Identification of ASF/SF2 as a Critical, Allele-Specific Effector of the Cyclin D1b Oncogene

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Abstract

The cyclin D1b oncogene arises from alternative splicing of the CCND1 transcript, and harbors markedly enhanced oncogenic functions not shared by full-length cyclin D1 (cyclin D1a). Recent studies showed that cyclin D1b is selectively induced in a subset of tissues as a function of tumorigenesis; however, the underlying mechanism(s) that control tumor-specific cyclin D1b induction remain unsolved. Here, we identify the RNA-binding protein ASF/SF2 as a critical, allele-specific, disease-relevant effector of cyclin D1b production. Initially, it was observed that SF2 associates with cyclin D1b mRNA (transcript-b) in minigene analyses and with endogenous transcript in prostate cancer (PCa) cells. SF2 association was altered by the CCND1 G/A870 polymorphism, which resides in the splice donor site controlling transcript-b production. This finding was significant, as the A870 allele promotes cyclin D1b in benign prostate tissue, but in primary PCa, cyclin D1b production is independent of A870 status. Data herein provide a basis for this disparity, as tumor-associated induction of SF2 predominantly results in binding to and accumulation of G870-derived transcript-b. Finally, the relevance of SF2 function was established, as SF2 strongly correlated with cyclin D1b (but not cyclin D1a) in human PCa. Together, these studies identify a novel mechanism by which cyclin D1b is induced in cancer, and reveal significant evidence of a factor that cooperates with a risk-associated polymorphism to alter cyclin D1 isoform production. Identification of SF2 as a disease-relevant effector of cyclin D1b provides a basis for future studies designed to suppress the oncogenic alternative splicing event.

Introduction

The cyclin D1b variant, produced via alternative splicing of the CCND1 transcript (1, 2), is a potent oncogene that harbors distinct functions from full-length cyclin D1 (cyclin D1a; refs. 3–5). Unlike cyclin D1a, cyclin D1b independently confers cellular transformation (4, 5). In addition, only the cyclin D1b isoform has the capacity to promote anchorage-independent growth and cell invasiveness (6). Further confirmation of novel oncogenic capabilities was identified in mouse models, wherein animals expressing human cyclin D1b under the bovine K5 promoter showed increased papilloma multiplicity (3). Given the enhanced oncogenic function of cyclin D1b, it is imperative to define the mechanisms that regulate cyclin D1b production in systems of clinical relevance.

The alternative splicing event that produces the cyclin D1b transcript (referred to as transcript-b) arises from failure to splice at the CCND1 exon 4–intron 4 boundary. Due to intrinsic transcriptional termination, cyclin D1b lacks exon 5–encoded sequences and contains a novel COOH-terminal domain of unknown function (1, 2). Previous studies showed that transcript-b/transcript-a ratios are enhanced in selected tumor types, thus providing evidence that the alternative splicing event may be altered as a function of tumorigenesis or tumor progression (6–10). Lending support to this posit, recent analyses of a large cohort of prostate cancer (PCa) specimens revealed that cyclin D1b (but not cyclin D1a) is induced in PCa as compared with nonneoplastic tissue (11). These findings were of interest, as cyclin D1b has specialized functions in this tumor type that are hypothesized to promote tumor progression (7).

Despite the compelling evidence identifying cyclin D1b as a potent, novel oncogene, the tumor-associated factor(s) that promote the alternative splicing event remain poorly defined. It has long been suggested that a polymorphism within the exon 4 splice donor site (G/A870) might contribute to transcript-b production, wherein the A allele was suggested to favor the alternative splicing event (1, 12, 13). Recent analysis using minigenes supported this contention,
and analysis of nonneoplastic prostate tissue showed that the presence of the A allele predicted for higher transcript-b production; however, the effect of the A allele was lost in tumor tissue, thus indicating that tumor-associated factor(s) likely bypass or modify the effect of the G/A870 polymorphism with regard to transcript-b production (11). Here, the present study identifies the SF2 (also known as ASF or SRp30a) RNA binding protein as a critical, allele-selective factor that associates directly with transcript-b and modulates cyclin D1b production in model systems of cancer relevance. Importantly, analyses of tumor tissue further support a model wherein tumor-associated elevation of SF2 specifically enhances cyclin D1b expression in human disease. Together, these findings provide a mechanism by which CCND1 alternative splicing is controlled in tumorigenesis, and identify SF2 as a critical regulator of cyclin D1b oncogene production.

Materials and Methods

Cell culture, transfections, generation of stables. LNCaP, C33A, and LAPC4 cell lines were obtained, cultured, and transfected as previously described (7, 14). C33A stable cell lines were generated by transfecting the individual expression constructs encoding empty vector, or individually introduced by stable transfection into C33A cells, harboring either the G or A870 allele (Fig. 1A) were independently introduced into LNCaP, LAPC4, C33A, and C33A-derived stable cell lines) were harvested and maintained as previously described (18). DT40-ASF cell line was a generous gift from James Manley (Cell and Molecular Biology, Columbia University, New York, NY) and DT40-ASF cells were transfected as using the Amazax Nucleofector protocol.

C33A stable cell lines were generated by transfecting the indicated expression constructs encoding empty vector, or individual cyclin D1 minigenes and selected with 400 μg/mL of G418 (MP Biomedicals). Clonal isolates were screened for expression by immunoblot. Isolates used herein are denoted as C33A-Vec, C33A-G1 (containing the G870 allele minigene), and C33A-A1 (containing the A870 allele minigene).

Plasmids. The pCGT7, pCGT7-ASF/SF2, and pCGT7-SRp40 expression constructs were generous gifts from Adrian Krainer (Biological Sciences, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY) and have been previously described (14, 15). The pCEP4-ASF/SF2 was a generous gift from Woan Yuh-Tarn (Cell Biology and Signal Transduction, Institute of Biomedical Sciences, Taipei, Taiwan) and was previously described (20). The cyclin D1 minigenes were previously described (11).

Immunoblotting. Cells were harvested, lysed in NETN, and subjected to SDS-PAGE and immunoblotting as previously described (14, 15). Immunoblots were performed using anti-sera against ASF/SF2 (Invitrogen), β-tubulin (Sigma), cyclin D1a (Neomarker, Ab3), cyclin D1b (7, glyceraldehyde-3-phosphate dehydrogenase (Invitrogen), or T7 (Novagen), as indicated.

RNA isolation, PCR, PCR-restriction fragment length polymorphism, and real-time PCR. RNA was isolated using TRIzol according to the protocols of the manufacturer. PCR analyses and primer sequences for transcript-a, transcript-b, and glyceraldehyde-3-phosphate dehydrogenase were previously described (7, 15, 21). The PCR-restriction fragment length polymorphism (PCR-RFLP) was performed as previously described (7, 22); briefly, RNA immunoprecipitation (RIP)-recovered products were subjected to a second amplification using primers designed for RFLP analyses. The product was then digested and visualized after electrophoresis by ethidium bromide. Real-time PCR for transcript-b was performed using the Syber Green protocol from Applied Biosystems and a 7900F Real-time PCR machine.

Immunohistochemistry and AQUA system analysis. Immunohistochemistry and AQUA analyses were performed as previously described (11) using a human prostate cancer array (SuperBio Chips Labs) and antisera indicated above. Comparison of relative SF2 levels from microarrays were analyzed using one-way ANOVA. Correlations of SF2 with cyclin D1a and D1b AQUA expression levels was completed using Spearman correlation coefficients, with Bonferroni correction of P values for multiple comparisons.

RNA immunoprecipitation. RIPs were performed as previously described (23). Briefly, cells (LNCaP, LAPC4, C33A, and C33A-derived stable cell lines) were harvested and nuclear extracts prepared by resuspending in isotonic buffer. After a 7-minute incubation on ice, samples were centrifuged at 700 × g for 7 minutes and nuclei were isolated, resuspended in buffer supplemented with 90 mmol/L of NaCl and 0.5% Triton X-100, and sonicated. After centrifugation at 5,000 × g for 15 minutes, nuclear extracts were precleared for 1 hour and immunoprecipitated with ASF/SF2 antibody or mouse IgG antibody. The antibody-antigen complex was precipitated by the addition of protein G-Sepharose beads (Invitrogen) for 3 hours at 4°C with rotation. Beads were washed thrice with lysis buffer and an aliquot was eluted in SDS sample buffer for immunoblot analysis. The remaining beads were incubated with lysis buffer in the presence of RNase free) DNase (Ambion) for 15 minutes at 37°C and washed thrice with lysis buffer before incubation with 50 μg of proteinase K (Roche) for 15 minutes at 37°C. Coprecipitated RNA was then extracted by the TRizol procedure and used for reverse transcription-PCR analyses.

Results

G/A870 polymorphism alters cyclin D1b production and SF2 binding. Given the enhanced oncogenic function of the cyclin D1b variant (3–5), and the established observation that cyclin D1b levels are enhanced as a function of prostate tumorigenesis (7, 11), it is imperative to discern the mechanism(s) underpinning the alternative splicing event. As was recently reported, the CCND1 G/A870 polymorphism plays a context-specific role in the alternative splicing event, wherein the A allele favors cyclin D1b production in minigene expression studies in which the alleles were individually examined (11). These studies were validated here, wherein minigenes harboring either the G or A870 allele (Fig. 1A) were independently introduced by stable transfection into C33A cells, which have been previously shown to harbor low to undetectable levels of endogenous cyclin D1 isoforms (24). Introduction of the G allele minigene (stable line C33A-G1), resulted in detectable expression of both CCND1 transcripts (a and b), and a preference towards transcript-a and cyclin D1a protein was observed (lane 2). Transscript-b levels were comparatively increased in the presence of the A allele minigene (lane 3), consistent with previous studies in which the minigenes were individually analyzed in parallel (11).
Subsequent analyses of individual minigene studies in spontaneously immortalized CV1 cells or viral oncoprotein immortalized RWPE-1 prostate epithelial cells (25, 26) were also carried out. Similar findings were observed in both nontumorigenic model systems, in which the A allele predisposed to transcript-b and cyclin D1b production (Supplementary Fig. S1). These studies further support the premise that in isolated comparisons, the G/A870 polymorphism influences CCND1 alternative splicing.

As G/A870 lies within the splice donor site, it was reasoned that the polymorphism might influence RNA binding protein recognition or activity. The splicing factor binding resource ESEfinder3.1 (27, 28) was therefore used to predict distinctions in the profile of associated splicing factors between the G and A-870 allele splice donor sites. As shown, binding of SF2 was suggested to be altered in both position and strength by changes in the polymorphic site (Fig. 1C). To initially assess whether SF2 could play a role in CCND1 alternative splicing, RIP was performed using the same stable cell lines described in Fig. 1B. Using standard techniques, RNA associated with either SF2-specific or control antisera were isolated, reverse transcribed, and detected by PCR amplification. As illustrated in Fig. 1D (top), transcript-b was only weakly detected in control cells and immunoprecipitates thereof (lanes 1–3). In cells containing the G allele minigene (C33A-G1), SF2 readily associated with transcript-b, providing the first evidence that SF2 associates with this mRNA species (lanes 4–6). SF2 association with transcript-b was reduced in cells containing the A allele minigene (lanes 7–9), as was confirmed by quantitative reverse transcription-PCR (Fig. 1D, bottom). For these analyses, signals observed in C33A-Vec cells were set to “1” for ease of comparison. The finding that SF2 binding is influenced by the polymorphism was subsequently confirmed in additional stable isolates of minigene integration (Supplementary Fig. S2A) as well as through transient analyses (B). Together, these data strongly indicate, for the first time, that the G/A870 polymorphism influences recognition by the SF2 splicing factor.

**SF2 specifically correlates with cyclin D1b in prostate cancer.** The observation that the G/A870 polymorphism may alter SF2 association with transcript-b was of interest, given reports that cyclin D1b, not cyclin D1a, is induced as a function of prostate tumorigenesis (7, 11), and that cyclin D1b has oncogenic activity (3–5). Intriguingly, analyses of gene microarray data from human PCa showed that SF2 expression increases with tumor progression (Fig. 2A; refs. 6–8).

![Figure 1. SF2 associates with transcript-b and shows allele preference in minigene analyses.](image-url)
This observation was further validated upon screening a panel of PCa cell lines, wherein it was revealed that SF2 expression is lowest in nontransformed RWPE-1, and as compared with cells derived from primary and distant metastases of prostate cancer (Supplementary Fig. S3). Among the cancer cell lines representative of hormone therapy-sensitive disease, SF2 was relatively low in cells known to express lower levels of cyclin D1b (LNCaP) and higher in cells of this subtype known to express high levels of cyclin D1 (LAPC4; refs. 7, 11). For the androgen receptor-negative cells, unexpectedly high levels of expression were observed in PC3 cells, which exhibit the most aggressive phenotype in vivo with regard to metastases (32). To probe the effect of SF2 on cyclin D1b production in human tumors, comparative analyses of nuclear SF2 and cyclin D1 (a and b isoforms) expression was objectively analyzed using serial sections of PCa specimens and quantitative AQUA analyses. Representative images of tumors scoring with low SF2 (Fig. 2B, top) or high SF2 (bottom) are shown. Signals were quantified across each specimen within the nuclear compartment (DAPI positive, blue) of epithelially derived carcinoma cells (cytokeratin positive, green), and resultant data are plotted in Fig. 2C. As shown, tumors expressing low SF2 exhibited low cyclin D1b expression; conversely, tumors with high SF2 scored high for cyclin D1b. Quantification of all tumors examined revealed a significant correlation between SF2 and cyclin D1b (P = 0.023), but not cyclin D1a (P = 0.19). Coexpression of cyclin D1b and SF2, in serial sections, was observed in glandular epithelial cells (data not shown). Together, these data show that SF2 expression is strongly correlated with only the cyclin D1b isoform in human disease.
**SF2 modulates cyclin D1b production in multiple model systems.** Because SF2 predicted for high cyclin D1b in PCa, the effect of SF2 on cyclin D1b production was examined in model systems of disease relevance. Initially, LNCaP cells, which express low endogenous levels of cyclin D1b, were used (7). Epitope-tagged SR proteins (SRp40 or SF2) were individually introduced (Supplementary Fig. S4) by transient assays with high transfection efficiency (Supplementary Fig. S5), and the effect on CCND1 mRNA isoform expression determined (Fig. 3A). Consistent with previous results, these cells express low levels of endogenous transcript-b (lane 1), and SRp40 failed to elicit changes in either CCND1 transcript (lane 2). Significantly, SF2 promoted a dramatic increase in transcript-b expression without altering transcript-a (lane 3). Quantification revealed a ∼2.7-fold increase in transcript-b following SF2 introduction (right), thus providing the first functional evidence for SF2-mediated regulation of cyclin D1b. Increased expression of SF2 in LNCaP cells also resulted in an increase in cyclin D1b protein expression (Supplementary Fig. S4). Unfortunately, depletion of endogenous SF2 in PCa models using short interfering RNA were unsuccessful (data not shown), consistent with previous observations that knockdown of SF2 induces cell death (33). As such, a previously developed DT40-ASF/SF2 cell line was used (DT40-ASF), in which endogenous SF2 was replaced with a tet-repressible SF2 construct (Fig. 3B; ref. 18). In this system, SF2 expression was undetectable ∼24 hours following the addition of doxycycline. Previous reports indicated that 48 hours post-knockdown, the DT40-ASF cell line begins to undergo apoptosis (33). Thus, experiments analyzed end points after 24 hours, whereupon no loss of cell viability was noted (data not shown). As expected, no detectable cyclin D1 isoforms were recognized (Fig. 3B, left, lanes 1 and 2). Stable introduction of the G870 minigene revealed that although both isoforms were produced (left, lanes 4 and 5), suppression of endogenous SF2 (left, lane 5) diminished cyclin D1b (but not cyclin D1a) production. Similar results were observed at the level of the transcripts following depletion of SF2 (Fig. 3B, right). Collectively, these results identify SF2 as an effector of cyclin D1b production in multiple model systems.

**Endogenous SF2 associates with both alleles in PCa cells.** As it was observed that elevated SF2 induces cyclin D1b in PCa (Fig. 2), and that SF2 differentially binds the transcript dependent on G/A870 (Fig. 1), the effect of the polymorphism on SF2 association was investigated in PCa cells. First, LAPC4 cells were used, which are homozygous for the A870 allele (7). Consistent with the individual minigene analyses in Fig. 1, endogenous SF2 associates with the endogenous transcript-b in these cells (Fig. 4A). RFLP analyses of the SF2-associated transcript was also performed (Fig. 4B). These observations show that in PCa, SF2 can associate with transcript-b generated by the A870 allele; however, as individual minigene analyses in Fig. 1 indicated a preference for SF2 to associate with transcript-a from the G870 allele (when compared in isolation), the most critical analyses were generated in LNCaP cells, which are heterozygous for the polymorphism (shown as genotype control in Fig. 4B). This model system afforded the first opportunity to dissect the effect of SF2 on G870-derived versus A870-derived transcripts in the same model system. As expected, SF2 was associated with total transcript-b in this model system (Fig. 4C). Using the SF2-bound and recovered transcript, two key determinations were made. First, RFLP analyses of the total transcript (Fig. 4D, lane 1) revealed that ∼61% of the endogenous transcript-b was derived from the G allele and 39% from the A allele, thus indicating that in the endogenous setting, both alleles significantly contribute to transcript-b production. Intriguingly, RFLP analyses and

![Figure 3. Cyclin D1b production was induced by SF2 in multiple model systems.](image-url)

**Figure 3.** Cyclin D1b production was induced by SF2 in multiple model systems. A, LNCaP cells were transfected with constructs encoding empty vector, T7-SRp40, or T7-SF2, harvested after 48 hours and examined for the expression of indicated transcripts. Representative PCR (left) and quantification by qPCR of at least three independent experiments (right). B, DT40-ASF/SF2 cells were transfected with plasmids encoding either empty vector or the G870 minigene. Transfected cells were split into populations treated with vehicle or doxycycline for 24 hours. Cells were harvested, lysed, and subjected to immunoblot analyses with the indicated antisera (left) or RNA was isolated and subjected to reverse transcription-PCR analyses for the indicated transcripts (right).
quantification of the SF2-bound fraction (Fig. 4D, lane 2) resulted in a similar ratio of transcript generated from the G and A alleles, based on at least five independent analyses and quantification (Fig. 4D, bottom). Thus, these data show that endogenous SF2 could associate with both transcripts when present, but shows a slight preference for the G870-derived transcript.

**SF2 predominantly associates with and produces transcript-b from the G allele.** Given the observation that elevated SF2 correlates with high cyclin D1b in human PCa and is sufficient in PCa model systems to induce cyclin D1b production, the effect of the G/A870 polymorphism for this event was determined. As shown, SF2 levels were elevated through ectopic expression of an HA-tagged allele in cells heterozygous for the polymorphism and that express low endogenous cyclin D1b (Supplementary Fig. S6), so as to mimic tumor-associated SF2 induction. Subsequent analyses (Fig. 5A) confirmed SF2-mediated enhancement of overall transcript-b levels as a function of the G/A870 allele (generated from the input band) or SF2-associated transcript (generated from the SF2-RIP studies) were quantified quantified from at least five independent experiments (bottom). Averages and SEM are shown. The ratio of transcript-b as A to G (A/G) is shown for the representative image.

**Figure 4.** Endogenous SF2 can associate with transcript generated from both G/A870 alleles in PCa. A, asynchronous LAPC4 cells were harvested and subjected to a RIP. An aliquot of immunoprecipitated complexes was subjected to SDS-PAGE and immunoblot to validate SF2 recovery (left). From the remaining sample, RNA was isolated, converted to cDNA, and analyzed for the presence of transcript-b by PCR (representative sample, right). qPCR quantification of at least four independent experiments is shown (bottom). P value determined by ANOVA. B, input and SF2-recovered transcripts from A were amplified with primers required for RFLP analyses of the CCND1 polymorphism, which have been previously described (38). Following amplification, the PCR product was ScrFI digested and visualized on an agarose gel. Genotype control is from amplification of genomic DNA from LNCaP cells. C, asynchronous LNCaP cells were treated similar to A. Relative SF2 pulldown and transcript-b recovery are shown. Quantification was from at least five independent RIP experiments. D, analyses of input and SF2-associated transcripts by RFLP from G is shown (top). Relative band intensities of endogenous, overall transcript-b levels as a function of the G/A870 allele (generated from the input band) or SF2-associated transcript (generated from the SF2-RIP studies) were quantified from at least five independent experiments (bottom). Averages and SEM are shown. The ratio of transcript-b as A to G (A/G) is shown for the representative image.
transcripts after SF2 induction or in control cells. First, it was observed that SF2 predominantly resulted in an induction of transcript-b from the G870 allele (Fig. 5B, lane 1 versus lane 3); quantified in C). These data implicate SF2 as an allele-selective modifier of the alternative splicing event. Second, to determine whether this action of SF2 was direct, RFLP analyses of the SF2-bound fraction was compared in cells with steady-state SF2 (control) versus those with elevated SF2 expression (Fig. 5B, compare lanes 2 and 4). For ease of comparison, the percentage of SF2 bound to the A870-derived transcript (relative to input) in control cells was set to “1”, and relative association determined for each (Table 1). As shown, SF2 association with the G allele was statistically unchanged under conditions mimicking tumor-associated SF2 elevation. By contrast, SF2 association with the A allele was enhanced by ~2-fold under these conditions.

Collectively, these data suggest a model (summarized in Fig. 6) in which SF2 elicits allele-selective effects on cyclin D1b production in prostate cancer that are dose-dependent. Under steady state conditions, SF2 binds with slight preference to transcripts generated from the G870 allele; concordantly, the G allele accounts for 61% of transcript-b production with the A allele accounting for the remaining 39%. These data are consistent with the supposition that SF2 acts (potentially directly) to suppress splicing at the intron 4–exon 4 boundary, and that this event is facilitated by the G870 allele. Elevated SF2, such as observed in human disease, can modestly enhance SF2 association with the A allele transcript, but induced SF2 remains predominantly associated with and produces cyclin D1b from the G allele transcript.

**Table 1. Relative SF2 association**

<table>
<thead>
<tr>
<th>% Allele</th>
<th>Control</th>
<th>SF2</th>
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</thead>
<tbody>
<tr>
<td>A</td>
<td>1.0</td>
<td>1.92 ± 0.57</td>
</tr>
<tr>
<td>G</td>
<td>5.34 ± 0.80</td>
<td>4.42 ± 0.80</td>
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**Discussion**

Here, we identify SF2 as a dose-dependent effector of cyclin D1b production, and provide evidence of a tumor-associated mechanism that alters the influence of the G/A870 polymorphism. Although minigene analyses of individual alleles (Fig. 1) and evaluation of nonneoplastic human tissue support a role for the A870 allele in promoting transcript-b and resultant cyclin D1b production, the influence of the A allele is thought to be relieved in PCa (11). The present data shows that the RNA-binding protein SF2, which is induced as a function of PCa progression, predicts for cyclin D1b (not cyclin D1a) elevation in human disease (Fig. 2). By contrast, cyclin D1b production was attenuated in model systems of SF2 depletion (Fig. 3). Functional studies in PCa cells heterozygous for the polymorphism unexpectedly showed that SF2 predominantly associates with and induces transcript-b derived from the G870 allele; however, association with and production of transcript-b from the A allele could still occur (Figs. 4 and 5). Together, these studies provide a novel mechanism by which cyclin D1b oncogene production is induced in human disease, and identify tumor-associated SF2 as an allele-selective effector of cyclin D1b.

Despite the potent oncogenic activity of cyclin D1b, knowledge of the factor(s) that regulate the CCND1 alternative splicing event are poorly defined. The present identification of SF2 as an effector of transcript-b and cyclin D1b production using both in vitro models and analyses of human tumors provides strong evidence linking splicing factor deregulation to oncogene activation. It is tempting to speculate as to whether SF2 could cooperate with few effectors of cyclin D1b production that were identified in other tissue types. For example, in colorectal cells, it was observed that knockdown of the SWI/SNF chromatin remodeling complex subunit Brahma (BRM) increased transcript-b production without altering transcript-a (34). These findings are of note,

![Figure 5](image-url)
as BRM was recently shown to be significantly downregulated in human PCA (35), and it has yet to be determined whether BRM loss might also affect SF2 levels. In a separate study, a chromosomal translocation-derived transcription factor known to be upregulated in Ewing’s sarcoma (EWS-FLI1) was found to enhance cyclin D1b production by diminishing the rate of transcriptional elongation (10). More recently, it was shown that Sam68 promotes cyclin D1b production through a splicing-repressive mechanism by blocking U1-70k association, a constitutive spliceosome accessory factor of the U1 small nuclear ribonucleoprotein that is necessary for 5′ splice site recognition (36, 37). It is well established that chromatin remodeling complexes could alter RNA Pol II accessibility by alteration of the native chromatin structure (38); moreover, pre-mRNA splicing occurs cotranscriptionally, and is aided by the function of SR proteins (including SF2) which can bind to Pol II and selected SWI/SNF subunits (BAF155 and BAF53A; ref. 39). Therefore, an attractive hypothesis is that SF2 could act in concert with either BRM or EWS-FLI1 to modulate the CCND1 splicing event. Given the marked protumorigenic activity of cyclin D1b, these collective observations further underscore the importance of delineating the mechanisms that regulate or influence the SF2-mediated alternative splicing event in models of disease relevance.

With regard to clinical relevance, it is notable that in PCA cells, SF2 exhibited an allele-selective effect on the alternative splicing event. Previous studies showed that in nonneoplastic tissue, the A870 allele was associated with higher transcript-b production but that the influence of the A allele was lost in PCA specimens (11); these findings suggested that tumor-associated factors might either bypass the effect of the polymorphism or bolster the production of transcript-b from the G allele. The present data supports the hypothesis that SF2 may serve as such a factor because SF2 induction (such as occurs in human disease) predominantly binds to transcript-b derived from the G allele and promotes the accumulation of this transcript. Production of transcript-b still occurs from the A allele (~40%), however, this seems to remain unaltered following modulation of SF2 expression, thus it will be of interest to examine the functional relationship between SF2 and the A allele. Examination of how SF2 influences allele-specific cyclin D1b production in other tumor types in which cyclin D1b levels are elevated as a function of tumorigenesis (e.g., colon, bladder, or breast carcinoma) will be critical (6, 9, 40, 41). Given the propensity of SF2 to preferentially bind to and induce cyclin D1b from the G allele, the present data indicate that SF2 may promote intron inclusion at the CCND1 exon 4–intron 4 boundary, and precedence for a splicing repressor function of SF2 was previously established for the MNK2 kinase (42). It cannot be presently ruled out that the effect of SF2 could be manifested through other means, given the ability of SF2 to affect mRNA metabolism, mRNA transport and/or stability, and mTOR-mediated translation (43, 44). Future analyses will be directed at defining the action of SF2 at the exon 4–intron 4 boundary.

Finally, the present findings provide new insight into a potential means through which SF2 promotes cellular transformation. It is noteworthy that SF2 could independently induce transformation and induce tumor growth in vivo (42), thus demonstrating phenotypes similar to those observed with cyclin D1b (3, 5). As SF2 levels correlated with cyclin D1b in human PCA, these data implicate cyclin D1b as a possible downstream effector of SF2-mediated cellular transformation in the prostate. Additional mechanisms are predicted to contribute to this event, as perturbations in spliceosome function and RNA processing proteins have been recently identified as major contributors to genomic instability (45). Importantly, dysregulation of splicing factors has also been shown to accelerate PCA progression and metastases, such as observed by deregulated expression of SRp40, or in the presence of specific, cancer risk–associated polymorphisms in the intronic region of the KLFL tumor suppressor that create novel SRp40 binding sites (46). Given the disease relevance of this event, it will be imperative to determine not only the consequence of SR protein dysregulation, but whether these events act in concert to promote tumor progression. Ongoing studies suggest that tumor-associated SF2 induction

Figure 6. Model of SF2 activity. Under steady-state conditions, ~60% of detected transcript-b is generated from the G870 allele, and SF2 predominantly binds to the G870-derived transcript. SF2 elevation, as associated with PCA progression, enhances association with the A870 allele, but the observed increase in transcript-b production is exquisitely associated with the G870 allele. No Δ, no change.
may induce and enhance the migration and invasion phenotype in prostate cancer cells (data not shown), providing the impetus to discern the effect of SF2 on the development of tumor metastases.

In summary, our study identifies SF2 as a novel, clinically relevant effector of CCND1 alternative splicing, capable of promoting allele-specific induction of cyclin D1b in prostate cancer. The findings presented are among the first to determine how the cyclin D1b oncogene is enhanced in human disease, and provide the foundation for future studies directed at developing mechanisms to target oncogene induction.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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