified in 49 samples (22%); and TCT to CCT in codon 45 (45P), resulting in the replacement of serine by proline, was identified in 27 samples (12%). Further, in nine cases (4%), we also detected a small in-frame deletion (Table 4). In six cases (3%), other point mutations in exon 3 of the *CTNNB1* gene were found:

- in codon 41 (41I), the replacement of threonine by isoleucine was identified in three samples.
- in codon 34 (34A), the replacement of glycine by arginine was identified in one sample (and detection of a change of nucleotide in intron 3 of *CTNNB1* gene (c.241 + 2T >A), involving the site of splicing).
- in codon 37 (37A), the replacement of serine by phenylalanine was identified in one sample.
- one sample presented two point mutations in exon 3 *CTNNB1*: one in codon 33 (33T) resulting in the replacement of serine by threonine and one in codon 34 (34A) resulting in the replacement of glycine by arginine.

None of the 175 lesions mimicking desmoid tumors analyzed harbored any *CTNNB1* mutations.

No correlations were found between the presence of *CTNNB1* gene mutations and the following variables: age at diagnosis, sex, tumor site, tumor size and type of specimens (Table 3). When analyzing the incidence of the specific *CTNNB1* gene mutations, tumors in extra-abdominal sites had a higher incidence of the 45F mutation ($P=0.0023$). Furthermore, among extra-abdominal sites, tumors in the extremities had a higher incidence of the 45F mutation ($P=0.005$). No other associations were noted (Table 4).

Discussion

Our study confirms previous findings that *CTNNB1* mutations are highly prevalent in sporadic desmoid tumors^{9,14,15} and that desmoid *CTNNB1* mutational spectra are very restricted.^{9,16,17} Only three specific mutations are reported: two involving codon 45 (p.Ser45Pro and p.Ser45Phe) and one involving codon 41 (p.Thr41Ala). This study is the first to our knowledge to report the presence of other point mutations of exon 3 of *CTNNB1* in desmoid tumors. These new point mutations are located in codon 41 (resulting in the replacement of threonine by isoleucine), in codon 34 (resulting in the replacement of glycine by arginine), in codon 37 (resulting in the replacement of serine by phenylalanine) and in codon 33 (resulting in the replacement of serine by threonine). The exon 3 *CTNNB1* point mutations have already been described, but only in rare epithelial neoplasms and with a very low frequency.^{18–25} Indeed, β -catenin mutations are not exclusive to desmoid tumors and are also reported for several epithelial neoplasms at various prevalence levels. Table 5 quotes the main studies^{18–25} searching for exon 3 *CTNNB1* mutations in different carcinoma (thyroid, ovary, uterine, prostate, colorectal, hepatoblastoma and hepatocarcinoma) with prevalence and type of mutations. The observed mutations are identical to the desmoid tumor mutations in 6% of all carcinomas studied and reported, which represents 28% of the exon 3 *CTNNB1* mutations. However, from a morphological point of view, making the difference histologically between such neoplasms and desmoid tumors does not cause diagnostic problems.

The main focus of this study was to concentrate on the differential diagnosis of desmoid tumors from low-grade sarcomas, myofibroblastic benign lesions and reactive processes. The existence of *CTNNB1* mutations in spindle cell lesions, which morphologically imitate desmoid tumors would detract from the value of detecting these mutations for a diagnostic purpose. To the best of our knowledge, this is the first study on exon 3 *CTNNB1* mutations (characteristic of sporadic desmoid tumors) in a large cohort of spindle cell lesions. None of the 175 spindle cell lesions, including low-grade sarcoma (low-grade fibromyxoid sarcoma and low-grade

Table 4 Characteristics of desmoid tumors by *CTNNB1* genotype

<i>CTNNB1</i> characteristics	41A (%)	45F (%)	45P (%)	Deletion in exon 3 (%)	P-value*
<i>N</i>	132 (59)	49 (22)	27 (12)	9 (4)	
<i>Age</i>					0.1192
Median, years	41	37	40	58	
Range	10–88	1–80	7–80	39–71	
<i>Sex</i>					0.7329
Male	36 (56)	15 (23)	10 (16)	3 (5)	
Female	96 (63)	34 (22)	17 (11)	6 (4)	
<i>Tumor site</i>					0.0023
Abdominal cavity	41 (78)	6 (11)	5 (9)	1 (2)	
Abdominal wall	32 (63)	6 (12)	11 (22)	2 (3)	
Extra-abdominal	55 (51)	36 (34)	11 (10)	5 (5)	0.005
Head and neck	7 (54)	4 (31)	2 (15)	0	
Trunk	23 (59)	9 (23)	4 (10)	3 (8)	
Extremities	25 (45)	23 (42)	5 (9)	2 (4)	
Unknown	4	1	0	1	
<i>Tumor size</i>					0.9425
Median, mm	45	51.5	40	45	
Range	5–200	10–130	8–260	10–100	
Unknown	54	21	14	4	
<i>Sample</i>					0.1292
Core needle biopsy	27 (49)	18 (33)	7 (13)	3 (5)	
Chirurgical biopsy and surgical excision	105 (65)	31 (19)	20 (12)	6 (4)	

41A, 45F, 45P, mutated residues; *n*, number of patients.*P-value: differences were considered statistically significant when $P < 0.05$. Significant P-value is shown in bold.**Table 5** *CTNNB1* mutations reported in previous studies in epithelial neoplasms

Article	Tumor type	Number of exon 3 <i>CTNNB1</i> mutations/ number of the cohort	Codon mutated (number of cases)
Garcia-Rostan <i>et al</i> ¹⁸	Anaplastic thyroid carcinoma	19/31	17, 20, 22, 33, 36, 37, 38, 40, 41, 42, 43, 44, 45, 46, 47, 49, 52, 54, 55, 58, 60
Oliva <i>et al</i> ¹⁹	Endometrioid tumors of borderline malignancy of the ovary	7/8	32(2), 33(3), 37(2)
Palacios <i>et al</i> ²⁰	Endometrioid ovarian borderline tumor and carcinomas	3/11	37(2), 41A(1)
Voeller <i>et al</i> ²¹	Prostate carcinoma	5/104	31(1), 33(2), 41A(1) , del 45(1),
Koch <i>et al</i> ²²	Hepatoblastoma	27/52	32(2), 34(3), 37(1), 41A(7) large del(14),
Miyoshi <i>et al</i> ²³	Hepatocellular carcinomas	14/75	32(5), 33(1), 34(1), 41A(1) , 45F(2) , 45P(2) , large del(2)
Fukuchi <i>et al</i> ²⁴	Uterine endometrium adenoarcoma	10/76	33(1), 37(2), 41A(2) , 41I(2), 45C(1), 45F(2)
Mirabelli-Primdahl <i>et al</i> ²⁵	Colorectal carcinomas with high- frequency MSI	13/53	41A(3) , 41I(2), 45P(4) , 45F(3) , large del(1)
Mirabelli-Primdahl <i>et al</i> ²⁵	Colorectal carcinomas with stable or low-frequency MSI	0/27	

Abbreviations: del, deletion; MSI, microsatellite instability.

Exon 3 *CTNNB1* point mutations identical to desmoid tumor is shown in bold.

sarcoma not otherwise specified), GIST, sarcomatoid carcinoma, malignant peripheral nerve sheath tumor, synovial sarcomas, benign proliferations (myofibroma, perineurioma, fibrothecoma, fibroma, lipofibromatosis and fibroblastoma) and reactive processes (nodular fasciitis, myositis and scar),

harbored exon 3 *CTNNB1* mutations. Recently, using a small cohort, Colombo *et al*²⁶ suggested that *CTNNB1* genotyping can be useful in lesions where the differential diagnosis includes desmoid tumors, particularly in cases of suspected recurrence. Previously, Amary *et al*⁹ failed to detect the common

Table 6 *CTNNB1* mutations reported in previous sarcoma studies

Article	Tumor type	Number of exon 3 <i>CTNNB1</i> mutations/N of cohort	Codon mutated (number of cases)
Iwao <i>et al</i> ²⁷	Soft-tissue tumors	2/62	
	MFH, osteosarcoma, synovial sarcoma, liposarcoma, malignant schwannoma	2/51	SS: codon 32(1) MFH: codon 45P(1)
Kuhnen <i>et al</i> ²⁸	Benign tumors	0/11	
Saito <i>et al</i> ²⁹	Pleomorphic-type MFH	1/22	MFH: codon 37(1)
	Synovial sarcoma	4/49	Codon 32(3) Codon 37(1)
Sato <i>et al</i> ³	Synovial sarcoma	0/15	
Sakamoto <i>et al</i> ²⁴	Liposarcoma and MFH	6/39	
	WDLs 'lipoma-like'	0/10	
	WDLs 'sclerosing'	0/8	
	DDLs	2/12	Codon 37(1) Codon 39(1) Codon 40(1) Codon 42(1) Codon 43(1) Codon 45P(1)
	MFH	4/9	
Saito <i>et al</i> ³²	Soft tissue sarcomas	0/27	
	MFH	0/10	
	LMS	0/10	
	MPNST	0/5	
	SFT	0/2	

Abbreviations: DDLs, dedifferentiated liposarcoma; MFH, malignant fibrous histiocytoma; MPNST, malignant peripheral nerve sheath tumor; LMS, leiomyosarcoma; SFT, solitary fibrous tumor; SS, synovial sarcoma; WDLs, well-differentiated liposarcoma lipoma-like. Exon 3 *CTNNB1* point mutations identical to desmoid tumor is shown in bold.

CTNNB1 mutations in 57 spindle cell lesions but this cohort contained mainly cases of superficial fibromatosis. However, it should be noted that the 10 cases of low-grade fibromyxoid sarcoma did not present exon 3 *CTNNB1* mutations, as was observed in our study. In addition, some studies have reported *CTNNB1* mutations in various sarcomas. The various published studies looking for *CTNNB1* mutations in soft tissue sarcomas are summarized in Table 6.^{8,27–32} These studies showed that the prevalence of exon 3 *CTNNB1* mutations in soft tissue sarcomas is very low. Rare cases of exon 3 *CTNNB1* mutations were reported in synovial sarcoma and malignant fibrous histiocytoma. In most of these cases, this point mutation is situated in different codons (32, 37, 39, 40, 42, 43) from those generally observed in desmoid tumors (41 and 45). A mutation typical of a desmoid tumor (p.Ser45Phe) was observed in only two sarcoma cases (malignant fibrous histiocytoma). However, the high-grade atypia of malignant fibrous histiocytoma excludes them from the differential diagnosis of desmoid tumors.

When making a morphological diagnosis of a desmoid tumor in an intra-abdominal situation, searching for exon 3 *CTNNB1* mutations (characteristic of sporadic desmoid tumors) turns out to be essential for the diagnostic approach. The presence of typical exon 3 *CTNNB1* mutations allows us to make the diagnosis of sporadic desmoid tumors. On the other hand, the absence of exon 3 *CTNNB1* mutations in this intra-abdominal location should suggest a family type of desmoid tumor and could

help to select patients for whom *APC* gene mutations should be tested (Gardner's syndrome).

By comparing sequencing results from the formalin-fixed paraffin-embedded tissue samples paired to the frozen tumor specimens in a small cohort, Domont *et al*¹⁵ have previously shown the feasibility of β -catenin gene sequencing using formalin-fixed paraffin-embedded tissues. In this study, we demonstrate in a large series that the use of formalin-fixed paraffin-embedded tissue samples is completely relevant and useful in daily routine practice. Furthermore, we show the feasibility of performing these analyses on core needle biopsies in the daily practice. Indeed, approximately one-third of our cases corresponded to such micro biopsies ($n=150$, 34%). In the field of sarcoma care, the current gold standard is based on the use of core needle biopsy.

CTNNB1 sequencing is easy to conduct and reproducible using formalin-fixed paraffin-embedded tissue obtained via core needle biopsy. Our study shows that sequencing of *CTNNB1* exon 3 mutations is a specific diagnosis tool/test, which can resolve difficult situations in daily practice such as distinguishing desmoid tumors from benign or malignant fibroblastic lesions (eg, low-grade fibromyxoid sarcoma, GIST, leiomyosarcoma, sarcomatoid carcinoma, synovial sarcoma, nodular fasciitis, scar and other reactive processes). This finding is particularly useful to resolve cases where the histological interpretation of tumor samples resulting from core needle biopsies is complicated. Differentiating these three categories of lesions

(desmoid tumor, sarcoma/carcinoma and reactive processes) becomes particularly important given the locally aggressive but non-metastasizing nature of deep fibromatosis, and the recent 'wait and see' approach for the management of desmoid tumor.⁶

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Disclosure/conflict of interest

The authors declare no conflict of interest.

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