CRX is a Diagnostic Marker of Retinal and Pineal Lineage Tumors

Citation

Published Version
doi://10.1371/journal.pone.0007932

Permanent link
http://nrs.harvard.edu/urn-3:HUL.InstRepos:10198690

Terms of Use
This article was downloaded from Harvard University’s DASH repository, and is made available under the terms and conditions applicable to Other Posted Material, as set forth at http://nrs.harvard.edu/urn-3:HUL.InstRepos:dash.current.terms-of-use#LAA

Share Your Story
The Harvard community has made this article openly available. Please share how this access benefits you. Submit a story.

Accessibility
CRX Is a Diagnostic Marker of Retinal and Pineal Lineage Tumors

Sandro Santagata, Cecile L. Maire, Ahmed Idbaih, Lars Geffers, Mick Correll, Kristina Holton, John Quackenbush, Keith L. Ligon

Introduction

Pineal parenchymal tumors predominantly affect children, and account for approximately one-quarter of all neoplasms of the pineal region [1]. These tumors exhibit a spectrum of clinical aggressiveness that include pineocytomas, which are low-grade well-differentiated and indolent tumors often with large pineocytomatous rosettes; pineoblastomas, which are high-grade poorly-differentiated aggressive embryonal tumors with dense sheets of poorly differentiated small cells and pineal parenchymal tumors of intermediate differentiation (PPTID), which have an intermediate grade and prognosis[2-7]. The appropriate pathologic classification and grading of tumors of the pineal region is essential for determining clinical management and prognosis[8], however, the diagnostic evaluation is often difficult due to the inherently small size of the biopsies for diagnosis and the wide array of tumor types that can involve the pineal gland[3,9].

Background: CRX is a homeobox transcription factor whose expression and function is critical to maintain retinal and pineal lineage cells and their progenitors. To determine the biologic and diagnostic potential of CRX in human tumors of the retina and pineal, we examined its expression in multiple settings.

Methodology/Principal Findings: Using situ hybridization and immunohistochemistry we show that Crx RNA and protein expression are exquisitely lineage restricted to retinal and pineal cells during normal mouse and human development. Gene expression profiling analysis of a wide range of human cancers and cancer cell lines also supports that CRX RNA is highly lineage restricted in cancer. Immunohistochemical analysis of 22 retinoblastomas and 13 pineal parenchymal tumors demonstrated strong expression of CRX in over 95% of these tumors. Importantly, CRX was not detected in the majority of tumors considered in the differential diagnosis of pineal region tumors (n = 78). The notable exception was medulloblastoma, 40% of which exhibited CRX expression in a heterogeneous pattern readily distinguished from that seen in retino-pineal tumors.

Conclusions/Significance: These findings describe new potential roles for CRX in human cancers and highlight the general utility of lineage restricted transcription factors in cancer biology. They also identify CRX as a sensitive and specific clinical marker and a potential lineage dependent therapeutic target in retinoblastoma and pineoblastoma.

Abstract

Background: CRX is a homeobox transcription factor whose expression and function is critical to maintain retinal and pineal lineage cells and their progenitors. To determine the biologic and diagnostic potential of CRX in human tumors of the retina and pineal, we examined its expression in multiple settings.

Methodology/Principal Findings: Using situ hybridization and immunohistochemistry we show that Crx RNA and protein expression are exquisitely lineage restricted to retinal and pineal cells during normal mouse and human development. Gene expression profiling analysis of a wide range of human cancers and cancer cell lines also supports that CRX RNA is highly lineage restricted in cancer. Immunohistochemical analysis of 22 retinoblastomas and 13 pineal parenchymal tumors demonstrated strong expression of CRX in over 95% of these tumors. Importantly, CRX was not detected in the majority of tumors considered in the differential diagnosis of pineal region tumors (n = 78). The notable exception was medulloblastoma, 40% of which exhibited CRX expression in a heterogeneous pattern readily distinguished from that seen in retino-pineal tumors.

Conclusions/Significance: These findings describe new potential roles for CRX in human cancers and highlight the general utility of lineage restricted transcription factors in cancer biology. They also identify CRX as a sensitive and specific clinical marker and a potential lineage dependent therapeutic target in retinoblastoma and pineoblastoma.
bulb-ended cilia with a 9+0 axial skeleton protruding into an intracytoplasmic lumen, microtubular sheaves, and vesicle-crowned and annulate lamellae [12–13] but such features are not present reliably enough for routine clinical diagnosis. Pinea1 parenchymal tumors have been shown to express antigens found in the retina including retinal S-antigen[16,17], transducin[18,19], and interphotoreceptor retinoid-binding protein, rod opsin, cone opsin, and cellular retinaldehyde-binding protein[20]. Conversely, normal human retina and retinoblastoma express retinal and pineal antigens consistent with incomplete retinal lineage differentiation, and a bias towards cone photoreceptor antigens[21]. The common lineage connection between the pineal and retina is further exemplified by the occurrence of pineoblastoma in patients with retinoblastoma, a phenomenon termed trilateral retinoblastoma[22–24]. This shared heritage strongly suggests that lineage-restricted biomarkers found in the developing retina and pineal may be useful not only as immunohistochemical markers in the diagnosis of retino-pineal tumors but possibly in the etiology or treatment of these tumors.

As a class, transcription factors are emerging as highly reliable tools in the pathologic diagnosis of human solid tumors[25]. Recently, our group and others demonstrated that lineage-restricted transcription factors such as OCT4 and NANOG are robust markers for the diagnosis of germ cell tumors, including those in the central nervous system[26–29]. Crx is an Otx-like homeobox transcription factor critical for photoreceptor differentiation and for maintenance of the transcriptional regulatory networks essential for normal retinal development [30] and pineal function[31–33]. Mutations in the human CRX gene lead to photoreceptor degeneration and the retinal diseases cone-rod dystrophy 2 (CORD2), Leber congenital amaurosis type VII (LCA7), and retinitis pigmentosa, late onset dominant[34–36]. Consistent with these findings, Crx null mice demonstrate a lineage dependent role for this TF in proper development of retinal stem/progenitor cells leading to subsequent photoreceptor degeneration[37]. In addition, while the pineal gland appears grossly normal in post-natal Crx null mice, pineal-specific gene expression is reduced and circadian entrainment is attenuated[39]. Little is known about CRX expression or function in human cancer, although several studies have described its expression in retinoblastoma cell lines. Given its restricted expression and functional relevance in pineal and retinal cell lineages we sought to more comprehensively establish whether CRX might serve as a robust TF marker for research and diagnostic evaluation of retino-pineal tumors.

In this study we demonstrate expression of Crx in normal and neoplastic cells of retinal and pineal lineage and demonstrate the utility of immunohistochemistry for Crx in discriminating pineal parenchymal tumors from other lesions that often enter the differential diagnosis of pineal masses.

**Materials and Methods**

**Ethics Statement**

This study was conducted according to the principles expressed in the Declaration of Helsinki. All work on human tissues was conducted on anonymous excess archival human material from the Departments of Pathology at Children's Hospital, Boston and Brigham and Women's Hospital. The research study was approved by the Children's Hospital Boston Institutional Review Board for Human Research and also the Brigham and Women's Hospital Institutional Review Board for Human Research as an excess tissue protocol. The data were analyzed anonymously and therefore both review boards did not require specific written consent from patients for this study.

**Tissue Samples**

Paraffin blocks from surgical resection specimens spanning a 10 year period (1998–2008) were obtained as anonymous specimens from Children’s Hospital, Boston and Brigham and Women’s Hospital, Boston, in accordance with the regulations of the review boards of both institutions for excess tissue. Diagnoses were confirmed based on World Health Organization diagnostic criteria. Surgical resection samples consisted of five normal pineal tissue, three pineal cysts, five pineoblastoma, four pineocytoma, four pineal parenchymal tumor of intermediate differentiation, nine CNS germinoma, four CNS embryonal carcinoma, ten medulloblastoma, five supratentorial primitive neuroectodermal tumor, five atypical teratoid/rhabdoid tumor, five Langerhan’s cell histiocytosis, five neurocytoma, 12 glioblastoma, 12 anaplastic oligodendroglioma, five meningioma, five choroid plexus carcinoma, six anaplastic ependymoma, five metastatic carcinoma (one lung adenocarcinoma, one ductal carcinoma of the breast, one neuroendocrine carcinoma, one renal cell carcinoma and one melanoma) and enucleation specimens of retinoblastoma. Paraffin blocks of ten pineals from post-mortem examination were also obtained from the archives of Brigham and Women’s Hospital. The pineal tumor samples were consecutive samples that had sufficient tissue present in the block for research use. The study was designed in light of recommendations from the STARD (STAndards for the Reporting of Diagnostic accuracy studies) statement. http://www.stard-statement.org/

**Slide Preparation, Immunohistochemistry and Scoring**

Specimens were fixed in 10% buffered-formalin, four-micron sections were generated from paraffin blocks and slides were stained with hematoxylin and eosin (H&E). Serial sections of the paraffin blocks were cut and these slides were used for immunohistochemical studies. The antigen, clone, dilution, antigen retrieval conditions and vendors of the primary antibodies are listed in Table 1 and all antibodies are publicly available.

<table>
<thead>
<tr>
<th>Antigen</th>
<th>Clone</th>
<th>Dilution</th>
<th>Antigen Retrieval</th>
<th>Vendor</th>
</tr>
</thead>
<tbody>
<tr>
<td>CRX</td>
<td>Polyclonal Rabbit (H-120)</td>
<td>1:100</td>
<td>Citrate; Microwave</td>
<td>Santa Cruz Biotechnology, Santa Cruz, CA</td>
</tr>
<tr>
<td>OCT3/4 (POU5F1)</td>
<td>Monoclonal Mouse (C-10; sc-5279)</td>
<td>1:2000</td>
<td>Citrate, Steamer</td>
<td>Santa Cruz Biotechnology, Santa Cruz, CA</td>
</tr>
<tr>
<td>Olig2</td>
<td>Polyclonal Rabbit (AB9610)</td>
<td>1:15K</td>
<td>Citrate; pressure cooker</td>
<td>Millipore</td>
</tr>
<tr>
<td>GFAP</td>
<td>Polyclonal Rabbit (Z 0334)</td>
<td>1:20K</td>
<td>Pressure cooker citrate</td>
<td>DAKO</td>
</tr>
<tr>
<td>Synaptophysin</td>
<td>Monoclonal Mouse (SY38)</td>
<td>1:200</td>
<td>no treatment</td>
<td>DAKO</td>
</tr>
</tbody>
</table>

Table 1. Antibody Panel Used In This Study.
Expression Profiling Analysis

Expression profiling analysis of cell lines was performed using the publicly available Oncomine resource (http://www.oncomine.org/main/mianx.jsp) [42] and the publicly available datasets contained within the Oncomine database. Analysis was done using the t-test method for determining significance of CRX expression across multiple datasets for normal and cancer cell lines. All data was collected using U133 Plus 2.0 Affymetrix arrays. Global cancer cell line analysis was done using an unpublished but publicly available dataset created by Wooster et. al. in collaboration with GlaxoSmithKline which contained data from 316 cancer cell lines. Representative cell lines of pineal origin were not present in this dataset.

Meta-analysis of Crx expression was also assessed in a wide range of tumor types. Raw data files downloaded from public resources were first processed using the MAS5.0 algorithm implemented in Bioconductor to obtain detection calls and the 3’ to 5’ signal ratios for control probesets: GAPDH and β-ACTIN. All the CEL files were processed using the RMA algorithm implemented in Bioconductor to generate normalized expression values. Expression values were scaled by computing the median expression value for each sample and then processed using a custom script to scale the RNA-derived expression values such that each array will have the same median intensity. Expression profiling data from 1936 individual tissue samples and 929 individual cell line preparations were evaluated in this manner.

Sequence Alignment

Sequence alignment (Smith-Waterman algorithm) of human CRX immunogen (amino acids 166 to 285) was performed with OTX1 and OTX2. The alignment conservation annotation is based on the AMAS method of multiple sequence alignment analysis[43]. The image was generated using Jalview 2.4.

Results

Crx mRNA Is Restricted to the Retina and Pineal

To determine the degree of lineage restriction of Crx during development, we performed in situ hybridization on whole animal sections to detect Crx RNA at embryonic and postnatal stages. In 14.5 days post coitus NMRI mouse embryos (E14.5) Crx expression was restricted to the developing ventricular zone (VZ) progenitor cells of the retina and the pineal gland (Fig. 1A-D). At 7 postnatal days (P7), strong signal was detected in the outer nuclear layer of the retina with weak signal present in the inner nuclear layer (data not shown). In the brain of P7 mice, strong Crx RNA expression was mainly restricted to the pineal gland in C57BL/6 mice (Fig. 1E, 1F). Weak expression of Crx RNA was, however, also detected in the soft tissues of the face (Fig. 1A) and in a thin layer of the periventricular VZ progenitors of the developing posterior cerebral hemispheres (Fig. 1C). A similar pattern of expression to that seen in the NMRI embryo was also observed at stage E14.5 in C57BL/6 mouse embryos with a riboprobe recognizing a different portion of the Crx transcript (data not shown) in images obtained from the genepaint database (http://www.genepaint.org)[40,41].

Characterization of Anti-CRX Antibody H120

In light of the fact that CRX protein expression in situ has not been extensively analyzed, we sought to determine whether CRX expression might be similarly restricted in human at the protein level. To validate the specificity of the rabbit polyclonal antibody used in these studies (Table 1; Santa Cruz H120 anti-Crx) for through commercial sources. Controls, as appropriate, were used and visualization was attained using the Envision Plus Detection System (Dako, Carpinteria, CA). Competition experiments were performed using recombinant proteins expressed in bacteria GST-Crx and the unrelated protein GST-Cry1 (Abnova H00001406-P01 and H00001407-P01) as well as Glutathione-S-Transferase (GST) alone (Millipore 12–350). Equimolar amounts of protein and anti-Crx antibody were incubated together for 30 minutes at room temperature and then applied to tissue sections as described above. Grading of immunoreactivity was based on the following semiquantitative approach by two neuropathologists (SS and KL): 0, no tumor cells demonstrating nuclear (for Crx) or membranous/cytoplasmic staining (for GFAP, Synaptophysin); 1+, <5% of tumor cells reactive; 2+, >5%–25% of tumor cells reactive; 3+, >25%–50% of tumor cells reactive; 4+, >50%–75% of tumor cells reactive; 5+, >75% of cells reactive.

Immunoblotting

50 ng and 20 ng of indicated proteins were spotted on nitrocellulose membranes. Blocking was performed for 1 hr using 5% BSA in PBS-T, followed by application of rabbit polyclonal anti-Crx antibody (H120; 1:400 dilution in 0.1%BSA/PBS-T) for 30 min, 3 washes with PBS-T and incubation with anti-rabbit secondary antibody conjugated with HRP (1:5000 dilution in 0.1%BSA/PBS-T). Following an additional three washes with PBS-T, the membrane was developed with chemiluminescent substrate (Thermo, SuperSignal West Pico 34078).

In Situ Hybridization

Analysis of the expression pattern of Crx mRNA was conducted using GenePaint.org, an interactive publically available in situ hybridization (ISH) atlas of gene expression patterns in mouse development, we performed in situ hybridization on whole animal sections to detect Crx RNA at embryonic and postnatal stages. In 14.5 days post coitus NMRI mouse embryos (E14.5) Crx expression was restricted to the developing ventricular zone (VZ) progenitor cells of the retina and the pineal gland (Fig. 1A-D). At 7 postnatal days (P7), strong signal was detected in the outer nuclear layer of the retina with weak signal present in the inner nuclear layer (data not shown). In the brain of P7 mice, strong Crx RNA expression was mainly restricted to the pineal gland in C57BL/6 mice (Fig. 1E, 1F). Weak expression of Crx RNA was, however, also detected in the soft tissues of the face (Fig. 1A) and in a thin layer of the periventricular VZ progenitors of the developing posterior cerebral hemispheres (Fig. 1C). A similar pattern of expression to that seen in the NMRI embryo was also observed at stage E14.5 in C57BL/6 mouse embryos with a riboprobe recognizing a different portion of the Crx transcript (data not shown) in images obtained from the genepaint database (http://www.genepaint.org)[40,41].

Animal Procedures

For immunohistochemistry studies, tissue specimens including brain and eye were harvested from E14.5 mouse pups that either had one (Crx+/−) or both (Crx −/−) alleles disrupted [39]. The specimens were snap frozen in liquid nitrogen and sections were prepared by cryostat sectioning. Genotyping was performed as previously described [39] and using probes designed by Transnetyx Inc.

Animal Welfare Statement

All animals were handled in strict accordance with good animal practice as defined by the European Communities Council Directive of November 24, 1986 (86/609/EEC) and under authorization of Az 32.22/Vo (‘‘Ordnungsamt der Stadt Göttingen’’). All animals were euthanized for analysis using procedures approved by the appropriate institutional animal welfare committee.

Expression Profiling Analysis

Expression profiling analysis of cell lines was performed using the publicly available Oncomine resource (http://www.oncomine.org/main/mianx.jsp) [42] and the publicly available datasets contained within the Oncomine database. Analysis was done using the t-test method for determining significance of CRX expression across multiple datasets for normal and cancer cell lines. All data was collected using U133 Plus 2.0 Affymetrix arrays. Global cancer cell line analysis was done using an unpublished but publicly available dataset created by Wooster et. al. in collaboration with GlaxoSmithKline which contained data from 316 cancer cell lines. Representative cell lines of pineal origin were not present in this dataset.

Meta-analysis of Crx expression was also assessed in a wide range of tumor types. Raw data files downloaded from public resources were first processed using the MAS5.0 algorithm implemented in Bioconductor to obtain detection calls and the 3’ to 5’ signal ratios for control probesets: GAPDH and β-ACTIN. All the CEL files were processed using the RMA algorithm implemented in Bioconductor to generate normalized expression values. Expression values were scaled by computing the median expression value for each sample and then processed using a custom script to scale the RNA-derived expression values such that each array will have the same median intensity. Expression profiling data from 1936 individual tissue samples and 929 individual cell line preparations were evaluated in this manner.

Sequence Alignment

Sequence alignment (Smith-Waterman algorithm) of human CRX immunogen (amino acids 166 to 285) was performed with OTX1 and OTX2. The alignment conservation annotation is based on the AMAS method of multiple sequence alignment analysis[43]. The image was generated using Jalview 2.4.

Results

Crx mRNA Is Restricted to the Retina and Pineal

To determine the degree of lineage restriction of Crx during development, we performed in situ hybridization on whole animal sections to detect Crx RNA at embryonic and postnatal stages. In 14.5 days post coitus NMRI mouse embryos (E14.5) Crx expression was restricted to the developing ventricular zone (VZ) progenitor cells of the retina and the pineal gland (Fig. 1A-D). At 7 postnatal days (P7), strong signal was detected in the outer nuclear layer of the retina with weak signal present in the inner nuclear layer (data not shown). In the brain of P7 mice, strong Crx RNA expression was mainly restricted to the pineal gland in C57BL/6 mice (Fig. 1E, 1F). Weak expression of Crx RNA was, however, also detected in the soft tissues of the face (Fig. 1A) and in a thin layer of the periventricular VZ progenitors of the developing posterior cerebral hemispheres (Fig. 1C). A similar pattern of expression to that seen in the NMRI embryo was also observed at stage E14.5 in C57BL/6 mouse embryos with a riboprobe recognizing a different portion of the Crx transcript (data not shown) in images obtained from the genepaint database (http://www.genepaint.org)[40,41].

Characterization of Anti-CRX Antibody H120

In light of the fact that CRX protein expression in situ has not been extensively analyzed, we sought to determine whether CRX expression might be similarly restricted in human at the protein level. To validate the specificity of the rabbit polyclonal antibody used in these studies (Table 1; Santa Cruz H120 anti-Crx) for...
recognition of Crx we took a combination of sequence alignment, immunoblotting and immunohistochemistry approaches. OTX1 and OTX2 are the proteins with the highest sequence identity to CRX in the genome of human and mouse. An alignment of the protein sequences in the region of human CRX that was used to generate the polyclonal antibody (amino acids 166 to 285) reveals that the overall identity between CRX and OTX1 (30%) and OTX2 (40%) is low reducing the likelihood of antibody cross-reactivity (Fig. 2A). In fact in this region, homology is limited to stretches of three amino acids or less (with only one region of CRX and OTX1 sharing four amino acids), which is an insufficient length to likely support significant cross-reactivity of the antibody via a shared epitope.

We next performed immunoblots following SDS-PAGE resolution of lysates from human retina, human retinoblastoma cells and 293T cells with exogenously expressed Crx protein. Interestingly, we were unable to detect any band corresponding to Crx in any of these denatured lysates (data not shown). In fact no bands at all (background) were detected under these conditions. Incubation of the same Western blot with another antibody available through Santa Cruz (Q17 monoclonal) detected a band of the appropriate size. These findings led us to hypothesize that the H120 antibody was recognizing a conformational epitope rather than a linear epitope, a relatively frequent event according to published studies[44]. To test this we performed dot blots of native (non-denatured) GST-CRX protein purified from bacteria and were successfully able to detect the native protein with the H120 Crx antibody while we were unable to detect control unrelated proteins or GST alone (Fig. 2B).

Since the H120 anti-Crx antibody recognizes a conformational rather than a linear epitope, we further characterized the specificity of the antibody in the context of in vivo staining. We demonstrate that the H120 anti-Crx antibody recognizes a strong signal in appropriate regions of the developing retina of E14.5 mice that are heterozygous for Crx (Crx+/−) but that the signal is completely absent in the retina of Crx knockout mice (Crx−/−) which lack only the Crx protein through homologous recombination[39](Fig. 2C). In addition, the pattern of immunoreactivity detected in the mouse CNS using the H120 anti-CRX antibody (retina and pineal) mirrors the pattern of CRX mRNA expression and not that of OTX1 and OTX2 mRNA expression as determined by in situ hybridization (Fig. S1). To further address the specificity of the antibody in the context of human tissue, we performed competition assays with purified CRX protein and show on tissue sections of human retinoblastoma and adjacent uninvolved retina that the immunostaining with the H120 anti-Crx antibody can be completely competed away with 1:1 molar amounts of purified GST-Crx protein in both normal retina and the retinoblastoma tumor cells (Fig. 2D).

CRX Protein Is Highly Expressed in Human Retina and Pineal

Having characterized the specificity of the antibody for recognition of Crx, we turned to evaluating the pattern of expression of CRX in the human eye and pineal. Analysis of normal appearing adult human retina (Fig. 3A,3B) demonstrates strong expression in the ventricular zone of the retina (A, B) and in the developing pineal which appears as a diverticulum in the diencephalic roof of the third ventricle (C, D). Crx in the brain of a P7 C57BL/6 mouse (Genepaint Set ID MH1082) demonstrates strong expression restricted to the pineal primordium (E, F)[40,41].

doi:10.1371/journal.pone.0007932.g001

Figure 1. Strong expression of Crx mRNA is highly restricted to the retina and pineal during normal murine development. RNA in situ hybridization using antisense riboprobes for Crx at developmental stage E14.5 in NMRI mouse embryos (Genepaint Set ID DA117) demonstrates strong expression in the ventricular zone of the retina (A, B) and in the developing pineal which appears as a diverticulum in the diencephalic roof of the third ventricle (C, D). Crx in the brain of a P7 C57BL/6 mouse (Genepaint Set ID MH1082) demonstrates strong expression restricted to the pineal primordium (E, F)[40,41].

CRX in Retino-Pineal Cancer
and horizontal cells. Intranuclear staining was absent in ganglion cells (Fig. 3B).

Expression of CRX protein in the human pineal was also evaluated by immunohistochemistry in eight pineal surgical resection specimens that contained either normal pineal (n = 5) (Fig. 2C) or a pineal cyst (n = 3) (Fig. 3E). In all eight specimens intranuclear staining was present in >85% of pineocyte nuclei (Fig. 3D, 3F). Gliotic regions composing the cyst wall were negative for intranuclear CRX immunostaining (Fig. 3F) as were inflammatory cells and endothelial and smooth muscle cells composing blood vessels. To note, expression of CRX was detected by immunohistochemistry in none of the ten post-mortem pineal specimens evaluated. The presence of CRX in surgically-derived pineal specimens but the absence of CRX immunostaining in autopsy-derived tissue likely reflects the labile nature of the antigen and highlights the importance of performing CRX immunohistochemistry on recent resection specimens that have undergone prompt formalin-fixation after resection.

CRX Is a Sensitive Marker for Retinoblastoma and Pineal Parenchymal Tumors

CRX protein expression was evaluated by immunohistochemistry in 22 enucleation specimens for histologically confirmed retinoblastoma (Fig. 4A, 4C). 21 of the 22 cases (>95%) demonstrated strong intranuclear CRX immunoreactivity in most tumor cells (Fig. 4B, 4D) with strong staining evident in both well-differentiated regions demonstrating Flexner-Wintersteiner rosettes (Fig. 4D) as well as in moderately and poorly differentiated regions (Fig. 4B). CRX immunostaining was negative in the regions of optic nerve adjacent to the retinoblastoma (Fig. 4B, lower right portion of field). CRX immunostaining was absent in necrotic regions and often in morphologically viable cells surrounding these necrotic regions. In addition, we noted CRX expression was weak or absent in the central portion of large tumors while the peripheral portions and the associated retina demonstrated strong expression. These findings, in addition to the absence of CRX staining in post-mortem pineal tissue, suggest that the CRX antigen is moderately labile and needs to be evaluated in well-fixed tissue.

CRX expression was also evaluated by immunohistochemistry in 13 pineal parenchymal tumors that were classified according to WHO criteria. Included among these were four pineocytoma (W.H.O. Grade I) (Fig. 5A), four pineal parenchymal tumors of intermediate differentiation (W.H.O. Grade II/III) (Fig. 5C), and five pineoblastoma (W.H.O. Grade IV) (Fig. 5E). These tumors had previously solely been evaluated with GFAP and synaptophysin to arrive at a clinical diagnosis (Table 2). Twelve of the 13 cases demonstrated intranuclear staining for CRX (4 of 4 pineocytoma, Fig. 5B; 4 of 4 pineal parenchymal tumor of intermediate differentiation, Fig. 5D; and 4 of 5 pineoblastoma Fig. 5F). Four of the five pineoblastoma demonstrated intranuclear staining in >50% of tumor cells, 3 of the 4 pineal parenchymal
tumors of intermediate differentiation demonstrated intranuclear staining in 50% of tumor cells and 3 of the 4 pineocytoma demonstrated intranuclear staining in 50% of the tumor cells (Table 2). The heterogeneity of CRX staining in a portion of the tumor samples may reflect biological heterogeneity within these tumors. Of these pineal parenchymal tumors, 12 of 13 demonstrated immunoreactivity for synaptophysin, currently the most widely used marker of pineal tumors, in 75% of tumor cells and 12 of 13 demonstrated immunoreactivity for GFAP, a glial marker, in 5% of tumor cells. Examination of serial sections showed that the CRX staining correlated precisely to regions of synaptophysin signal in a highly specific manner in 100% of cases. In all, the data suggest that CRX is a sensitive diagnostic marker for tumors of pineal lineage and can be used effectively along with synaptophysin and GFAP in the diagnostic evaluation of these tumors.

CRX Is a Specific Marker for Tumors of Pineal/Retinal Lineages

The diagnosis of tumors of the pineal region is often difficult due to the range of tumor types that can affect this region and the often minute size of the biopsy that is provided for definitive diagnosis. To investigate the specificity of CRX in the diagnosis of tumors of pineal/retinal lineage, we performed immunohistochemistry for CRX on a number of tumor types that frequently enter the differential diagnosis of pineal masses (Fig. 6A–6F). Intranuclear immunoreactivity was not detected in a broad range of tumors...
examined including five atypical teratoid/rhabdoid tumors (Fig. 6A, 6B), nine germinoma (Fig. 6C, 6D), five primitive neuroectodermal tumors (Fig. 6E, 6F), four embryonal carcinoma, five choroid plexus carcinoma, six anaplastic ependymoma, five metastatic carcinoma, five neurocytoma, five Langerhans cell histiocytosis, five meningioma and 24 high-grade diffuse gliomas (12 glioblastoma and 12 anaplastic oligodendrogliomas).

Pathologic distinction of medulloblastoma from pineoblastoma can occasionally pose a clinical challenge given that these poorly differentiated tumors are morphologically indistinguishable and larger tumors may grow to involve both the superior cerebellum and pineal regions. Interestingly, four of ten medulloblastoma (Fig. 6G) demonstrated a subpopulation of scattered cells with positive intranuclear CRX staining (Fig. 6H). Two of the cases showed immunoreactivity in <5% of the tumor cells, one case in 5–25% of tumor cells and one in 25–50% of tumor cells. While this heterogeneous pattern of immunoreactivity is noteworthy, none of the cases demonstrated the robust, uniform pattern of CRX immunostaining most often seen in pineoblastoma.

A specific example of the practical diagnostic use of CRX immunohistochemistry can be provided by a recent case evaluated at Children’s Hospital, Boston of a high-grade neoplasm of the pineal region (Fig. 7A). This tumor represented the frequent diagnostic challenge presented by tumors of the pineal. This particular tumor was identified as a high-grade neoplasm of uncertain origin based on a minute surgical biopsy specimen. A panel of lineage specific transcription factors including CRX (pineal), OLIG2 (diffuse glioma) and OCT4 (germ cell tumors) were utilized to “decode” the lineage of the tumor. In this case CRX and the germ cell transcription factor OCT4 were negative and showed no intranuclear reactivity in tumor cells (Fig. 7B and 7C), while OLIG2 exhibited strong nuclear staining (Fig. 7D) consistent with a high-grade glioma arising principally in the pineal region.

As seen in Figure 7B, we also found that a low percentage of tumors demonstrated weak granular cytoplasmic immunoreactivity for CRX. This pattern of cytoplasmic staining was particularly seen in gliomas, Langerhans cell histiocytosis, central neurocytoma, primitive neuroectodermal tumor and renal cell carcinoma. In addition, the cytoplasm of lymphocytes demonstrated weak to moderate immunoreactivity as noted in tumors bearing many of these cells such as some germinoma. The cytoplasmic pattern of staining appears to be consistent with cross-reactivity within the endoplasmic reticulum and/or secretory granules and was not considered to be specific staining.

Finally, to more broadly investigate the extent of CRX expression across many types of cancer and normal tissues, we performed a meta-analysis of expression profiling data from a wide range of cancer tissues, normal tissue controls and cancer cell lines using a wide sampling of publicly available datasets (Table S1). Meta-analysis of 1,934 primary tumor and normal tissue samples of various types revealed high levels of Crx expression was restricted to a subset of medulloblastoma specimens, particularly those of anaplastic subtype (Fig. 8A). Publicly available datasets from retinoblastoma or pineoblastoma were not identified in this analysis. Furthermore, examination of a comprehensive panel of 318 different human cancer cell lines (Wooster et al.; Oncomine database of transcriptome profiles [42,48,49]) using both Oncomine analysis methods (Figure 8B,C), as well as the normalization methods used in tumor tissues above (Fig. S2) demonstrated that the highest relative level of CRX expression was present in the sole retinoblastoma cell line (Y79) present in the dataset (Fig. 8B and 8C) and that moderate levels of CRX expression were also noted in two medulloblastoma cell lines (D341-Med and D283-Med) and a handful of other non-CNS tumor cell lines. Overall, the vast majority of tumor lines showed no evidence of consistent expression of CRX, including 8 glioma cell lines and 1 central PNET cell line. No expression profiles of tumors or cell lines of pineal parenchymal origin were available for comparison within public databases.

Discussion

Advances in the study of the normal pineal and pineal region tumors has been limited in part due to their very infrequent occurrence, with tumors of the pineal region accounting for less than 0.1% of all intracranial tumors. Here we hypothesized that

---

### Table 2. Immunohistochemical Staining Results on Pineal Parenchymal Tumors.

<table>
<thead>
<tr>
<th>Case Number</th>
<th>Tumor</th>
<th>Age (years)</th>
<th>Gender</th>
<th>CRX</th>
<th>GFAP</th>
<th>Synaptophysin</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Pineocytoma</td>
<td>71</td>
<td>Female</td>
<td>2+</td>
<td>0</td>
<td>5+</td>
</tr>
<tr>
<td>2</td>
<td>Pineocytoma</td>
<td>56</td>
<td>Female</td>
<td>4+</td>
<td>0</td>
<td>4+</td>
</tr>
<tr>
<td>3</td>
<td>Pineocytoma</td>
<td>61</td>
<td>Male</td>
<td>4+</td>
<td>0</td>
<td>4+</td>
</tr>
<tr>
<td>4</td>
<td>Pineocytoma</td>
<td>54</td>
<td>Male</td>
<td>4+</td>
<td>3+</td>
<td>2+</td>
</tr>
<tr>
<td>5</td>
<td>PPTID</td>
<td>2</td>
<td>Female</td>
<td>4+</td>
<td>0</td>
<td>4+</td>
</tr>
<tr>
<td>6</td>
<td>PPTID</td>
<td>30</td>
<td>Male</td>
<td>2+</td>
<td>0</td>
<td>4+</td>
</tr>
<tr>
<td>7</td>
<td>PPTID</td>
<td>44</td>
<td>Female</td>
<td>4+</td>
<td>0</td>
<td>5+</td>
</tr>
<tr>
<td>8</td>
<td>PPTID</td>
<td>36</td>
<td>Female</td>
<td>4+</td>
<td>0</td>
<td>4+</td>
</tr>
<tr>
<td>9</td>
<td>Pineoblastoma</td>
<td>4</td>
<td>Male</td>
<td>4+</td>
<td>1+</td>
<td>5+</td>
</tr>
<tr>
<td>10</td>
<td>Pineoblastoma</td>
<td>12</td>
<td>Female</td>
<td>4+</td>
<td>0</td>
<td>5+</td>
</tr>
<tr>
<td>11</td>
<td>Pineoblastoma</td>
<td>13</td>
<td>Male</td>
<td>5+</td>
<td>0</td>
<td>5+</td>
</tr>
<tr>
<td>12</td>
<td>Pineoblastoma</td>
<td>9</td>
<td>Female</td>
<td>5+</td>
<td>1+</td>
<td>5+</td>
</tr>
<tr>
<td>13</td>
<td>Pineoblastoma</td>
<td>8</td>
<td>Female</td>
<td>0</td>
<td>0</td>
<td>4+</td>
</tr>
</tbody>
</table>

Table 2 Legend:
0 indicates no staining; 1+, <5% tumor cells reactive; 2+, 5% to 25% tumor cells reactive; 3+, 26% to 50% tumor cells reactive; 4+, 51% to 75% tumor cells reactive; 5+, >75% tumor cells reactive. GFAP, Glial Fibrillary Acid Protein; Pineal Parenchymal Tumor of Intermediate Differentiation (PPTID).

doi:10.1371/journal.pone.0007932.t002
lineage restricted transcription factors for retino-pineal progenitors might represent useful diagnostic and investigational tools as has been demonstrated in other cancers[28,29,50,51]. The molecular-genetic similarity between the retina and pineal and the remarkably restricted expression pattern of Crx mRNA suggested a distinct opportunity for employing Crx as a candidate biomarker. Our studies of RNA ISH in whole embryos and brain confirm the remarkable lineage restriction of this gene across the whole mouse embryo. Furthermore, our studies in human systems using IHC and expression profiling data validate that such lineage restriction is highly preserved in humans as well. Given that CRX protein expression had not been previously as well studied, we find that the RNA and protein expression are highly conserved with no significant differences detected in our study.

From a diagnostic standpoint, we find that 90% of retinoblastoma and 90% of pineal parenchymal tumors display significant intranuclear expression of CRX while none of the tumors entering the differential diagnosis of pineal masses display intranuclear CRX immunoreactivity. These findings highlight that CRX is both a sensitive and specific marker for tumors of pineal and retinal lineage and that its use should be further evaluated for routine application as an essential component of the standard workup of tumors of the pineal region. Previous studies using non-TF markers of photoreceptor lineage have also supported the lineage conservation between tumors of these two regions, but due to their non-nuclear and less consistent expression have found little diagnostic acceptance in clinical practice[20,52]. These same studies in the retina had concluded that retinoblastomas represented a bias towards cone differentiation, and the presence of strong CRX staining supports this given its more specific role in development of cone photoreceptors[52]. Also, while immunohistochemistry for CRX may be of practical utility in the classification of biopsies of the central nervous system it may also be valuable in unequivocally ascribing peripheral metastases in bone marrow and elsewhere to a known primary ocular retinoblastoma as well as in the evaluation of cerebrospinal fluid cytological specimens in patients with retinoblastoma, pineoblastoma and pineal parenchymal tumor of intermediate differentiation. Finally we find that CRX is a new sensitive and specific marker for retinoblastoma and pineal parenchymal tumors that should be useful in the diagnostic evaluation of pineal masses when used as part of a panel of immunohistochemical markers including synaptophysin and GFAP.

An interesting finding in this study is that CRX is expressed in a heterogeneous subpopulation of cells in four out of the ten medulloblastomas that were analyzed. Photoreceptor differentiation has previously been demonstrated in medulloblastoma with retinal S-antigen and rhodopsin antigens detected by immunohistochemistry[53–55]. A recent study classifying medulloblastoma based on gene expression profiles identified five molecular-genetic subtypes, two of which demonstrated photoreceptor differentiation[56]. These subtypes represented approximately 40% of medulloblastoma cases, similar to our findings, and had increased RNA expression of the photoreceptor transcription factors CRX, NRL and NR2E3. In addition, they were associated with clinical presentation at a younger age (<3 years of age) and more aggressive biological behavior with an increased risk of metastases.
at the time of diagnosis. These findings support the pathologic and molecular heterogeneity of medulloblastoma [57,58] and suggest that in addition to a role in the diagnosis of pineal and retinal tumors, CRX immunohistochemistry may provide critical information in determining subtype classification and poor prognosis in cases of medulloblastoma [59].

Lineage-specific transcription factors have increasingly been demonstrated as important tools in the diagnostic workup of a range of tumor types including OCT4 and NANOG in peripheral and CNS germ cell tumors[28,29], MYF4 in tumors with myogenic differentiation[60], OLIG2 in tumors with glial differentiation[61], TTF1 in thyroid tumors, BSAP (PAX5) in B-cell neoplasms[62], Brachyury in chordomas [63] and hemangioembromas [64] and CDX2 in gastrointestinal tumors[65]. CRX represents a new addition to this group and suggests that additional useful markers may be discovered through systematic identification of lineage restricted transcription factors in a broader range of tumors.

Figure 8. Expression profiling analysis demonstrates CRX expression is highly lineage-restricted across a broad range of cancer tissues and cell lines. Analysis of CRX mRNA expression was assessed using publically available expression profiling data from over 1900 primary tumor samples and demonstrates elevated expression of CRX predominantly in medulloblastoma samples (A). Pineal parenchymal tumor data is not available. Oncomine data from 316 human cancer cell lines demonstrates 26 lines with significant expression of CRX relative to other lines as demonstrated in a scatter plot (B). All expression levels are relative to the total dataset. The highest relative expression level was present in the sole retinoblastoma cell line (Y79) within the dataset (C). High level expression was also noted in the only two medulloblastoma cell lines present in the dataset (D341 and D283). Other CNS tumor cell lines showed no significant increase in CRX expression (8 astrocytoma, 1 PNET). Additional validation using same independent normalization methods as for tissues produced similar results (Fig. S2). Data utilized in construction of plots is provided as Tables S1 and S2.

doi:10.1371/journal.pone.0007932.g008
Evidence from Fevre-Montagne et al. demonstrates that at least seven genes are specifically expressed in pineoblastoma versus other tumors of pineal parenchymal origin. Consistent with our results showing that the frequency and intensity of expression of CRX protein is similar in pineoblastoma, PPT1D and pineo-octoma, CRX was not among the list of genes which discriminated classes of pineal parenchymal tumors. Among the seven discriminatory genes from Fevre-Montagne et al., were the three transcription factors HoxD13, Pitx2 and Pou4F2 [2], which unlike the highly lineage-restricted pattern of expression seen for Crx, are expressed in lineage-nonrestricted patterns. The use in tandem of both lineage-restricted and lineage-nonrestricted transcription factors as components of a diagnostic panel has been used in the evaluation of germ cells tumors where lineage-restricted transcription factors like Otx4 and Nanog can be used alongside lineage-nonrestricted transcription factors like Sox2 [29] and Sox17 [66]. This panel of transcription factors permits, first, the confident identification of a germ cell tumor and second, the more subtle discrimination between germ cell tumor subclasses such as seminoma/germinoma, embryonal carcinoma, yolk sac tumor and choriocarcinoma. The findings of Fevre-Montagne et al. suggest that CRX along with HoxD13, Pitx2 and Pou4F2 might form the core transcription factor code permitting an objective immunohistochemical and molecular subclassification of pineal parenchymal tumors.

Within the field of cancer research, extensive effort continues to be directed at identifying oncogene pathways that are activated in cancer with the goal of developing targeted therapeutic with specific signaling pathways. An emerging body of evidence, however, supports the concept that tumors may also be dependent on the same lineage-specific transcription factors which critically regulate the normal tissue restricted developmental progenitor cells [50,51,67]. This dependence for survival and proliferation on critical cellular constituents that are not mutated and that alone do not serve to transform cells (sometimes called ‘non-oncogene addiction’) represents an under-explored opportunity for development of targeted cancer therapies directed at these components and pathways. Such pathways also have the added benefit of reduced off-target effects due to their inherent lineage restriction. Our study suggests CRX might represent just such a target in retinoblastoma, pineoblastoma, and possibly even a subset of medulloblastoma. Functional studies of CRX in these cancers would certainly seem warranted, given the known dependency of medulloblastoma and medulloblastoma cell lines. The Glaxo-Smith-Kline human cancer cell line dataset was normalized and analyzed for expression of the CRX specific probeset 217510. Highest expression was seen in two medulloblastoma cell lines and the single retinoblastoma cell line in the dataset. Most other cell lines showed little to no expression of CRX.

Found at: doi:10.1371/journal.pone.0007932.s001 (2.18 MB TIF)

CRX Expression in Human Tissues

Table S1

Table S2

Acknowledgments

We thank Lena Liu, Marian Slaney and Lilliam Cruz for slide preparation and Mei Zheng for performing part of the immunohistochemistry. We thank Dr. Connie Cepko and Shateenah Kae Barnes for kindly providing us with Crx knockout mice.

Author Contributions

Conceived and designed the experiments: SS JQ KLL. Performed the experiments: SS AI LG MC KH JQ KLL. Contributed reagents/materials/analysis tools: AI LG. Wrote the paper: SS AI KLL.

References


