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Biology and Treatment of Rhabdoid Tumor

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Abstract

Rhabdoid tumor is a rare, highly aggressive malignancy that primarily affects infants and young children. These tumors typically arise in the brain and kidney, although extrarenal, non-central nervous system tumors in almost all soft-tissue sites have been described. *SMARCB1* is a member of the SWI/SNF chromatin-remodeling complex and functions as a tumor suppressor in the vast majority of rhabdoid tumors. Patients with germline mutations or deletions affecting *SMARCB1* are predisposed to the development of rhabdoid tumors, as well as the genetic disorder schwannomatosis. The current hypothesis is that rhabdoid tumors are driven by epigenetic dysregulation, as opposed to the alteration of a specific biologic pathway. The strategies for novel therapeutic approaches based on what is currently known about rhabdoid tumor biology are presented.

Keywords

rhabdoid; *SMARCB1*; SWI/SNF

I. INTRODUCTION

Rhabdoid tumor (RT) is a rare and highly malignant tumor that arises predominantly in the brain (referred to as atypical teratoid/RT [AT/RT]), kidney (RT of the kidney [RTK]), or soft tissues (extrarenal RT, malignant RT [MRT]). Frequent sites for extrarenal RTs include the skin, liver, and lung, although tumors in almost all soft tissues, including the orbit, thymus, uterus, bladder, and neck, have been reported. The peak incidence is between 1 and 4 years of age, although classic RTs in adults have been described.

Children, typically in their first year of life, may also present with more than one primary RT, consistent with a genetic predisposition to cancer. These infants typically have a central nervous system (CNS) AT/RT and RTK, or an AT/RT and a lung or liver tumor. Bilateral

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RTKs occur but are much less frequent than bilateral Wilms tumors of the kidneys, accounting for 2% of RTK cases.¹ Brain and spine imaging studies should, therefore, always be performed in a newly diagnosed patient with a renal or extrarenal RT. Similarly, imaging studies to rule out a renal tumor are indicated for a patient with AT/RT.

Epidemiologic studies of RT have been limited by the fact that this is a rare disease. Heck et al.² performed the first population-based epidemiologic analysis of RT as part of an Air Pollution and Childhood Cancer Study in the state of California. They reported an association of RT with low birthweight, preterm birth, and late-term delivery. Of interest, twin pregnancies were associated with RT, which also was noted by Nicolaides et al.³ and Bourdeaut et al.⁴ Nicolaides et al.³ and Cecen et al.⁵ each reported a single case of RT in a patient born after in vitro fertilization, and we are aware of 3 children conceived by in vitro fertilization who developed AT/RTs in the first year of life (unpublished data). Although some studies suggest a small increased risk for cancer with the use of assisted reproductive technologies,⁶ this remains controversial.⁷

Histologically, RTs contain characteristic filamentous cytoplasmic inclusions, large nucleoli, and abundant eosinophilic cytoplasm. A variety of neural, epithelial, mesenchymal, or ependymal patterns may also be present, making the histologic appearance quite variable and clinical diagnosis difficult.⁸ CNS AT/RTs typically comprise rhabdoid cells and areas of primitive neuroepithelial tissue resembling a primitive neuroectodermal tumor (PNET), as well as mesenchymal and/or epithelial elements.⁹ In the past, this complex histologic pattern routinely led to misclassification of AT/RTs, most often as medulloblastoma/PNET.^{9,10} Some AT/RTs display only the PNET component, and the diagnosis relies on molecular genetic analysis. It is assumed that the cell of origin for RTs is a primitive stem cell with the capacity for divergent differentiation, possibly derived from the neural crest.⁸

II. GENETICS OF RT

The majority of RTs arise as a consequence of homozygous inactivation of the *SMARCB1/INI1/hSNF5/BAF47* gene.^{11,12} Loss of expression of the protein permitted the development of an immunohistochemistry (IHC) assay¹³ that is based on the loss of nuclear expression of the protein in tumor cells, with retained expression in normal cells (Fig. 1). This IHC assay can be used in the vast majority of cases to help make a clinical diagnosis of RT. Loss of expression of SMARCB1 is also observed in other tumors with inactivation of the locus, including epithelioid sarcoma, cribriform neuroepithelial tumor, chordoma, and medullary renal cell carcinoma.^{14–20} Therefore, while the loss of SMARCB1 expression by IHC is highly sensitive, it is not specific. Correlation with other histologic and immunophenotypic findings, the patient's age, and the location of the tumor is required to make a clinical diagnosis. RTs may also arise in the setting of a previously benign tumor in both the brain^{21,22} and peripheral nervous system^{23,24} following acquisition of a *SMARCB1* mutation and/or deletion. The loss of expression of SMARCB1 by IHC clearly distinguishes the rhabdoid areas from the other (less malignant) components of the tumor.

Versteeg et al.¹¹ first reported somatic mutations of the *SMARCB1/hSNF5* gene in renal and extrarenal RT, followed shortly thereafter by a report by Biegel et al.¹² of germline and

somatic mutations in *INI1/hSNF5* in patients with RTs of the brain, kidney, and soft tissues.¹² *SMARCB1* (*SWI/SNF* related, matrix-associated, actin-dependent regulator of chromatin, subfamily B, member 1) is now the recommended nomenclature to replace human sucrose nonfermenting gene number 5 (*hSNF5*), integrase interactor 1 (*INI1*), or 47-Kd *Brg1/Brm*-associated factor (*BAF47*).

SMARCB1 is a member of the human *SWI/SNF* complex.^{25,26} The *SWI/SNF* complex acts in an adenosine triphosphate-dependent manner to remodel chromatin and thus leads to the activation and repression of gene transcription. Whole-exome sequencing studies of primary RTs²⁷ have shown that biallelic mutations or copy number alterations of *SMARCB1* seem to be both necessary and sufficient to cause cancer; there were no other consistent coding sequence or copy number changes identified. Stabilization of an epigenetically altered genome is thought to contribute to tumorigenesis, but the specific genes that contribute to transformation are not yet known.

Among patients newly diagnosed with RT, 25–30% have a germline alteration of *SMARCB1* that predisposed them to cancer.^{4,28} In our patient cohort the median age at diagnosis for patients with germline *SMARCB1* alterations was 6 months (range, 1 day to 5 years) compared with a median age at diagnosis of 1.5 years (range, 1 day to 32 years) for patients with sporadic tumors.

Virtually all of the complete *SMARCB1* deletions or larger 22q11.2 germline deletions that include *SMARCB1* are de novo. The majority of germline *SMARCB1* mutations in patients with RT are also de novo. Interestingly, the germline *SMARCB1* deletions more frequently affect the paternal allele, whereas there seems to be a small bias for mutations to be present on the maternal allele, especially when they are inherited.²⁸ Because of the ascertainment bias for a child with a RT, inherited germline mutations often are passed down from an unaffected parent. Because there is reduced penetrance of RT associated with a germline alteration of *SMARCB1*, the long-term risk for cancer in carriers of mutations or deletions of *SMARCB1* is not yet known. Gonadal mosaicism also has been observed in several families^{28,29}; therefore, parents need to be counseled appropriately about their recurrence risks and options for prenatal testing. Schwannomatosis (OMIM 162091) is characterized by the presence of multiple nerve tumors, which are histologically benign but may cause serious morbidity. Patients may also have meningiomas, and, in some cases, the schwannomas may transform into malignant sarcomas, requiring surgical intervention and chemotherapy. Approximately 50–60% of families with schwannomatosis have germline mutations in *SMARCB1*.^{30,31} We and others have described families with germline mutations or intragenic deletions or duplications in *SMARCB1* in which the adult carriers of the mutations had fibromas or schwannomas and their affected children had RTs. Because the schwannomas may not develop until the third or fourth decade of life, individuals who have a germline *SMARCB1* alteration must, therefore, be counseled about their own risk for both benign and malignant tumors, in addition to the cancer risks for their offspring. There does seem to be some genotype–phenotype correlation for the types of mutations that occur in schwannomatosis versus RT, as described below.

The spectrum of germline mutations, deletions, and duplications from 70 patients with RT is shown in Fig. 2. Approximately 20% of the germline alterations are deletions in chromosome band 22q11.2 that include all of *SMARCB1*, whereas 25% of the patients have a partial deletion or duplication involving 1–5 exons of the gene. The remaining patients have a variety of truncating mutations caused by single base point mutations or insertions/deletions leading to a frameshift. Splicesite mutations are the least common type of mutations observed in children who first present with a RT. By contrast, splicesite mutations and point mutations in exons 1 and 9 are more frequent in families with schwannomatosis.^{30,31}

The 3 most frequently detected germline specific mutations in *SMARCB1* are c.118C>T in exon 2, c.157C>T in exon 2, and c.472C>T in exon 4.^{4,12,28} With the exception of the exon 9 frameshift mutations (described below), the same mutations predispose carriers to AT/RT, renal RT, and, to a lesser extent, extrarenal RT. The majority of extrarenal RTs are sporadic and arise as a consequence of homozygous loss of *SMARCB1* caused by deletions, unbalanced 22q11.2 translocations, or monosomy 22. The most frequent second hit in patients with a germline mutation is a large 22q deletion or monosomy 22, or a copy number neutral loss of heterozygosity (CN-LOH) generating event that unmask the mutation or deletion on the remaining allele.

The distribution of *SMARCB1*-and chromosome 22-inactivating mutations, deletions, and CN-LOH in 200 sporadic AT/RTs, renal RTs, and extrarenal RTs is shown in Table 1. In the majority of tumors (43%) there is a mutation in one allele, and the second copy of the gene is lost as a result of a structural deletion in 22q11.2, monosomy 22, or an acquired CN-LOH event. Compound heterozygous mutations are infrequent in these patients (4%). Partial deletions and duplications are detected in approximately 15% of tumors. Homozygous deletions of exons 1–9 of *SMARCB1* are present in approximately 40% of RTs overall, although there is an unequal distribution with respect to anatomic location. Approximately 25% of AT/RTs, 40% of renal RTs, and 70% of extrarenal RTs have homozygous deletions of the entire locus.

The mutations in sporadic RTs include single base pair point mutations and insertion/deletion or frameshift mutations that are predicted to introduce a novel stop codon (Fig. 3). The majority of mutations result in nonsense-mediated decay, although this has not formally been proven in most cases. The highest frequency of coding sequence mutations among the sporadic RTs occurs in exon 9 (Fig. 3). Two single base deletions in codons 381 (c.1143delG) and 382 (c.1145delC) are somatic in origin and are associated exclusively with AT/RT.¹² Mutations in exon 2 and exons 4–7 are frequently observed in RTK and AT/RT. Four specific mutations—c.118C>T, c.157C>T, c.472C>T, and c.601C>T in exons 2, 2, 4, and 5, respectively—are highly recurrent, although they do not seem to be specific to the brain or kidney.^{4,12,28} Mutations in exons 1 and 3 are rare, and a mutation in exon 8 has been documented in only one RT in our cohort (unpublished data) in a patient with schwannomatosis.³² Splice site mutations are rare in primary RTs, and missense mutations have not yet been reported.^{4,28}

The 2 most common mutations in AT/RT are single base deletions in exon 9: c.1143delG and c.1145delC (Fig. 3B). Interestingly, neither of these frameshift mutations has been detected as a predisposing mutation in blood from patients with RT or schwannomatosis. These 2 frameshift mutations are not predicted to be subject to nonsense-mediated decay, and theoretically this would result in the addition of 100 amino acids to the protein. Similar to other RTs with coding sequence alterations, there is no expression of the protein by IHC in AT/RTs with these 2 exon 9 deletions.¹³ It is possible that this mutation functions as a dominant-negative mutation during early development, which is an area for future research.

Although *SMARCB1* is the predominant gene altered in RTs, approximately 2–3% of tumors with rhabdoid histology retain expression of the SMARCB1 protein on IHC and do not display inactivating mutations in the gene. A small number of families and patients with RT with germline or somatic mutations of *SMARCA4*, which is the primary ATPase in the SWI/SNF complex, have now been reported.^{33,34} A variety of solid tumors in children and adults, such as medulloblastoma, the most common malignant brain tumor in children, have mutations in *SMARCA4*. To date, however, the only other tumor type to demonstrate biallelic inactivation of *SMARCA4*, consistent with a cancer-predisposing germline mutation and second somatic alteration, is small cell carcinoma of the ovary, hypercalcemic type (SCCOHT).^{35–37} Based on the relatively early age at presentation, and the presence of rhabdoid-appearing cells on histology, it has been proposed that SCCOHT represents another type of extrarenal RT.³⁸ The germline mutations in SCCOHT included both missense and truncating mutations, typically with loss of the wild-type allele as the second inactivating event in the tumor.

Interestingly, mutations in a variety of SWI/SNF proteins, including ARID1A, ARID1B, SMARCA2, SMARCA4, SMARCE1 and SMARCB1, have recently been reported in patients with genomic disorders such as Coffin-Siris syndrome (CSS)^{39–43} or Nicolaides Barrister syndrome^{43–45} who do not seem to be at increased risk for cancer, as well as in patients with unexplained intellectual disability or autism.^{46,47} Most patients with CSS and *SMARCB1* alterations have heterozygous missense mutations, which are so far distinct from the typical nonsense mutations that occur in patients with RT or the splice site mutations that often occur in familial schwannomatosis. We studied 1 patient with CSS and a missense mutation in exon 9 who developed multiple schwannomas but not RT.⁴⁸ As whole-genome sequencing moves into the area of prenatal testing, the prediction of whether such mutations will result in a genomic disorder or increased risk for malignancy will become extremely challenging.

III. HISTORICAL TREATMENT AND OUTCOMES

Patients with AT/RT have, until recently, been treated according to institutional preference or nonspecific infant brain tumor protocols, combining surgery, possible radiation therapy, and chemotherapy. In general, drugs have included some combination of platinum agents, epipodophyllotoxins, oxazaphosphorines, vinca alkaloids, methotrexate, and anthracycline, with or without intrathecal directed medications (methotrexate, hydrocortisone, cytarabine, mafosfamide) and/or high-dose chemotherapy with stem cell rescue.^{49–56} While the optimal “standard” therapy remains debated, the prognosis has improved from early reports to nearly

50% overall for AT/RT, but for RTK it remains unchanged at approximately 20–25%.^{1,57,58} Efforts by the Children’s Oncology Group (COG) to improve the cure rate of AT/RT (protocol ACNS0333 [www.clinicaltrials.gov identifier NCT00653068]) use a combination of surgery; 2 cycles of induction chemotherapy (cisplatin, cyclophosphamide, etoposide, vincristine, methotrexate); consolidation therapy with 3 cycles of high-dose chemotherapy with stem cell rescue (thiotepa, carboplatin); and age- and stage-directed radiation therapy. By contrast, the Dana Farber Consortium AT/RT study (www.clinicaltrials.gov identifier NCT00084838) uses a more protracted approach to combination therapy with surgery, age- and stage-directed radiation, and chemotherapy lasting approximately 1 year in duration, in part based on historic rhabdomyosarcoma group therapy, including vincristine, dactinomycin, cyclophosphamide, cisplatin, doxorubicin, temozolomide, and intrathecal methotrexate, cytarabine, and hydrocortisone.⁵¹ In Europe the registry study (Eu-Rhab) for all RT (AT/RT, RTK, MRT) recommends using combination therapy including surgery, radiotherapy, and chemotherapy (vincristine, dactinomycin, cyclophosphamide, doxorubicin, ifosfamide, carboplatin, etoposide), and intrathecal methotrexate and permissive use of high-dose chemotherapy with stem cell rescue (carboplatin, thiotepa).⁵⁹

Before study AREN0321 (www.clinicaltrials.gov identifier NCT00335556), in the United States, RTKs specifically were historically treated along-side Wilms’ tumors in National Wilms’ Tumor Study trials with regimens used for the treatment of Wilms’ tumors, including vincristine, dactinomycin, and doxorubicin, with or without cyclophosphamide. The outcomes attained with these regimens were poor.^{1,57} NWTS-5 adopted a different treatment strategy consisting of carboplatin and etoposide alternating with cyclophosphamide (regimen RTK). Preliminary analysis of patients treated with regimen RTK revealed no clear improvement compared with previous studies, leading to study closure. Subsequent case reports demonstrated that ifosfamide-carboplatin-etoposide or ifosfamide-etoposide chemotherapy alternating with vincristine-doxorubicin-cyclophosphamide can be efficacious against RTK,^{52,60,61} providing the rationale for study AREN0321 regimen UH-1 (vincristine-doxorubicin-cyclophosphamide alternating with cyclophosphamide, carboplatin, etoposide), as well as the similar Eu-Rhab registry regimen. In study AREN0321, patients with stage 4 measurable RTK or MRT were initially eligible for vincristine/irinotecan window therapy, but none of the 3 patients with RT who were enrolled in the window responded, leading to closure of such window therapy for patients with RT. Preliminary analysis of regimen UH-1 does not, unfortunately, demonstrate clear improved outcome compared with historical data; however, further analyses are in process. While some authors discuss a potential role for even higher doses of alkylator therapy and/or high-dose chemotherapy for RTK and MRT, analogous to approaches drafted for AT/RT,^{62,63} no formal trial has demonstrated a therapeutic advantage in the treatment of non-CNS RT, and any further intensification of therapy is challenged by the fact that current regimens already maintain a toxicity-related mortality of approximately 5%, as well as significant morbidity.⁶⁴

In sum, while the prognosis for select patients—particularly those with localized RT associated with an older age and lower stage disease—has improved some,^{1,65,66} the overall outcomes of RT remain poor despite maximized therapy intensity, mandating the discovery

and integration of targeted novel therapy, which is likely to emerge from a deeper understanding of RT biology and additional preclinical investigation

IV. RT BIOLOGY AND TARGETED THERAPY

Current preclinical investigations aiming to expand therapy options and improve the survival of infants and children with RT have focused largely on the specific interrogation of *SMARCB1*-related biology and potential therapeutic targets (Table 2), as well as nonspecific preclinical efforts conducted through the Pediatric Preclinical Testing Program (PPTP), using 2 RT cell lines and xenografts for testing of new agents emerging from the pharmaceutical industry.

SMARCB1 plays a critical role in epigenetic regulation, cell cycle progression, and signaling crosstalk, all of which provide fertile ground for preclinical and clinical investigation. *SMARCB1* functions as a classic tumor suppressor and is the primary gene responsible for malignant RT pathophysiology. While homozygous inactivation of *Smarcb1* in mice exhibits embryonic lethality, 20% of heterozygous *Smarcb1* mice that are normal at birth ultimately develop sarcomas at a median age of 1 year, following a second hit to the *Smarcb1* locus. All mice with conditional biallelic inactivation of *Smarcb1* develop cancer, with a median onset of 11 weeks, making this one of the most aggressive cancer predisposition genotype–phenotype correlations yet described.^{67,68} As mentioned, RTs are generally diploid and genomically stable, lacking additional recurrent gene amplifications or deletions beyond *Smarcb1* loss. The *SWI/SNF* complex, perturbed in the setting of *Smarcb1* loss, acts in an adenosine triphosphate–dependent manner to remodel chromatin, regulating gene transcription and DNA repair. Considering the lack of cooperating mutations and aggressive neoplasia, RT is perhaps the quintessential tumor driven by epigenetic dysregulation.

A. Epigenetic Targeting

The evolving field of epigenetics has provided access to targeted therapy aiming to alter methylation and acetylation patterns within cancer cells.⁶⁹

Somewhat speculative at this point, the loss of *SMARCB1* is postulated to result in a global failure to release the repressive H3K27 trimethylation mark present on bivalently modified histones, mediated by the polycomb complex 2, resulting in widespread epigenetic modifications and leading to arrested development and abnormal proliferation, potentially via histone methylation processes.⁷⁰ The polycomb group family of proteins represses transcription by mediating histone 3 lysine-27 trimethylation. Two members of the polycomb complex 2, *CBX6* and *EZH2*—the latter a histone methyltransferase—are upregulated in RT (Fig. 4). ZNF217, an organizer of repressive histones, is also significantly upregulated in RT and is capable of demethylating H3K4me3 and methylating H3K27 through interaction with *EZH2*.^{70,71} *EZH2* inhibitors are now in clinical development (Table 2), and one report by investigators associated with the company Epizyme documents in vitro and in vivo activity against RT, albeit delayed,⁷² potentially limiting efficacy in more rapidly dividing and morbidly aggressive RT. *EZH2* inhibition also has been shown to sensitize RT cells to the effects of radiation.⁷³

In addition to EZH2 histone methyltransferase targeting, preclinical investigations have demonstrated anti-RT effects with histone deacetylase inhibitors (HDACi) and demethylating agents.^{74–79} HDACi sensitization of RTs to radiation therapy and sensitization to anthracycline-based therapy also has been demonstrated in RT cell lines.^{74,75,80}

Importantly, the strategy for future treatment of patients with RT should include the addition of new agents concurrent with, or before, standard chemotherapy. DNA damage response pathways, apoptosis signaling components, DNA repair components, and drug transporters each include genes subject to epigenetic control in cancer and relevant to chemotherapy disease resistance.^{81–83} For example, multidrug (doxorubicin and cisplatin)–resistant human MCF-7 breast adenocarcinoma cells demonstrate loss of global DNA methylation, loss of histone H4 lysine 20 trimethylation, increased phosphorylation of histone H2 serine 10, and diminished expression of Suv4–20h2 histone methyltransferase compared with parental MCF-7 cells.⁸⁴ Subsequent investigations have demonstrated that DNA methyltransferase inhibition with 5-azacytidine reduces MDR1 promoter methylation in MCF-7 cells, with changes in chromatin structure.⁸⁵ MLL1, a histone methyltransferase specific for H3K4 that is transcriptionally activated through interaction with SMARCB1, as previously discussed, has been shown to be required for MDR1 promoter methylation and chemoresistance.⁸⁶ Chemotherapeutic drugs can upregulate MDR1 with associated H3 acetylation and induction of methylated H3K4 within the MDR1 locus.⁸⁷ Similar to MDR1, *ABCG2* gene expression is dependent on DNA methylation.⁸⁸ EZH2, upregulated in RT, is essential for chemotherapy resistance in cisplatin resistant cell lines, likely through H3K27 methylation.⁸⁹ Removal of H3K27 methylation resensitizes drug-resistant ovarian carcinoma cells to cisplatin by increasing DNA-platinum adduct formation resulting from increased access of cisplatin to target DNA sequences.⁹⁰ Further, DNA methyltransferase inhibition enhances chemosensitivity to cisplatin.⁹¹ Last, microRNAs themselves, which are suppressed in RT, can mediate drug sensitivity.⁹² Specifically, suppression of mir451 imparts doxorubicin resistance in MCF-7 cells.⁹³ Thus, it is possible that DNA or histone methylation inhibitors may sensitize cells to the effects of standard chemotherapy via a reversal of resistance mechanisms.

The COG completed a trial of decitabine in combination with doxorubicin and cyclophosphamide in children, which is of potential interest in RT, though concerns regarding adequate pharmacodynamic demethylation and toxicity have thus far limited advancement.⁹⁴ In pediatric-focused trials, decitabine/vorinostat chemotherapy combination therapies have advanced with anthracycline-based combination therapy in relapsed leukemia (www.clinicaltrials.gov identifier NCT01483690) and with alkylator therapy for brain tumors.⁹⁵

B. CDK4/CDK6/CyclinD/RB

Reports to date have demonstrated that *SMARCB1* loss can promote cell cycle progression resulting from upregulation of targets of the p16INK4a-Rb-E2F pathway, primarily including cyclin D1 (upregulated in primary RTs) as well as several cyclin-dependent kinases (CDKs).^{70,96} Rb family loss has been shown to increase rhabdoid tumorigenesis,⁹⁷

and reintroduction of SMARCB1 into RT cell lines leads to G1 arrest and decreased cyclin D1 transcription,⁹⁸ whereas ablation of *CyclinD1* abrogates malignant RT evolution in mouse models.⁹⁹ Tumor development in *Smarb1*-deficient mice is greatly accelerated in the absence of functional p53 protein.¹⁰⁰ These findings suggest a cooperative effect between *SMARCB1* and the *pRB*, *CyclinD1*, and *Tp53* pathways.

Flavopiridol, a nonspecific CDK inhibitor, has inhibited RT cell growth with synergy demonstrated with tamoxifen in tumor models.¹⁰¹ The CDK4/6 inhibitor LEE011 is currently in phase I/II investigation in pediatric patients with perturbed RB/CyclinD1/CDK4/6 pathway signaling, with specific focus on RT and neuroblastoma (www.clinicaltrials.gov identifier NCT01747876). Other CDK4/6 inhibitors are in active development (Table 2).

C. Aurora-A-Kinase

Aurora-A-kinase is expressed at high levels in RT and is repressible with *SMARCB1* reintroduction into RT cells via transcriptional downregulation. In addition, small interfering RNA targeting of Aurora A induces RT cell death in vitro,¹⁰² and additional data from PPTP testing of the aurora-A-kinase inhibitor MLN8237 (Alisertib) demonstrated in vivo activity in RT xenografts.¹⁰³ Such data prompted the COG Rhabdoid Tumor Working Group to endorse the phase II trial of Alisertib in pediatric solid tumors via the inclusion of an RT stratum (ADV0921; www.clinicaltrials.gov identifier NCT01154816). Unfortunately, none of 4 patients demonstrated an objective response to further accruals before study closure. Nonetheless, an institutional study (www.clinicaltrials.gov identifier NCT02114229) continues to investigate Alisertib in patients with RT, either as a single agent for recurrent/refractory disease or as part of combination therapy with chemotherapy, surgery, and radiation to treat AT/RT. While trial NCT02114229 is not designed to test concurrent Alisertib and radiation exposures, preclinical data suggest a potential role for Alisertib as a radiation sensitizer in the treatment of RT.¹⁰⁴

D. Additional Potential Targets

SMARCB1 loss leads to increased expression of GLI1, noted in RT primary tumors, supporting a role in the biology of the sonic hedgehog pathway and suggesting that downstream inhibition of the pathway is worth further preclinical and possibly clinical testing.⁵⁹ Microarray experiments have further suggested interferon therapy or downmodulation of PLK1,¹⁰⁵ as well as osteopontin and endostatin,⁷⁰ as worthy of further consideration. Additional genomic studies are underway as part of the National Cancer Institute–sponsored “Therapeutically Applicable Research to Generate Effective Treatments” (TARGET) initiative, inclusive of RTs derived from the COG biobank (AREN10B2).

E. PPTP Investigation in RT

The PPTP uses several RT cell lines (BT-12 and CHLA-266) and xenografts (BT29, KT16, KT14, KT12) in the study of new agents. Interestingly, these studies started with the validation of traditional chemotherapeutic agents such as vincristine, cyclophosphamide, and cisplatin. While widely used, vincristine failed to show an effect in BT29 and yielded growth

delay in KT14 and KT12 only.^{106,107} Cyclophosphamide and cisplatin therapy each resulted in a partial response and a complete response in KT16, respectively (a xenograft that trended toward increased sensitivity with other agents as well), and growth delay in BT29 and KT14. Additional activity was noted for AZD2171 (vascular endothelial growth factor [VEGF] receptor inhibitor), ispinesib (antimitotic), SU11248 (VEGF receptor inhibitor), rapamycin (mammalian target of rapamycin inhibitor), SVV001 (oncolytic), PR-104 (alkylator), GSK923295A (centromere protein E inhibitor), MLN8237 (aurora-A-kinase inhibitor), cabozantinib (VEGF receptor/c-Met inhibitor), and RG7112 (MDM2 inhibitor).^{103,108–116} Interesting additional negative results included in vitro assessment of the HDACi vorinostat (SAHA), showing high half-maximal inhibitory concentration (>2 μM) values, as well as limited activity with the HDACi JNJ-26481585 (quisinostat),^{117,118} limited growth delay in vivo with topotecan,¹¹⁹ and lack of in vitro or in vivo activity with CDK1/2/5/9 inhibitor SCH727965 (Dinaciclib).¹²⁰ While correlations of such preclinical testing with clinical activity in patients remains unproven, these data suggest several classes of drugs worth consideration of further clinical investigation, including VEGF multi-tyrosine kinase inhibitors as well as novel antimitotic therapies.

V. CONCLUSIONS AND FUTURE DIRECTIONS

RT remains a biologically fascinating, quintessential model of epigenetically controlled aggressive neo-The efforts of registry studies, cooperative group biological and clinical trials, and independent investigator– driven exploration of rhabdoid genomics; exploration of SMARCB1-driven biology, targeting epigenetic determinants of disease; and collaboration with the pharmaceutical industry to advance further preclinical and clinical testing are all imperative to advancing this important cause. Importantly, not only will such advances benefit patients and families affected by rhabdoid and related tumors, the results of such investigations are likely to be generalizable to a wide array of *SMARCB1*-dependent cancers and the epigenetic control of neoplasia in general.

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ABBREVIATIONS:

AT/RT	atypical teratoid/rhabdoid tumor
CNS	central nervous system
COG	Children's Oncology Group
CSS	Coffin-Siris syndrome
CN-LOH	copy number neutral loss of heterozygosity
CDK	cyclin-dependent kinase

HDACi	histone deacetylase inhibitor
IHC	immunohistochemistry
MRT	malignant rhabdoid tumor
PPTP	Pediatric Preclinical Testing Program
PNET	primitive neuroectodermal tumor
RT	rhabdoid tumor
RTK	rhabdoid tumor of the kidney
SCCOHT	small cell carcinoma of the ovary, hypercalcemic type
SMARCB1	<i>SWI/SNF</i> related, matrix-associated, actin-dependent regulator of chromatin, subfamily B, member 1
VEGF	vascular endothelial growth factor

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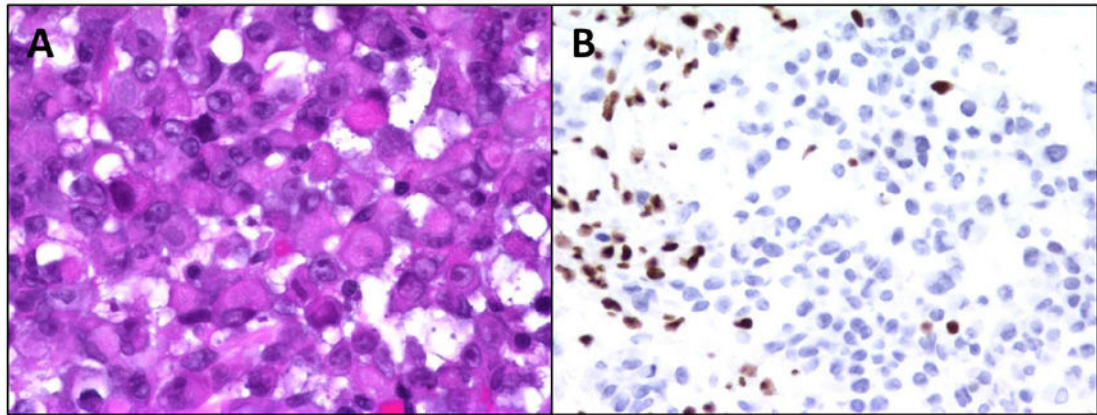


FIG. 1: Histology of a metastatic abdominal malignant rhabdoid tumor. **A:** Hematoxylin and eosin staining (magnification $\times 60$) demonstrates the presence of rhabdoid cells. **B:** Loss of SMARCB1 is seen by immunohistochemistry (magnification $\times 40$). (Reprinted with permission from Dr. Bruce Pawel, Department of Pathology & Laboratory Medicine, The Children's Hospital of Philadelphia, Philadelphia, Pennsylvania.)



FIG. 2:
 Distribution of germline mutations, deletions, and duplications in *SMARCB1* from 70 patients with rhabdoid tumor. Exons, introns, and genetic alterations are not drawn to scale. Stacked symbols are used to identify mutations recurring at the same nucleotide position. Indel, insertion/deletion.

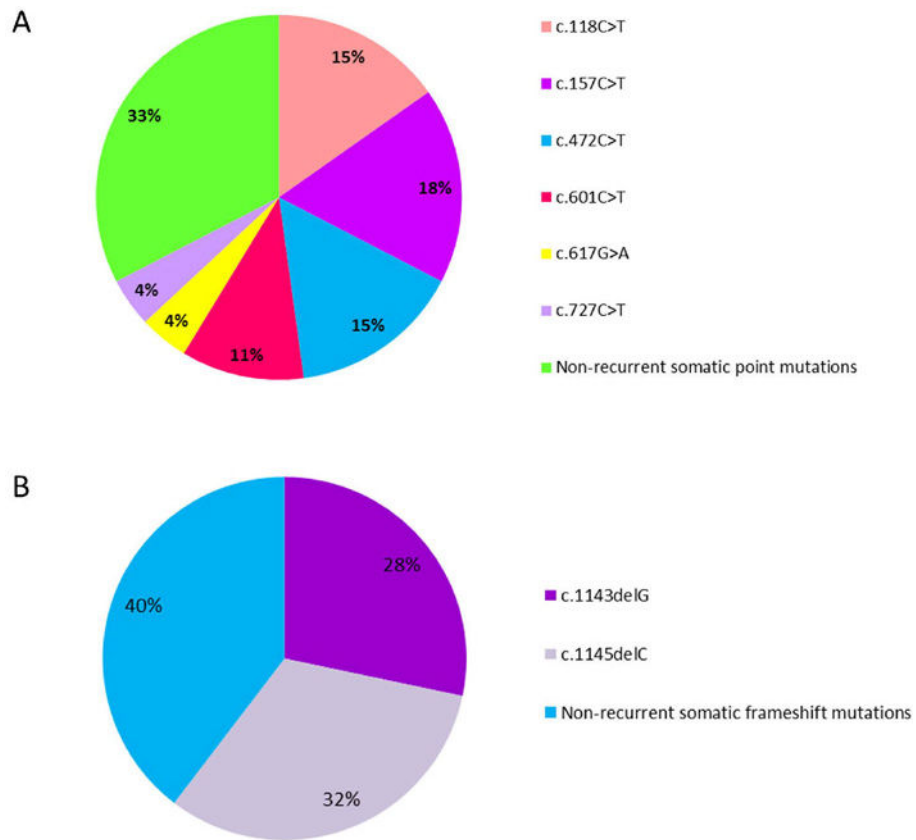
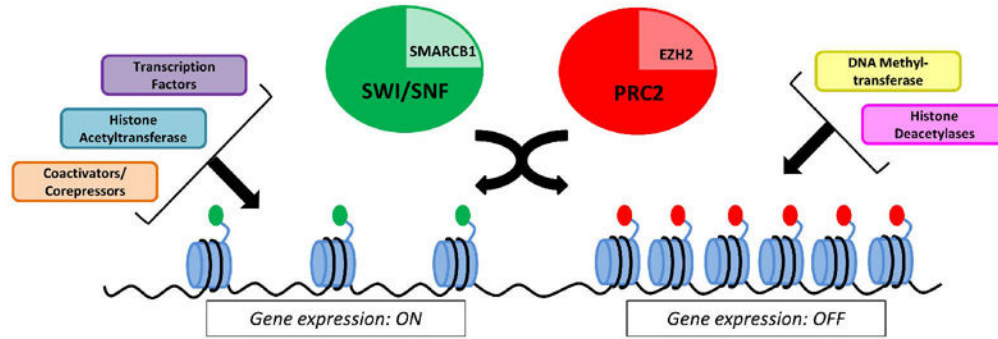
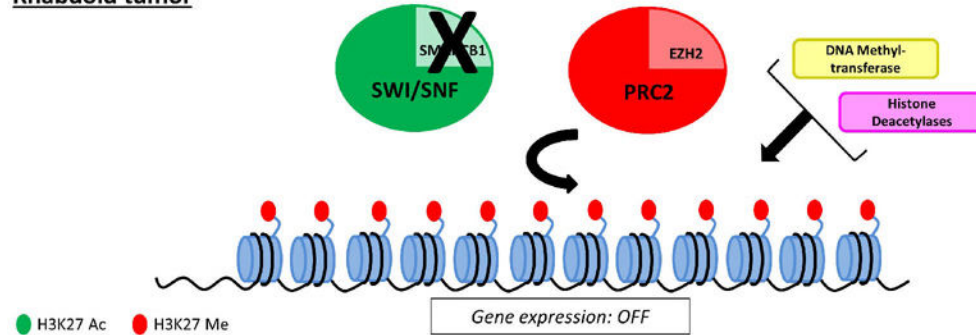


FIG. 3: Somatic point mutations (**A**) and frameshift mutations (**B**) identified in 200 sporadic rhabdoid tumors. Somatic point mutations and frameshift mutations were identified in a total of 46 and 53 patients, respectively.

Normal cell (lineage specific differentiation)**Rhabdoid tumor****FIG. 4:**

Regulation of gene expression by SWI/SNF and Polycomb repressive complex 2 (PRC2) complexes. During lineage-specific differentiation, the SWI/SNF complex, which includes SMARCB1, interacts with transcription factors, histone acetyltransferases, and transcriptional regulators to activate expression of target genes. Acetylation of histone H3K27 is present at transcriptionally active genes. Opposing the SWI/SNF complex is the PRC2 complex, which contains EZH2. PRC2 interacts with DNA methyltransferases and histone deacetylases to silence gene expression. The transcriptionally inactive genes are marked by methylation at histone H3K27. In rhabdoid tumors the loss of SMARCB1 expression prohibits the normal functions of the SWI/SNF complex, resulting in altered gene expression.

TABLE 1:Acquired *SMARCB1* Alterations in 200 Sporadic Rhabdoid Tumors

Allele 1 Alteration	Allele 2 Alteration				Total
	Mutation	Partial Gene Deletion / Duplication	Whole Gene Deletion	CN-LOH	
Mutation	8 (4%)	1 (0.50%)	58 (29%)	27 (13.5%)	94 (47%)
Partial gene deletion / duplication	—	5 (2.5%)	14 (7%)	11 (5.3%)	30 (15 %)
Whole gene deletion	—	—	76 (38%)	—	76 (38%)
Total	8 (4%)	6 (3%)	148 (74%)	38 (19%)	200 (100%)

CN-LOH, copy number neutral loss of heterozygosity.

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TABLE 2:

Molecular Targets and Potential Inhibitors of Rhabdoid Tumors

Epigenetic Target	Mechanism of Action	Agent	Pediatric Development Comments
EZH2	Histone methylation	E7458, EPZ-6438, GSK2816126	Agents pending phase I investigation
DNMT	DNA methylation	Decitabine, 5-Azacitadine SGI-110	Decitabine: phase I single and combination studies complete
HDAC	Histone deacetylation	Vorinostat, Valproic acid, Romidepsin, Panobinostat, Quisinostat, Others	Vorinostat: phase I single and combination studies complete/ongoing
CDK4/cyclinD	G ₁ cell cycle arrest	Palbociclib, LEE011, P276-00, LY2835219	LEE-011: pediatric phase I/II (rhabdoid)
Aurora-A-kinase	Antimitotic	Alisertib, TAS-119, ENMD-2076, AMG900	Alisertib: pediatric phase II (rhabdoid)

CDK4, cyclin-dependent kinase 4; DNMT, DNA methyltransferase; EZH2, enhancer of zeste 2 polycomb repressor complex 2; HDAC, histone deacetylase.

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