

## High Diagnostic and Prognostic Value of Steroidogenic Factor-1 Expression in Adrenal Tumors

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**Context:** No immunohistochemical marker has been established to reliably differentiate adrenocortical tumors from other adrenal masses. A panel of markers like melan-A and inhibin- $\alpha$  is currently used for this purpose but suffers from limited diagnostic accuracy. We hypothesized that expression of steroidogenic factor-1 (SF-1), a transcription factor involved in adrenal development, is of value for the differential diagnosis of adrenal masses and predicts prognosis in adrenocortical carcinoma (ACC).

**Patients and Methods:** SF-1 protein expression was assessed by immunohistochemistry on tissue samples from 167 ACC, 52 adrenocortical adenomas (ACA), six normal adrenal glands, six normal ovaries and 73 neoplastic nonsteroidogenic tissues. In an independent cohort of 33 ACC and 58 ACA, SF-1 mRNA expression was analyzed. SF-1 expression was correlated with clinical outcome in patients with ACC.

**Results:** SF-1 protein staining was detectable in 158 of 161 (98%) evaluable ACC samples including 49 (30%) with strong SF-1 staining and in all normal and benign steroidogenic tissues. In addition, SF-1 mRNA expression was present in all 91 analyzed adrenocortical tumors. In contrast, SF-1 expression was absent in all nonsteroidogenic tumors. Strong SF-1 protein expression significantly correlated with poor clinical outcome: tumor stage-adjusted hazard ratio for death 2.46 [95% confidence interval (CI) = 1.30–4.64] and for recurrence 3.91 (95% CI = 1.71–8.94). Similar results were obtained in the independent cohort using RNA analysis [tumor stage-adjusted hazard ratio for death 4.69 (95% CI = 1.44–15.30)].

**Conclusion:** SF-1 is a highly valuable immunohistochemical marker to determine the adrenocortical origin of an adrenal mass with high sensitivity and specificity. In addition, SF-1 expression is of stage-independent prognostic value in patients with ACC. (*J Clin Endocrinol Metab* 95: E161–E171, 2010)

Adrenal masses are among the most frequent human tumors with a prevalence of at least 3% in a population over the age of 50 yr (1). Although the majority of these lesions represent benign adenomas, adrenocortical carcinomas and metastases amount to 5–10% of all tumors (1). Clinical symptoms and biochemical evidence of autonomous hormone excess may indicate the adrenocortical origin of the lesion. However, the differentiation of a nonfunctioning adrenocortical tumor from a metastasis of an extraadrenal malignancy or a nonsecretory pheochromocytoma is challenging. Due to their broad histomorphological heterogeneity, accurate typing of adrenal tumors often poses a major diagnostic problem, and conventional histology frequently offers no conclusive diagnosis of the origin of an individual neoplasm. Many malignant neoplasias metastasize to the adrenal gland including melanoma, breast, lung, renal, and gastrointestinal cancer, making this organ the fourth most common site of metastasis in humans (2, 3). Therefore, reliable immunohistochemical markers are required to establish the correct diagnosis. In 1990, Schröder *et al.* (4, 5) described a monoclonal antibody (D11) with high specificity for adrenocortical tissue. However, further studies suggested that immunoreactivity is observed only in the subset of well differentiated adrenocortical carcinoma (ACC) markedly limiting its use as a general marker for ACC (6–9). In addition, D11 is not commercially available and currently no longer accessible. Melan-A (MART-1) and inhibin- $\alpha$  were also suggested as putative markers for distinguishing primary from secondary adrenal tumors (10–13). However, they fail to recognize 28 and 31% of ACC, respectively (Table 1) (14–20). Thus, due to their limited sensitivity, none of the proposed markers for adrenocortical tumor has gained general acceptance (21, 22).

Already in 1995, Sasano *et al.* (7, 23) suggested steroidogenic factor-1 (SF-1; also known as Ad4BP and NR5A1) as a marker to differentiate between tumors of adrenocortical and nonadrenocortical origin. SF-1 is a transcription factor expressed primarily in the hypothalamus, pituitary, and steroidogenic organs like adrenal glands, testes, and ovaries. It plays a key role in the development of steroidogenic tissues (24, 25) and is involved in the regulation of steroid biosynthesis (26, 27).

Recent studies have demonstrated overexpression of SF-1 in most cases of childhood adrenocortical tumors (28, 29). Importantly, it was also shown that elevated levels of SF-1 lead to increased proliferation of human adrenocortical cells *in vitro* and to tumorigenesis in mice (30–32). Accordingly, SF-1-stimulated adrenocortical cell proliferation was inhibited *in vitro* by SF-1 inverse agonists (33). These observations suggest an important role of SF-1 in the pathogenesis of adrenocortical tumors. However, up to now, its value as a marker for ACC has been

investigated only in small series of eight, five, and four ACC samples, respectively (34–36).

Accordingly, in this study, we investigated not only the role of SF-1 as a diagnostic tool in adrenal tumors but also its prognostic value in ACC.

## Patients and Methods

### Patients and tissue

#### German cohort

Three hundred four tissue samples (231 derived from steroidogenic and 73 from nonsteroidogenic tissue) were collected between 1989 and 2008. Samples of steroidogenic tissues comprised 167 ACC in different stages of disease, 52 benign adrenocortical adenomas (ACA), six normal adrenal glands, and six normal ovaries (Table 2). Nonsteroidogenic tissues included carcinomas derived from kidney (n = 11), lung (n = 12), breast (n = 8), colon (n = 7), pancreas (n = 5), liver (n = 7), prostate (n = 4), endometrium (n = 2), and ovary (n = 3) and eight pheochromocytomas, three melanoma metastases, two lymphomas, and one seminoma. All patients donating adrenocortical tissues gave written informed consent for collecting tissue and clinical data, and the study was approved by the ethics committee of the University of Würzburg. The other tissues derived from the tissue bank at the Department of Pathology at the University of Würzburg and were analyzed in an anonymous fashion in accordance with a general decision of the local ethics committee. For ACC patients, detailed clinical data, including follow-up and survival data, were collected in a structured manner by the German ACC Registry (37). Resection of the primary tumor was considered complete (R0 resection) if surgical, pathological, and imaging reports gave no evidence for remaining disease. Presence of distant metastases or recurrence was evaluated at the time of diagnosis and during follow-up visits by computerized tomography of chest and abdomen every 3–6 months. Patients with histologically confirmed ACA are assumed to be cured, and no structured follow-up is recommended (38). Accordingly, in 38 of 52 patients, in whom clinical outcome data were available, no evidence for recurrence was found.

#### French cohort

An independent cohort of adrenocortical tumors (n = 91) derived from a French series (39). Only samples with undoubtful histological diagnosis and evaluable RNA microarray data were included (ACA n = 58, ACC n = 33). These tumors were prospectively collected by the COMETE network between 1993 and 2005. Patient characteristics and collection of clinical data are described in detail elsewhere (39–41). Written informed consent was obtained from all patients, and the study was approved by the institutional review board of the Cochin Hospital (Paris).

#### RNA extraction and analysis

RNA extraction and analysis was performed as described recently (39). Microarray analyses were performed using 3  $\mu$ g total RNA in each sample as starting material following the manufacturer's protocol, as previously described (39). The labeled cDNA was hybridized to HG-U133 Plus 2.0 Affymetrix GeneChip arrays (Affymetrix, Santa Clara, CA), and the chips were scanned with GCOS version 1.4.

**TABLE 1.** Overview of immunohistochemical markers for the diagnosis of adrenocortical tumors

Reference	ACC		ACA		NAG		Nonadrenocortical tumors	
	+	–	+	–	+	–	+	–
D11 (nuclear staining)								
Komminoth <i>et al.</i> , 1995 (8)	22	5			13	0	0	28
Schröder <i>et al.</i> , 1990 (4)	9	0	40	0	27	0	1	143
Schröder <i>et al.</i> , 1992 (5)	15	0	57	0				
Tartour <i>et al.</i> , 1993 (6)	8	10			3	0	0	103
Wajchenberg <i>et al.</i> , 2000 (9)	22	13	38	0	27	17		
Total	76	28	135	0	70	17	1	274
For ACC: sensitivity, 73%; specificity, 99%; positive predictive value, 98%; negative predictive value, 90%								
Inhibin- $\alpha$ (cytoplasmic staining)								
Arola <i>et al.</i> , 2000 (16)	23	7	46	19	10	0	0	20
Fetsch <i>et al.</i> , 1999 (17)	7	0	15	0			0	23
Jalali and Krishnamurthy, 2005 (15)	1	4	4	31			0	10
McCluggage <i>et al.</i> , 1998 (12)	4	0	15	0	20	0	0	15
Munro <i>et al.</i> , 1999 (13)	10	2	17	0	6	0		
Pan <i>et al.</i> , 2005 (14)	27	13	52	10			6	787
Pelkey <i>et al.</i> , 1998 (18)	12	3	18	5			2	52
Zhang <i>et al.</i> , 2003 (19)	0	5	51	10	3	0	0	5
Zhang <i>et al.</i> , 2004 (20)	28	17	50	16	23	0	0	47
Total	112	51	268	91	62	0	8	949
For ACC: sensitivity, 69%; specificity, 99%; positive predictive value, 93%; negative predictive value, 95%								
A103 (Melan-A) (cytoplasmic staining)								
Busam <i>et al.</i> , 1998 (10)	29	0	5	0			7	185
Ghorab <i>et al.</i> , 2003 (11)	10	1	21	0			1	142
Jalali and Krishnamurthy, 2005 (15)	4	1	32	3			0 <sup>a</sup>	8
Pan <i>et al.</i> , 2005 (14)	22	18	60	2			3	790
Zhang <i>et al.</i> , 2003 (19)	0	5	55	6	3	0	0	5
Zhang <i>et al.</i> , 2004 (20)	35	13	60	6	23	0	0 <sup>a</sup>	41
Total	100	38	233	17	26	0	11	1171
For ACC: sensitivity, 72%; specificity, 99%; positive predictive value, 90%; negative predictive value, 97%								

NAG, Normal adrenal gland.

<sup>a</sup> Melanoma samples were excluded from the analysis.

**TABLE 2.** Adrenocortical tissues: patients and tumor characteristics

	Age [yr (sd)]	Sex (male/female)	Size of the adrenal tumor [cm (sd)]
German series			
Normal adrenal gland (n = 6)	59 (17)	4/2	
ACA			
Aldosterone-producing adenoma (n = 26)	53 (11)	17/9	1.7 (0.9)
Cortisol-producing adenoma (n = 16)	50 (12)	4/12	3.4 (1.5)
Hormonally inactive adenoma (n = 10)	64 (11)	6/4	3.9 (3.0)
ACC <sup>a</sup>			
Primary tumor (n = 133 <sup>b</sup> )	49 (16)	48/85	12 (4.4)
ENSAT stage I (n = 5)	54 (24)	2/3	4.7 (0.3)
ENSAT stage II (n = 48)	48 (17)	19/29	11.9 (4.5)
ENSAT stage III (n = 40)	53 (14)	14/27	11.8 (3.6)
ENSAT stage IV (n = 34)	47 (18)	11/23	13.4 (4.4)
Local recurrence (n = 19)	46 (17)	9/10	
Distant metastases (n = 15)	44 (11)	3/12	
French series			
ACA			
Aldosterone-producing adenoma (n = 10)	48 (12)	4/6	2.5 (0.7)
Cortisol-producing adenoma (n = 29)	43 (11)	3/26	3.8 (1.6)
Hormonally inactive adenoma (n = 19)	54 (11)	3/16	4.2 (1.5)
ACC <sup>a</sup>			
ENSAT stage I (n = 1)	41	0/1	5
ENSAT stage II (n = 17)	44 (19)	1/16	11.1 (4.9)
ENSAT stage III (n = 5)	48 (5)	2/3	15.0 (1.4)
ENSAT stage IV (n = 10)	47 (19)	4/6	11.6 (3.2)

Data represent mean values (sd) or number.

<sup>a</sup> Tumor stage at the time of diagnosis was reported according to the European Network for the Study of Adrenal Tumors (ENSAT) classification (49).

<sup>b</sup> In six cases, tumor stage was not determined. Forty-eight ACC were cortisol secreting, 13 exclusively sex hormone or precursors secreting, seven aldosterone secreting, and 18 hormonally inactive. In 48 cases, no sufficient endocrine work-up was performed preoperatively or data were not available.

## Immunohistochemistry

Tissue samples from 167 ACC, 15 ACA, five normal adrenal glands, and 10 nonadrenocortical malignancies were assembled into three tissue microarrays (TMA) as recently described (42–44). Twenty-eight samples included in the TMA were analyzed as standard full sections to validate the array results. In addition, 107 tissue samples including one normal adrenal gland, six normal ovaries, 37 adrenal adenomas, and 63 nonsteroidogenic tumors were processed as standard full sections.

TMA and full sections were deparaffinized twice in 100% xylene (Sigma-Aldrich, Seelze, Germany) for 10 min with rehydration twice in 100 and 70% ethanol, followed by an extensive washing step with distilled water. Antigen retrieval was performed in 10 mM citric acid monohydrate buffer (pH 6) twice for 5 min at 750 W in a microwave oven. Endogenous peroxidase activity was quenched with 3% hydrogen peroxide/methanol solution for 10 min. Subsequently, blocking of unspecific protein-antibody interactions was performed with 20% human AB serum in Dulbecco's Phosphate-Buffered Saline (DPBS) for 1 h at room temperature. SF-1 protein was detected by incubation with monoclonal mouse antihuman SF-1 antibody (Perseus-Proteomics, Tokyo, Japan) 1:100 in DPBS for 17 h, with the reaction controlled with N-Universal Negative Control Mouse (Dako, Glostrup, Denmark). Signal amplification was achieved by En-Vision+ System Labeled Polymer-HRP Anti-Mouse (Dako) for 30 min and developed for 7 min with NovaRED Substrate Kit (Vector Laboratories, Burlingame, CA) according to the manufacturer's instructions. Nuclei were counterstained with Mayer's hemalaun for 2 min.

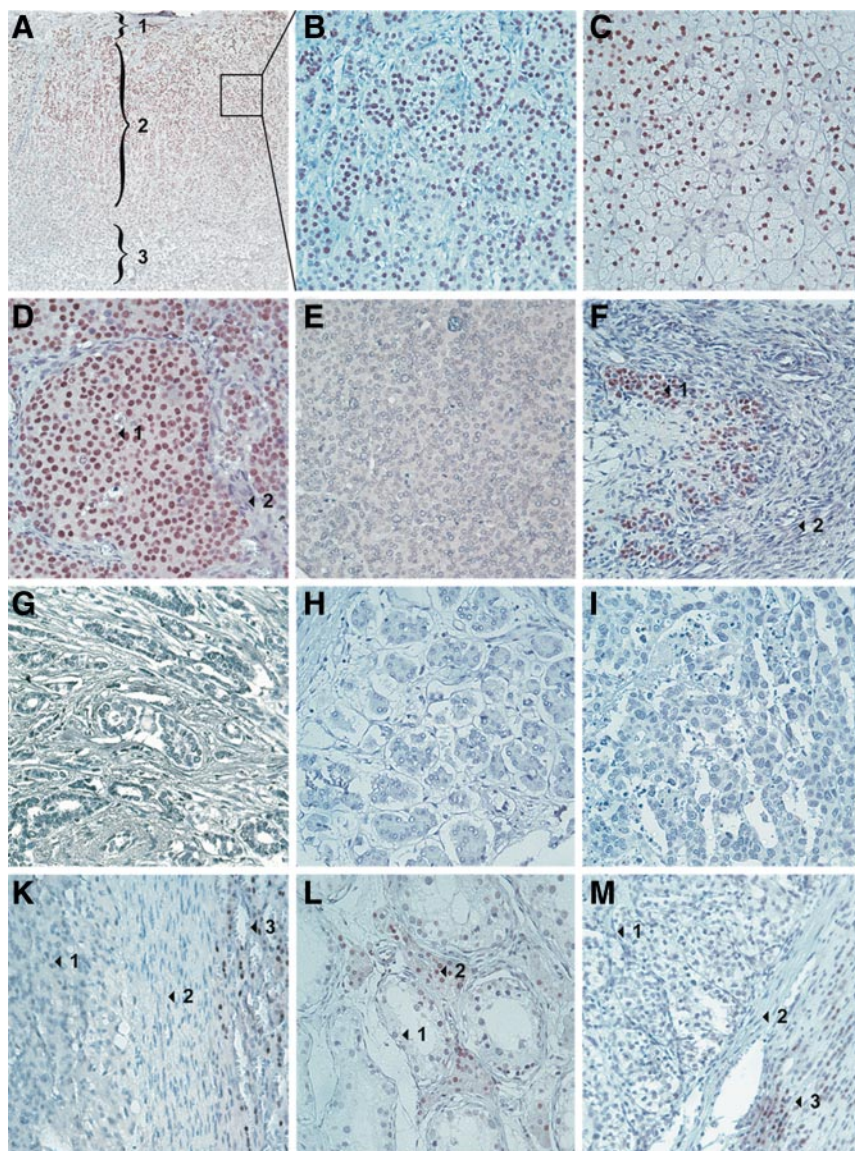
## Microscopic analysis

All slides were analyzed independently by two investigators. TMA samples were included in the analysis only if two or more evaluable cores were available after the staining procedure. Only nuclear staining was evaluated (23), and staining intensity was graded as negative (0), low to medium (1), or strong (2). The percentage of positive tumor cells was calculated for each specimen and scored 0 if 0% were positive, 0.1 if 1–9%, 0.5 if 10–49% and 1 if 50% or more. A semiquantitative H-score was then calculated by multiplying the staining intensity grading score with the proportion score as described (45). Where discrepancies were observed, results were double checked by both investigators together with a third observer. Samples of the TMA without staining were also reanalyzed in full tissue sections. Normal adrenal gland sections served as positive controls during all staining procedures and cells of the tumor stroma as internal negative control.

## Statistics

Characteristics of tumors and patients are presented as means with their respective sd values for normally distributed variables. The interobserver agreement for the scoring system was evaluated using Cohen's  $\kappa$ -coefficient and confirmed using Pearson's correlation coefficient. As cutoff for strong agreement of 0.81 was chosen for the  $\kappa$ -coefficient and 0.75 for Pearson's coefficient (46, 47). Categorical variables were compared by Fisher's exact test and  $\chi^2$  test. Correlation between endocrine activity of the tumor and SF-1 expression was analyzed using Spearman's correlation test. Affymetrix microarray data were normalized





**FIG. 1.** SF-1 protein expression in normal, benign, and malignant steroidogenic (A–F) and nonsteroidogenic neoplastic tissues (G–M): A, normal adrenal gland, including capsule (A-1), cortical zones (A-2, and magnification in B), and medulla (A-3); C, adrenocortical adenoma; D and E, adrenocortical carcinoma (D-1, tumor cells; D-2, fibroblasts); F, normal ovary; G, breast carcinoma; H, pancreas carcinoma; I, endometrium carcinoma; K, pheochromocytoma; L, intratubular germ cell neoplasia, including SF-1-positive Leydig cells (L-2); M, renal clear cell carcinoma, including adjacent adrenocortical cells (M-3).

using the robust multiarray averaging method (48). Survival analysis for ACC patients was calculated using the Kaplan-Meier method, and differences between groups were assessed with log-rank and Cox proportional hazards statistics. Overall survival was defined as time elapsed from primary resection of ACC to death or last follow-up visit. Recurrence-free survival was analyzed only in patients with European Network for the Study of Adrenal Tumors stages I–III (49) after complete resection and was defined as time from the date of tumor resection to the first evidence of relapse or last follow-up without evidence for disease. The Cox proportional hazards model was used for multivariate analysis to test the influence of sex, age, tumor stage, and endocrine activity of the tumors on SF-1-related survival. In the French ACC cohort, Cox analysis was used to determine tumor stage-adjusted survival with

SF-1 RNA expression as a continuous variable. Subsequently, a Kaplan-Meier regression analysis was performed using dichotomized categorical SF-1 values (cutoff value for this data set = 5.78).

Results are given as hazard ratios (HR) including 95% confidence interval (CI). The significance level was set at  $\alpha = 5\%$  for all comparisons. All statistical tests were performed using the SPSS software package (version 15.0.0; Chicago, IL).

## Results

### Immunohistochemical detection of SF-1 protein

As shown in Fig. 1, SF-1 staining was localized to the nucleus and was homogeneously distributed both in standard tissue slides and among the different cores from the same tissue sample in the TMA. Interobserver agreement for assessing SF-1 expression was strong with a  $\kappa$ -coefficient of 0.92 (95% CI = 0.87–0.97) and Pearson's correlation coefficient 0.86 (95% CI = 0.82–0.89). In agreement with previous publications (50), SF-1 was expressed in normal steroidogenic tissue (adrenal gland  $n = 6$  of 6 and ovary  $n = 6$  of 6). Within the adrenal gland, its expression was restricted to the cortex (Fig. 1A-2) with strong staining in the zona glomerulosa and zona fasciculata (Fig. 1B) and low staining intensity in the zona reticularis. No staining was observed in the capsular tissue and the medulla (Fig. 1A-1 and -2). In normal ovaries, strong SF-1 expression was detectable in theca and granulosa cells (Fig. 1F-1) but not in other cell types (Fig. 1F-2).

SF-1 was expressed in all benign adrenocortical neoplasias (Fig. 1C and Table 3). In ACC, SF-1 expression was detectable in 158 of 161 evaluable tissue samples (98%), and in 30% of samples ( $n = 49$ ), staining intensity was strong (Fig. 1, D and E). In both ACA and ACC, SF-1 staining pattern was independent of endocrine activity or the origin (primary tumor, local recurrence, or distant metastases) of the sample (Supplemental Table 1, published on The Endocrine Society's Journals Online web site at <http://jcem.endojournals.org>). Accordingly, in the French cohort, SF-1 mRNA expression was found in all 91 adrenocortical tumors using microarray analysis.

**TABLE 3.** SF-1 expression scores distribution in steroidogenic and nonsteroidogenic tissues

Tissue	n	SF-1 expression (H-score) (n)		
		Negative (0)	Low (1)	High (2)
Normal and benign steroidogenic tissues	64	0 (0%)	26 (41%)	38 (59%)
Normal adrenal gland <sup>a</sup>	6	0	3	3
Normal ovary	6	0	6	0
Inactive ACA	10	0	2	8
Aldosterone-producing adenoma	26	0	9	17
Cortisol-producing adenoma	16	0	6	10
ACC	161	3 (2%)	109 (68%)	49 (30%)
Primary tumor	130	3	84	43
Local recurrence	18	0	14	4
Distant metastases	13	0	11	2
Nonsteroidogenic tumors	73	73 (100%)	0 (0%)	0 (0%)
Breast carcinoma	8	8	0	0
Colon carcinoma	7	7	0	0
Hepatocellular carcinoma	7	7	0	0
Endometrial carcinoma	2	2	0	0
Melanoma metastasis	3	3	0	0
Non-Hodgkin lymphoma	2	2	0	0
Non-small-cell lung carcinoma	11	11	0	0
Ovarian carcinoma	4	4	0	0
Pancreatic carcinoma	5	5	0	0
Pheochromocytoma	8	8	0	0
Prostate carcinoma	4	4	0	0
Renal cell carcinoma	11	11	0	0
Seminoma	1 <sup>b</sup>	1	0	0
Small-cell lung carcinoma	1	1	0	0

<sup>a</sup> Only adrenocortical cells were positive, whereas cells of the medulla were negative.

<sup>b</sup> Only Leydig cells were positive.

In contrast, in none of the 73 tissues derived from nonsteroidogenic organs was SF-1 staining detectable (Table 3 and Fig. 1, G–M). The sample selection included all tumor entities that typically metastasize to the adrenal gland and pheochromocytomas that are sometimes difficult to distinguish histologically from ACC. Of note, Leydig cells within a seminoma (Fig. 1L-2) were SF-1 positive, whereas tumor cells were negative (Fig. 1L-1). Similarly, in a renal cell carcinoma, tumor cells were SF-1 negative (Fig. 1M-1), whereas invaded adrenocortical tissue showed strong SF-1 expression (Fig. 1M-3).

By analyzing all ACC samples and all tumor tissues derived from nonsteroidogenic organs, the sensitivity, specificity, positive predictive value, and negative predictive value for SF-1 in detecting ACC were 98.6, 100, 100, and 97.3%, respectively.

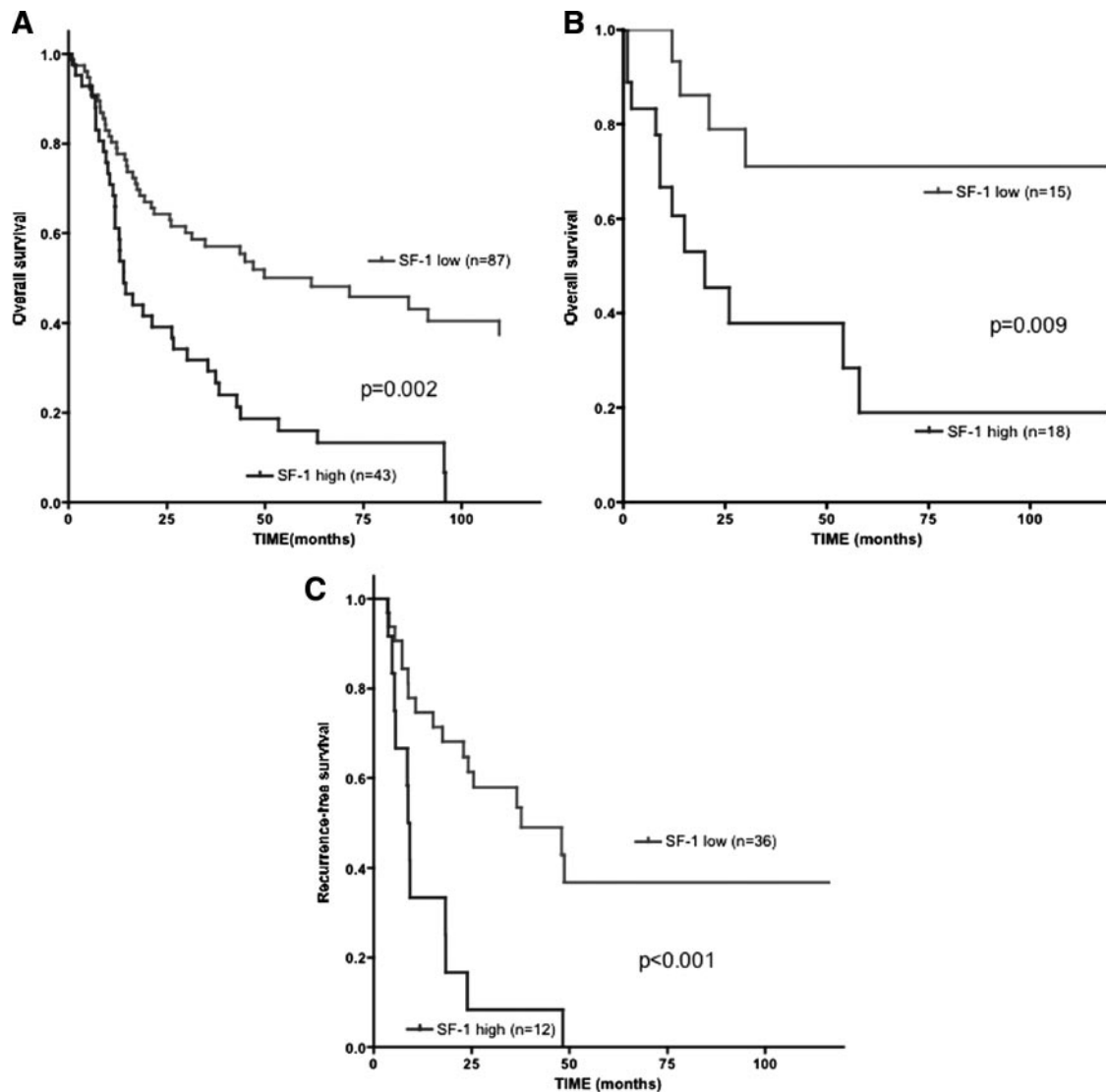
### Correlation of SF-1 expression and clinical outcome in patients with ACC

For survival analysis, only patients with tumor samples from primary surgery and sufficient follow-up data were included (n = 130). SF-1 expression was absent in only three, and SF-1 staining intensity was low in 84 and strong in 43 samples. In the high SF-1 expression group, 37 of 43 (86%) patients died from ACC and 39 of 43 (90%) had a tumor recurrence compared with 43 (51%) and 50 (59%) of 84 in

the low SF-1 expression group. Median overall survival was 14 months (95% CI = 9.9–18.1 months) in patients with strong SF-1 staining, whereas it was 49.8 months (95% CI = 5.96–93.7 months) in patients with low SF-1 staining intensity (Fig. 2A). Univariate analysis revealed a significant association between strong SF-1 expression and mortality [HR for death = 2.46 (95% CI = 1.57–3.87)], and in a multivariate model adjusted for tumor stage, sex, age, and endocrine activity of the tumors, the prognostic value of strong SF-1 expression remained unchanged [HR for death 2.46 (95% CI = 1.30–4.64); Table 4], confirming SF-1 expression as prognostic factor for survival in ACC.

Similar findings were found in the French ACC cohort using RNA microarray analysis. In this independent series, tumor stage-adjusted HR for death for continuous SF-1 values was 2.78 (95% CI = 1.32–5.86) and for dichotomized SF-1 values 4.69 (95% CI = 1.44–15.30; Fig. 2B).

In addition, we assessed the prognostic value of SF-1 expression after complete resection (n = 48). Median recurrence-free survival was significantly shorter in patients with strong SF-1 staining [8.8 months (95% CI = 7.7–9.9) vs. 37.7 months (95% CI = 9.8–65.6); Fig. 2C]. Again, multivariate analysis confirmed SF-1 expression as a prognostic factor [HR for recurrence = 3.91 (95% CI = 1.71–8.94); Supplemental Table 2].



**FIG. 2.** Kaplan-Meier estimates on overall survival (A and B) and recurrence-free survival (C) in patients with adrenocortical carcinoma according to SF-1 expression. A, Overall survival of all ACC patients of the German cohort with tumor samples from primary surgery (n = 130); B, overall survival of ACC patients of the French cohort (n = 33); C, recurrence-free survival only in the subgroup of German patients in whom complete resection was achieved (n = 48). SF-1 expression was determined by immunohistochemistry (A and C) and RNA microarrays (B) (for details see *Patients and Methods*).

## Discussion

Our large study including more than 161 evaluable ACC tissue samples indicates that SF-1 is a highly valuable immunohistological marker for the differential diagnosis of adrenal tumors. Only 2% of the 161 ACC samples, but all 73 nonadrenocortical tumors, were SF-1 negative, demonstrating that SF-1 has a much higher sensitivity and specificity to determine the adrenocortical origin of an adrenal lesion than has been reported for other immunohistological markers (Table 1). In addition, we provide the first evidence that high SF-1 expression is associated with poor clinical outcome in adults with ACC.

Histological diagnosis of ACC is often difficult, because ACC is a rare, morphologically heterogeneous tumor, and histomorphological criteria for the discrimination from

pheochromocytoma or metastases from extraadrenal neoplasias are not well established (7, 22, 51, 52). For all immunohistological markers proposed in the past such as D11, melan-A, or inhibin- $\alpha$ , the percentage of negative ACC samples were at least 25%, and the total number of ACC samples for each antibody was 163 at maximum (Table 1).

Expression of nuclear receptor SF-1 in adrenocortical cells has been documented previously (50), and its important role in adrenal development is well established (27). Accordingly, adrenocortical cells in normal adrenal glands as well as all benign adrenal adenomas were positive for SF-1 staining. Already in 1995, SF-1 had been suggested to be a useful marker in the differential diagnosis of ACC (23), but the results of only 17 ACC samples stained with SF-1 antibody were published (34–36). In addition, for many years, no re-



**TABLE 4.** Factors influencing overall survival according to univariate and multivariate analyses in patients with ACC (German cohort)

Variables	Univariate analysis			Multivariate analysis		
	HR	95% CI	P	HR	95% CI	P
Age <sup>a</sup>	1.00	0.99–1.02	0.509	1.01	0.99–1.02	0.340
Sex						
Male (n = 47) <sup>b</sup>						
Female (n = 83)	0.90	0.57–1.40	0.627	0.57	0.31–1.01	0.055
Tumor stage						
I–II (n = 53) <sup>c</sup>						
III (n = 40)	1.62	0.92–2.83	0.089	1.81	0.90–3.65	0.094
IV (n = 34)	3.94	2.25–6.88	<0.001	4.37	2.15–8.87	<0.001
Hormone secretion						
Nonsecreting (n = 17) <sup>d</sup>						
Glucocorticoids (n = 48)	1.12	0.56–2.20	0.753	1.02	0.48–2.15	0.966
Sex hormones (n = 13)	0.98	0.39–2.45	0.967	1.38	0.53–3.60	0.516
Mineralocorticoids (n = 6)	2.03	0.70–5.91	0.193	0.906	0.27–3.06	0.874
SF-1						
Negative + low (n = 87)						
High (n = 43)	2.46	1.57–3.87	<0.001	2.46	1.30–4.64	0.006

For survival analyses, only patients with tumor samples from primary surgery and sufficient clinical data (including follow-up) were included (n = 130).

<sup>a</sup> Age HR associated with one unit increase in the predictor.

<sup>b</sup> Male sex was taken as the reference category.

<sup>c</sup> Stage I–II was the reference category.

<sup>d</sup> Nonsecreting ACC was the reference category (in 46 patients, no information was available).

liable antibody against human SF-1 for paraffin-embedded tissue was available. In contrast, the antibody used in our study is now easily available for purchase.

The fact that two of the three ACC samples without SF-1 immunoreactivity were hormonally active (Supplemental Table 1) may point to methodological limitations of immunohistochemistry in cases of low SF-1 expression. This view is supported by the consistent SF-1 mRNA expression in all adrenocortical neoplasias in the French cohort. However, it is also possible that a small percentage of ACC are truly SF-1 negative, potentially harboring activating mutations downstream in the SF-1 pathway. This hypothesis has to be addressed in further investigations analyzing downstream targets of SF-1 (31).

In our study, detection of SF-1 staining in nonadrenal tissue was restricted to organs that are well known for SF-1 expression (53–55). In contrast, none of the investigated pheochromocytomas or tumors that usually metastasize to the adrenal gland revealed positive immunoreactivity against SF-1. In addition, SF-1 staining of Leydig cells within a seminoma and of adrenocortical cells adjacent to renal cancer (Fig. 1) demonstrates the accuracy of the method. Taken together, our results strongly confirm the hypothesis by Sasano *et al.* (7) that SF-1 is the best available marker for adrenocortical tumors. In our view, it, therefore, should become part of the routine diagnostic workup of adrenal tumors.

The second important finding of our study is the correlation of SF-1 expression and clinical outcome in patients with

ACC. It has been previously shown that the *SF-1* gene is amplified and overexpressed in childhood ACC (28, 29, 31) and that increased SF-1 dosage increases proliferation, decreases apoptosis of human adrenocortical cells, and induces adrenocortical tumors in transgenic mice (28, 29, 31). In addition, in adult ACC, chromosomal gains in 9q, where the SF-1 gene is located, have been described (56), suggesting that gene amplification may be the basis of SF-1 overexpression also in adult ACC. Therefore, there is increasing evidence that SF-1 dosage is critical for adrenal tumorigenesis (57). This concept is greatly supported by the demonstration of a reduced recurrence-free and overall survival in adult ACC patients exhibiting high SF-1 expression. The fact that this effect remains significant after adjusting for tumor stage and is also present in the French series indicates that SF-1 is not only a helpful diagnostic tool but also of important prognostic value.

At first glance, it seems to be a paradox that SF-1 is equally expressed in benign and malignant adrenocortical neoplasms and yet has such a strong and consistent association with prognosis in ACC. However, the action of SF-1 clearly varies depending on the cellular context. In differentiated adrenocortical cells, the major role of SF-1 is related to steroidogenesis with most of the steroidogenic enzymes possessing SF-1 response elements in their promoter (26, 27). However, SF-1 also plays a major role in fetal adrenal development by stimulating adrenal growth independent of its action on steroidogenesis (24, 25, 27). We hypothesize that in ACC, the cellular context resembles more the fetal phe-



notype, whereas benign tumors represent a differentiated phenotype. In agreement with this hypothesis is the fact that the level of SF-1 expression did not correlate with hormonal activity in our cohort. This view is further supported by the well-established overexpression of IGF-II in ACC (58). High IGF-II expression plays an important role in normal fetal adrenal development but is not found in adult adrenals or benign adrenocortical neoplasms (59–61). Thus, although SF-1 is obviously not causative for malignancy, it nonetheless may be a prerequisite for proliferation in ACC by providing a specific growth advantage on the background of oncogenic mutations. Similar molecular mechanisms have been described in other malignancies (62).

Currently, tumor stage is the only widely accepted prognostic marker in ACC. Few other markers have been suggested in the past for this purpose (44, 63, 64), but either their clinical value could not be confirmed or the immunohistochemical detection method is not established on a routine basis. Therefore, more reliable prognosis markers are needed to advise patients with ACC and a given tumor stage. Accordingly, if SF-1 immunohistochemistry will become part of the work-up in adrenal tumors, also prognostic information will be generated that may help to guide therapeutic decisions. This might be of special importance in patients after complete surgical resection, in whom a benefit of adjuvant therapy with mitotane (65) or radiotherapy of the tumor bed (66) has been suggested based on retrospective studies but is not yet generally accepted (67).

The negative association between SF-1 staining intensity and survival strengthens the concept of SF-1 being a crucial, dosage-dependent survival factor in this tumor entity. Therefore, SF-1 seems to be also an intriguing target for a therapeutic approach. Recently, SF-1 inverse agonists have been developed (68–70) and led to growth retardation of ACC cells (33), suggesting that these agonists might become useful future tools for treating ACC.

In conclusion, our study indicates that SF-1 is the best available immunohistological marker to determine the adrenocortical origin of an adrenal mass with high sensitivity and specificity. In addition, SF-1 expression is of stage-independent prognostic value in patients with ACC, suggesting that SF-1 plays an important role in the pathogenesis of this disease.

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