Detection of Novel Actionable Genetic Changes in Salivary Duct Carcinoma Helps Direct Patient Treatment

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Running title: Molecular characterization of salivary duct carcinoma
TRANSLATIONAL RELEVANCE

Broad based tumor genotyping is expediting the clinical development of effective targeted therapies, which is particularly helpful for patients with rare malignancies of poorly understood pathogeneses, who have limited therapeutic options. We applied a multiplexed tumor genotyping assay focused on clinically actionable targets, SNaPshot, and HER2 FISH to study salivary duct carcinoma (SDC), a rare and aggressive salivary gland tumor for which current chemotherapeutic regimens are largely ineffective. We identified mutually exclusive genetic aberrations in 15 of 27 (56%) tumors and detected, for the first time in SDC, activating mutations in the PIK3CA and BRAF genes while confirming the presence of HER2 gene amplification in a subset of cases. These findings were rapidly translated to clinical care expanding the therapeutic options for patients with SDC. Indeed, prospective clinical testing of 8 SDC patients identified actionable genetic alterations in 6 tumors, prompting treatment of all 6 patients with targeted therapies.
ABSTRACT

**Purpose:** Salivary duct carcinomas (SDC) are a rare and aggressive subtype of salivary gland cancers for which cytotoxic chemotherapy has limited efficacy. We investigated whether genotyping analysis could detect novel tumor-specific mutations that would help direct SDC patient treatment using targeted agents.

**Experimental Design:** We genotyped twenty-seven SDC archival specimens from patients followed at Massachusetts General Hospital and Massachusetts Eye and Ear Infirmary between 2000 and 2011. These included the tumors of 8 patients who were tested prospectively. Targeted mutational analysis of 13 clinically-relevant cancer genes was performed using SNaPshot multiplexed genotyping. FISH was performed to detect \( \text{HER2} \) gene amplification. Patient medical records and tumor histopathological features were retrospectively reviewed.

**Results:** Mutually exclusive genetic aberrations were detected in 15 of 27 (56%) tumors, including 2 (7%) mutations in \( \text{BRAF} \), 5 (19%) mutations in \( \text{PIK3CA} \), and 8 (30%) cases of \( \text{HER2} \) gene amplification. To our knowledge, this is the first time that \( \text{BRAF} \) and \( \text{PIK3CA} \) mutations have been reported in this tumor type. Prospective clinical testing of 8 SDC patients identified actionable genetic alterations in 6 tumors and influenced therapeutic decisions for all 6 patients.
**Conclusion:** SNaPshot molecular profiling identified novel genetic changes in SDCs, expanded the therapeutic options for patients with this rare tumor, and is changing SDC management at our institution. These findings highlight the importance of using broad based genetic profiling to expedite the identification of effective targeted therapies for patients with rare malignancies.
INTRODUCTION

Salivary gland cancers are rare, accounting for less than 5% of all cancers of the head and neck, and are amongst the most heterogenous primary tumors that arise in the body, with very different natural histories according to the specific histological subtypes.\(^{(1)}\) Salivary duct carcinomas (SDC) account for approximately 6% of all salivary gland cancers and are among the most aggressive salivary malignancies.\(^{(2)}\)

First described in 1968, SDC histopathology is characterized by solid and cribriform cell nests with central necrosis resembling ductal carcinoma of the breast.\(^{(3)}\) SDC can occur \textit{de novo} or as carcinoma ex-pleomorphic adenomas and primarily involve the major salivary glands (96%), particularly the parotid. The average age at diagnosis is 50 years and they tend to occur in men (approximately 75%). Patients typically present with an enlarging mass in the parotid accompanied by facial nerve dysfunction, and often with locally-advanced disease. Despite aggressive clinical management (complete surgical resection and chemoradiation) about 65% of patients with SDC die from progressive disease by 48 months.\(^{(4)}\)

In addition to the histological resemblance between SDC and breast ductal carcinoma, overexpression of the human epidermal growth factor receptor \textit{(HER2/neu)} is also a feature shared by both tumor types.\(^{(5-8)}\) Review of the literature indicates that approximately 37% of SDC (64 of 173 cases) exhibit strong (3+ score) \textit{HER2} overexpression, as assessed by immunohistochemistry, and 72% of these (46 of 64 cases) are positive for \textit{HER2} gene amplification, as
determined by fluorescence or chromogenic in situ hybridization (FISH or CISH).(9-17) In contrast to breast carcinoma, SDC are consistently negative for estrogen-\textit{alpha} and progesterone receptors, while the expression of androgen receptor is observed in the majority of cases.(18)

Given the rarity of the disease, establishing effective systemic therapy for such patients has been a challenge. Clinical trials are primarily limited to small phase II studies for patients with salivary gland cancers of multiple histologies, and have yielded modest response rates.(19, 20) The need for better therapies has prompted a number of efforts to characterize the biologic underpinnings of the various salivary gland histologies. With the rapidly expanding new generation of targeted therapies, we now have the ability to explore new treatments based on tumor-specific genetic markers. These approaches are especially critical in patients for whom no proven conventional treatment options are known.

We developed a multiplexed tumor genotyping clinical assay (SNaPshot) that has been adopted at our institution for over three years, to help guide patient treatment for various malignancies.(21) Clinical SNaPshot testing of one SDC patient detected a novel targetable mutation in the \textit{BRAF} oncogene (V600E). Based on this finding, we extended our genotyping efforts to a retrospective cohort of 19 SDC patients, and performed prospective clinical testing of 7 additional patients. We identified actionable genetic alterations in 15 (56\%) cases and our data impacted therapeutic decisions for 6 patients.
PATIENTS AND METHODS

Patient Selection
Salivary duct carcinoma cases diagnosed between 2000 and 2010 were identified by searching the Massachusetts General Hospital and Massachusetts Eye and Ear Infirmary records. Excess archival human material, in the form of formalin fixed paraffin embedded (FFPE) blocks, was retrieved for 19 patients and used under a research protocol approved by the institutional review board for human research (reference: 2008-P-002165; MGH). Between 2009 and 2011, eight patients were tested prospectively as part of their standard of care. SNaPshot tumor genotyping has been available at our institution as a clinical test since March or 2009, and is offered to any cancer patient at the discretion of the treating physician.(21) Prospective clinical genotyping is performed on FFPE surgical material and requires the patient’s written informed consent. Patient medical records were reviewed for demographics, treatment and outcomes. Stage at diagnosis was determined according to the American Joint Committee on Cancer (AJCC) guidelines.(22)

Genetic Analysis
Archival surgical specimens were reviewed by a pathologist (VN) to select the most appropriate tumor-enriched area for analysis. Total nucleic acid was extracted from FFPE tumor tissue obtained by manual macro-dissection, or by coring the paraffin block with a 1.5 mm dermal punch, followed by extraction
using a modified FormaPure System (Agencourt Bioscience Corporation).(21)

Multiplexed mutational analysis of a panel of 13 cancer genes, which included

**BRAF, EGFR, KRAS, NRAS, PIK3CA** and **TP53** (Supplementary Table S1), was

performed using a previously reported tumor genotyping protocol that was
developed by our group, and is based on Applied Biosystems' SNaPshot

platform.(21)

The mutational changes identified by SNaPshot genotyping were confirmed by
Sanger sequencing, using previously described conditions (21). For **PIK3CA** E545K
and H1047R mutations, we performed direct sequencing of M13-tagged PCR products
generated using the following primer pairs: **PIK3CA** exon 9, 5'-

TGTTAAACGACGAGCAGTCCTGTGAATCCAGAGGGGAAA-3' (forward) and 5'-
CAAGGAAACAGCTATGACCCATGCTGAGATCAGCCAAAT-3' (reverse); and **PIK3CA**
exon 20, 5’- TGTTAAACGACGACGAGTCATTTGCTCCAAACTGACCA -3’ (forward)
and 5’- CAGGAAACAGCTATGACCTGTGGAATCCAGAGTGAGCTT -3’ (reverse).

Thermocycling was performed at 95 °C for 8 min, followed by 45 cycles of 95 °C for 20
s, annealing at 58 °C (exon 20) or at 68 °C (exon 9) for 30 s and 72 °C for 1 min, and

one last cycle of 72 °C for 3 min.

Confirmation of **BRAF** V600E mutations was performed using direct sequencing of

PCR products generated using the following primer pair: **BRAF** exon 15, 5’-

TCATAATGCTTGCTGATAGGA-3’ (forward) and 5’-
GGCCAAAAATTTAATCAGTGA-3’ (reverse). Thermocycling was performed at 94
°C for 2 min, followed by 38 cycles of 94 °C for 30 s, annealing at 55 °C for 30 s and

72°C for 45 s, and one last cycle of 72 °C for 10 min.
Fluorescence in situ hybridization (FISH) was performed on 5-micron sections of FFPE tumor tissue, to evaluate copy number changes in the HER2 gene. Dual-color FISH was carried out using the PathVysion assay (Abbott Molecular), which includes one probe specific to the chromosome 17q HER2 locus and a copy number control probe recognizing centromere 17 (CEP17). HER2 gene amplification was determined following previously established guidelines, which define amplification as a HER2: centromere 17 (CEP17) signal ratio greater than 2.2 scored in 50 tumor nuclei.(23)

Immunohistochemistry

5-μm-thick tissue sections were cut from selected paraffin blocks, mounted onto charged glass slides and air dried overnight in a 58 °C convection oven. Immunohistochemical staining was performed on a fully automated Leica Bond Platform using the Leica Refine Detection Kit, including antigen retrieval (EDTA 9.0 for 20 minutes) and deparaffinization steps. We used the Androgen Receptor antibody from Dako (1:50 dilution). A positive control (section of known AR-positive prostate cancer) was run simultaneously. Immunostaining for AR was identified by a dark brown stain confined exclusively to the nucleus. Cases were considered positive if staining was observed in more than 50% of tumor cell nuclei, negative when seen in fewer than 5%, and weak or moderate if staining was detected in 5-20% or 21-50% of tumor cell nuclei, respectively.(24) All staining results were evaluated by a pathologist (PS).
Statistical Methods

Hypothesis tests for the association between clinico-pathological features and the *PIK3CA*, *BRAF*, and *HER2* status were conducted with Fisher exact tests. Survival curves were estimated using the Kaplan-Meier estimator; hazard ratios were estimated using the Cox proportional hazards model, and p-values for comparing survival distributions, were calculated using log-rank tests.
RESULTS

Clinical characteristics of the cohort

Patient demographics show a median age at presentation of 64 years (range 24-88), a high male to female ratio (8:1) and advanced disease at presentation, with 19 out of 27 (70%) patients presenting with lymph node metastasis and 4 out of 27 (15%) with distant metastasis (Tables 1 and 2). The majority (82%) of patients presented with stage IV disease (Table 1), and the overall prognosis was poor with 44% of initially resectable patients experiencing disease recurrence at a median of 10.03 months (range: 1.1-97.12) (Supplementary Table S2).

Representative images of SDC histology are illustrated in Supplementary Figure S1 (A-D) showing infiltrative ductal elements, cellular pleomorphism, high mitotic activity and an exquisite resemblance to ductal carcinoma of the breast. Characteristic positive staining for HER2 and for androgen receptor are also depicted (E and F, respectively). Additional histopathological features identified in our cohort are outlined in Table 2. Perineural and lymphovascular invasion were observed in 20 (74%) and 15 (56%) cases, extraglandular extension in 16 (59%) cases, and the presence of positive margins was detected in 14 (52%) tumors. Tumor cell necrosis was detected in 12 (44%) specimens. Lymph node involvement and extranodal extension were identified in 19 (70%) and 9 (33%) cases, respectively.
Molecular profiling of SDC identifies HER2 gene amplification and novel activating mutations in PIK3CA and BRAF

SNaPshot mutational profiling identified mutually exclusive point mutations in 7 of 27 (26%) SDC specimens, of which 24 were primary tumors and 3 were metastases (Supplementary Table S3). All mutations were confirmed by Sanger sequencing. Five (19%) tumors harbored activating mutations in the p110 alpha subunit of the phosphatidylinositol 3-kinase (PIK3CA) gene. Three of these substitutions were located within the kinase domain of PIK3CA (H1047R) (Fig. 1A), and the other 2 mapped to the helical domain (E545K) (Fig. 1B). In our cohort, patients with PIK3CA-mutant SDC presented with stage IV disease (5/5), perineural invasion (5/5), extraglandular extension (4/4), positive lymph nodes (5/5), and extranodal tumor extension in the three cases with available information (3/3) (Tables 1 and 2). While these features could be suggestive of a more aggressive tumor behavior, prognosis is universally poor in patients with this disease. In addition, we were limited by the size of our cohort, and found no statistically significant association between the presence of a PI3KCA mutation and any clinicopathological features, time to recurrence, or overall survival.

SNaPshot testing detected the BRAF V600E kinase activating mutation in two (7%) additional SDC cases (Fig. 1C). Both BRAF-mutant tumors had positive margins, exhibited lymphovascular invasion, and were identified in male patients who presented with stage IVA disease (Tables 1 and 2).

The HER2 gene encodes for a receptor tyrosine kinase often amplified and overexpressed in SDC. (5-17) Using FISH, we detected HER2 gene
amplification in 8 of 27 cases (30%). Representative images of SDC cases exhibiting normal HER2 copy number and HER2 gene amplification are illustrated in Figure 1 (D and E, respectively). Review of the pathology reports for all SDC cases revealed that HER2 IHC had been requested at the time of diagnosis for 12 of the 27 tumors. We found complete correlation between HER2 gene amplification by FISH and strong HER2 overexpression (3+ score) by IHC, for all SDC cases with available IHC data. None of the HER2-amplified tumors had concurrent point mutations in PI3KCA or BRAF. Six out of 8 (75%) patients with HER2-amplified tumors were male, and 7 (88%) presented with advanced disease (stage IV) (Table 1). Of the 8 HER2-amplified tumors, 7 (88%) had lymph node involvement, 6 (75%) showed perineural invasion and 5 (62%) presented with at least one of the following characteristics: positive resection margins, lymphovascular invasion, extraglandular extension or necrosis (Table 2). We found no statistically significant associations between the examined clinicopathological features and SDC HER2 status.

Immunohistochemistry analysis revealed that Androgen Receptor (AR) was strongly expressed by the majority of SDC in our cohort (24/27) confirming previous findings in the literature (Supplementary Fig. S1F). (18) Of the 3 SDC cases that were negative for AR expression: 2 exhibited HER2 gene amplification, as detected by FISH, and none of them harbored activating mutations in oncogenes detected by SNaPshot genotyping (Supplemental Table S3). The limited number of cases precluded any significant association between
the AR status of SDC tumors and other genetic changes or clinicopathological features.

Stratification of the overall patient population according to the mutational status of their tumors, revealed no statistically significant differences in outcome, either when each genetic alteration was analyzed separately or when the three types of changes were grouped together (Figure 2 and Supplementary Table S2). However, SDC patients whose tumors harbored a genetic abnormality (PI3KCA mutation, BRAF mutation or HER2 amplification) experienced a trend towards a reduced event free survival (EFS) (P=0.1102) when compared to patients whose tumors had no detectable oncogenic change (Figure 2B).

**Genotype-driven targeted therapies for SDC**

SNapShot genotyping of one SDC case was first requested as a clinical test for patient SDC-13 (Table 3). The finding of a BRAF V600E mutation in this patient’s tumor prompted the current study and his clinical case is presented below.

Patient SDC-13 was a 66-year-old male who presented with a large right parotid mass (6.2 cm in largest dimension) in June 2007, for which he underwent right total parotidectomy and modified radical neck dissection. Histology revealed stage IVA (22) SDC with positive surgical margins and 7 of 49 involved lymph nodes. Adjuvant radiotherapy to the parotid bed and ipsilateral neck irradiation (6400 cGy in 200 cGy fractions), with weekly concurrent carboplatin (AUC 1.5) and
paclitaxel (30 mg/m²) administration, lasted 7 weeks and was completed in December 2007.

In August 2008, routine FDG-PET-CT surveillance showed a solitary hypermetabolic L1 bone lesion that was treated with hemilaminotomy and facetectomy, followed by radiotherapy. Subsequent imaging in February 2009 showed new hypermetabolic bone lesions and mediastinal adenopathy. Monthly zoledronic acid infusions and cyclophosphamide plus doxorubicin were initiated, but chemotherapy was discontinued in October 2009 due to disease progression.

At that point, SNaPshot analysis of the tumor was performed. Identification of a \textit{BRAF} V600E mutation led to the patient’s enrollment in a phase II clinical trial investigating a MEK inhibitor in patients with \textit{BRAF}-mutant tumors. Treatment started in November 2009 and by March 2010 the disease appeared stable (22% reduction in mediastinal adenopathy), according to the Response Evaluation Criteria in Solid Tumors (RECIST). Eight months after initiation of therapy with the experimental MEK inhibitor (July 2010) a restaging CT showed an increase in mediastinal adenopathy (Figure 3A) and treatment was discontinued.

In August 2010 the patient enrolled in a phase I study of combined BRAF and MEK inhibitors GSK2118436 and GSK1123212. By September 2010 a restaging CT scan of the chest, abdomen and pelvis showed a partial response with a 52% decrease in mediastinal adenopathy and stable bone lesions (Figure 3B). The patient remained on this study for twelve months, until August 2011 when, after 14 cycles, imaging showed progressive disease.
In October 2011, the patient enrolled on a phase I clinical trial investigating combined PI3K/mTOR and MEK inhibitors. Shortly after starting the third cycle, head CT performed after a fall showed multiple new brain metastases. The patient came off study, elected to forgo whole brain radiotherapy and passed away in December 2011. In summary, 16 month after being diagnosed with advanced stage SDC and after undergoing two surgeries and several rounds of radiotherapy and chemotherapy, patient SDC-13 presented with new metastases and progressive disease. Discovery of a \textit{BRAF} V600E mutation in his tumor uncovered new therapeutic options and led to his enrollment in three consecutive clinical trials. He had partial responses to two of these protocols and his disease remained progression-free for a total of 20 months. His targeted treatments are summarized in Table 3 (patient SDC-13).

Three additional patients in our cohort entered clinical trials based on prospective SNaPshot genotyping data showing activating mutations in \textit{PIK3CA} (Table 3, SDC-20, SDC-21 and SDC-27). For patient SDC-20 with a \textit{PIK3CA} E545K mutant tumor, benefit from targeted agents was not negligible. He showed partial response to two experimental drugs and his combined progression-free survival lasted 8.7 months (Table 3). Patient SDC-21 harbored a \textit{PIK3CA} H1047R mutant tumor and her response to treatment was less remarkable, with progressive disease being detected just 8 weeks after enrollment in a study using a dual PI3K/mTOR inhibitor. Patient SDC-27 initiated treatment with a PI3K inhibitor at the time of writing, thus follow up information is still unavailable.
Finally, 2 of the 8 SDC patients with HER2-amplified tumors were tested prospectively and received off-label adjuvant treatment with the anti-HER2 monoclonal antibody trastuzumab (Table 3, SDC-24 and SDC-26). There was a period of disease stabilization in both cases, with one patient experiencing disease progression after 6 months and the other one after 1 year of treatment.
DISCUSSION

Targeted cancer therapies may represent the most promising strategy to fight rare aggressive malignancies that do not respond well to cytotoxic chemotherapy, such as salivary gland cancers. So far, targeted treatments used in salivary gland cancers have not always been adjusted to match particular histologic classes or specific genetic changes.(6, 19, 25) In all, few objective responses have been reported, and no agent has emerged as a standard of care for the treatment of loco-regionally recurrent and/or distant metastatic disease. In this study, we attempted to close the gap for one of the most aggressive subtypes of salivary gland cancers: salivary duct carcinoma.

Our approach uncovered novel and mutually exclusive mutations in PIK3CA (19%) and BRAF (7%). The discovery of PIK3CA variants in SDC provides a new genetic link between this malignancy and ductal carcinoma of the breast, further highlighting the similarities between these two tumor types. In addition, driver mutations in PIK3CA and BRAF are molecular targets for therapeutic agents under clinical development and could potentially represent new hope for patients suffering from this aggressive disease.

In agreement with previous reports, our patient population consisted primarily of males (89%) older than 50 years of age (median of 64 years), who presented with advanced disease (82% with stage IV).(4, 26, 27)

In addition to the histological resemblance between SDC and breast ductal carcinoma, another feature common to both tumor types is the strong overexpression of HER2, which is detected in a subset of cases and highly
correlates with amplification of the HER2 locus. We detected HER2 gene amplification in 8 of 27 (30%) SDC cases, consistent with the overall frequency reported in the literature (47 in 173 cases, 27%). (9-17)

For patients with HER2-positive breast cancer, treatment with anti-HER2 agents such as trastuzumab, can significantly improve disease-free and overall survival.(28-30) These findings provide a rationale for exploring the effects of trastuzumab in the treatment of HER2-positive SDC. So far, only a few SDC patients have been enrolled in treatment regimens that included HER2 antagonists, and some case reports have shown encouraging results with an occasional complete response.(13, 25, 31, 32)

In our study, 2 patients with HER2-amplified SDC were treated with adjuvant trastuzumab therapy (Table 3). They both experienced a period of stable disease after initiation of trastuzumab treatment, which lasted 6 months (SDC-26) and 1 year (SDC-24). The two patients are still alive at the time of writing, 13 and 33 months, respectively, since the date of diagnosis. Their survival is within the range previously described for reported cases of SDC patients treated with trastuzumab.(13, 31, 32)

Consistent with previous studies, the majority of SDC in our cohort (24/27) were AR-positive by IHC, including the 5 patients who were treated prospectively. Being AR so distinctively and strongly expressed in SDC, androgen deprivation therapy is emerging as a possible targeted approach for patients with this malignancy. In small series, androgen deprivation therapy has
shown clinical benefit in a discrete number of patients with AR positive SDC. (33, 34)

We identified activating mutations in PI3KCA (19%) and in BRAF (7%) in a subset of SDC that were AR-positive and negative for HER2 gene amplification. This is an interesting finding, as BRAF and PI3KCA encode for downstream targets of oncogenic signaling pathways triggered by the epidermal growth factor family of receptor tyrosine kinases, which include HER2 and EGFR. (35) Of note, a recent report described the presence of EGFR mutations in 9% of SDC. (15) Furthermore, while our manuscript was in preparation, another group reported PTEN loss in one patient with SDC. (36) PTEN is a negative regulator of PI3K signaling, thus loss of function of the PTEN tumor suppressor results in activation of the PI3K/AKT/mTOR pathway. (37)

The oncogenic roles of BRAF and PI3KCA have been extensively studied and supported by functional analyses in cell line and animal tumor models for other malignancies (38, 39), but this type of mechanistic data is still lacking for SDC. Of note, targeted inhibitors of BRAF and PI3K/mTOR signaling have shown promising results in a variety of cancers (40-43). While functional studies will be necessary to definitely assess SDC tumor dependency on these oncogenes, taken together with previous studies, our observations suggest that abnormal activation of intracellular pathways (such as PI3K/Akt/mTOR, and RAS/RAF/MEK/ERK) downstream of EGFR/HER2 signaling, may contribute to SDC tumorigenesis. The current data also raise the possibility that SDC
malignancy could be triggered by distinct genetic drivers, including mutations in 
\textit{PIK3CA}, \textit{BRAF} and \textit{EGFR}, loss of \textit{PTEN} and overexpression of \textit{HER2}.

\textit{PI3KCA} is mutated in a variety of epithelial tumors, including head and neck squamous cell carcinomas and breast cancer.\cite{44,45} Potent PI3K and PI3K/mTOR inhibitors are currently undergoing testing in genotype-driven clinical trials for patients with tumors carrying the hyperactive kinase. To our knowledge, this is the first time that activating mutations in \textit{PI3KCA} have been systematically studied and reported in SDC. In our cohort, 5 of 27 (19\%) specimens carried activating mutations in the kinase domain or in the helical domain of \textit{PI3KCA}, and had tumor features suggestive of more aggressive disease. Based on prospective genotyping, three patients (SDC-20, SDC-21 and SDC-27) enrolled in clinical trials that included PI3K, mTOR and MEK inhibitors (Table 3). In a recent report, two SDC patients with extensive cutaneous metastases were treated with the mTOR inhibitor temsirilimus, in combination with the antiangiogenic agent bevacizumab. Both patients responded rapidly and dramatically to therapy but the followup was short (<4 months), as their treatment was discontinued for reasons unrelated to the study drugs. \textit{PTEN} loss was identified in the tumor of one of the patients, and none of them harbored mutations in \textit{PIK3CA}.\cite{36} In our study, one patient (SDC-21) presented with progressive disease shortly (8 weeks) after initiation of treatment with an experimental PI3K/mTOR inhibitor, but patient SDC-20 had lasting partial responses to two targeted agents, maintaining progression-free disease for a total of 8.7 months (Table 3).
BRAF is a signaling component of the mitogen-activated protein kinase (RAS/RAF/MEK/ERK) pathway that promotes cell proliferation downstream of receptor tyrosine kinase signaling. The BRAF gene is mutated in a wide variety of cancers and the V600E mutation accounts for over 95% of all BRAF somatic variants described in human tumors.(46) Second generation BRAF inhibitors have shown impressive results in patients with BRAF V600E mutated malignant melanomas, with tumor regression being observed in the majority of cases.(47, 48) A strategy to overcome reactivation of the RAS/RAF/MEK/ERK pathway, which can occur in the context of acquired resistance when targeting BRAF, consists in inhibiting downstream targets of the pathway, like the MEK1/2 kinases. Multiple clinical trials are now testing MEK inhibitors in BRAF-mutant cancers. Therefore, it was interesting for us to detect BRAF V600E mutations in two of our patients (7%), and to use this information to guide treatment for one of them, who was tested as part of routine clinical management (SDC-13). This patient had partial response to two experimental treatments that used BRAF and MEK inhibitors, and his disease remained free from progression for a total of 20 months while on targeted therapy regimens (Table 3). Of note, in two recent clinical trials, treatment of BRAF-mutant advanced melanoma patients with vemurafenib resulted in median progression free survivals of 5.3 and 6.8 months.(47, 49) In all, patient SDC-13 survived 54 months after diagnosis, which compares favorably to previously reported survival of SDC.(4)

In conclusion, we identified novel mutations in SDC and, by prospectively testing 8 patients we detected actionable genetic alterations in 6 of them, which
helped guide their treatment with molecularly targeted therapies. While these are encouraging developments, it is hard to delineate clinical benefits in the few SDC patients who were treated with targeted agents based on somatic molecular findings (HER2 gene amplification or the presence of BRAF or PIK3CA mutations). Because SDC is so rare and typically presents as a high grade salivary cancer that requires nodal resection, the prognostic and therapeutic implications of our findings are difficult to access. At this point, there is no good estimate on what the expected time to disease progression should be, and it is unclear whether a few months of disease-free survival will translate into increased overall survival. Ultimately, larger studies with more homogeneous patient cohorts will be necessary to properly evaluate the clinical benefits of using targeted treatment strategies in SDC.

Our findings reiterate that broad base genetic profiling is a valuable approach in the identification of actionable mutations in rare tumors. We also demonstrate that, when applied to all tumor types in a clinical setting, large scale tumor genotyping strategies can enable the rapid translation of novel findings to patient care, which, if successful, could have a significant impact in rare and highly aggressive malignancies such as SDC.
FIGURE AND TABLE LEGENDS

Figure 1. Detection of PIK3CA and BRAF activating mutations and HER2 amplification in SDC

(A-C) SNaPshot mutational profiling was performed on nucleic acid extracted from SDC archival specimens run in parallel with a normal genomic DNA control. Examples of the three different mutated codons are shown with the black arrows pointing to the mutant alleles: PI3KCA H1047R (c.3140 A>G) in SDC-2 (A), PIK3CA E545K (c.1633G>A) in SDC-20 (B), and BRAF V600E (c.1799T>A) in SDC-13 (C). Assayed loci for each panel were as follows: (A) 1. PIK3CA 3140, 2. CTNNB1 101, 3. JAK2 1849, 4. BRAF 1798, 5. NRAS 37, 6. PIK3CA 1636, 7. APC 4348 and 8. APC 3340; (B) 1. KRAS 34, 2. EGFR 2235_49del F, 3. EGFR 2369, 4. NRAS 181, 5. PIK3CA 1633, 6. CTNNB1 94 and 7. CTNNB1 121; and (C) 1. EGFR 2235_49del R, 2. NRAS 38, 3. BRAF 1799, 4. NRAS 182, 5. PIK3CA 263, 6. TP53 742, 7. CTNNB1 95 and 8. CTNNB1 122. (D) HER2 FISH negative SDC display, on average, two red signals (HER2 probe Spectrum Orange: RP11-94L15) and two blue signals (Spectrum Aqua probe for chromosome 17 centromere) per nucleus (DAPI counterstaining). (E) HER2 FISH amplified SDC, showing clusters of red signals (HER2 probe) and 2 blue signals (chromosome 17 centromere probe) per nucleus (DAPI counterstaining).

Figure 2. Observed survival of 27 SDC patients according to molecular status.
Overall survival (A) and event-free survival (B) depicted according to the presence or absence of genetic abnormalities (*HER2* gene amplification, or mutations in *PI3KCA* or *BRAF*). Statistical analysis revealed no significant difference but showed a trend towards better survival for patients without a detected oncogenic abnormality.

**Figure 3. Effect of combination therapy with a BRAF and a MEK inhibitor in patient SDC-13, who carried a BRAF V600E-mutant tumor.**

(A) Pretreatment Chest CT scan showing enlarged mediastinal lymph nodes (arrows). (B) Post-treatment/restaging CT scan showing 52% shrinkage of mediastinal lymphadenopathy (arrows).

**Table 1. Baseline characteristics of SDC patients**

**Table 2. SDC tumor characteristics**

**Table 3. Summary of therapeutic decisions.** Prospective tumor genotyping helped guide treatment decisions for SDC patients whose tumors harbored oncogenic mutations.
REFERENCES


Figure 1
Nardi et al.

A Normal

Tumor<sub>SDC-2</sub>

<sup>PIK3CA</sup>  
<sub>H1047R</sub>

B Normal

Tumor<sub>SDC-20</sub>

<sup>PIK3CA</sup>  
<sub>E545K</sub>

C Normal

Tumor<sub>SDC-13</sub>

<sup>BRAF</sup>  
<sub>V600E</sub>

D

E
Figure 2
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A

Overall survival

- No abnormality
- At least one abnormality

Survival probability

HR: 1.487 (0.3652, 6.053)
P = 0.5774

Months

B

Event–free survival

- No abnormality
- At least one abnormality

Survival probability

HR: 2.191 (0.8185, 5.865)
P = 0.1102

Months
Figure 3
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Table 1. Baseline characteristics of SDC patients

<table>
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Table 2. SDC tumor characteristics

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* These features are relevant for adjuvant therapy
Table 3. Summary of therapeutic decisions. Prospective tumor genotyping helped guide treatment decisions for SDC patients whose tumors harbored oncogenic mutations.

<table>
<thead>
<tr>
<th>UPN</th>
<th>Genetic alteration</th>
<th>Treatment based on tumor genotype (TTP)*</th>
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</table>
| SDC-13| BRAF V600E (c.1799T>A) | Phase I clinical trial  
                          | MEK inhibitor (8 months)  
                          | Combination of BRAF inhibitor + MEK inhibitor (12 months)  
                          | Combination of PI3 kinase/mTOR inhibitor + MEK inhibitor (NA) |
| SDC-20| PI3KCA E545K (c.1633G>A) | Phase I clinical trial  
                          | PI3 kinase inhibitor (3.7 months)  
                          | Combination of PI3 kinase inhibitor + MEK inhibitor (NA)  
                          | TORC1/2 inhibitor (5 months) |
| SDC-21| PIK3CA H1047R (c.3140A>G) | Phase I clinical trial  
                          | PI3 kinase/mTOR inhibitor (8 weeks) |
| SDC-27| PIK3CA H1047R (c.3140A>G) | Phase I clinical trial  
                          | PI3 kinase inhibitor (ND) |
| SDC-24| HER2 amplification | Off label treatment  
                          | Concurrent RT + chemotherapy, followed by adjuvant trastuzumab for solitary metastasis (12 months) |
| SDC-26| HER2 amplification | Off label treatment  
                          | Concurrent RT + chemotherapy + trastuzumab, followed by adjuvant trastuzumab for initial post-operative therapy (6 months)  
                          | Off label treatment  
                          | Whole brain RT, followed by combination of trastuzumab + lapatinib for brain metastases (ND) |

* All treatment for metastatic disease except where noted. TTP: time to disease progression; NA: not applicable, patient experienced disease progression under treatment; ND: not determined, treatment ongoing.
Detection of Novel Actionable Genetic Changes in Salivary Duct Carcinoma Helps Direct Patient Treatment

Valentina Nardi, Peter M Sadow, Dejan Juric, et al.

Clin Cancer Res  Published OnlineFirst November 27, 2012.

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