Response to Pembrolizumab in a Patient With Xeroderma Pigmentosum and Advanced Squamous Cell Carcinoma

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INTRODUCTION

Xeroderma pigmentosum (XP) is a rare autosomal recessive disorder caused by a nucleotide excision repair deficit, resulting in sensitivity to UV radiation.¹ Individuals with XP are 10,000 times more likely to develop cutaneous squamous cell carcinoma (SCC), with initial presentation at a median age of 9 years.² Metastatic skin cancer is the leading cause of death (34%), with a median survival of 32 years.² Few options for effective systemic therapy of advanced cutaneous SCC are available,^{3,4} and there is no standard therapy for patients with XP who have developed metastatic skin malignancies.⁵ There is a critical need for effective therapy for advanced skin cancers, and patients with XP represent a unique need because they have the potential to suffer catastrophic adverse effects from standard chemotherapeutic agents.⁶

Immune checkpoint blockade has demonstrated efficacy in tumors characterized by high mutational burden, including SCC.7,8 Therefore, cutaneous SCC is a good candidate for additional investigation of response to checkpoint inhibitors.⁹⁻¹³ A recent phase I/II clinical trial demonstrated partial response in 41% of patients receiving the programmed cell death 1 (PD-1) inhibitor cemiplimab.¹⁴ Case reports in patients with XP and advanced SCC describe response with PD-1 inhibitors, including pembrolizumab.^{5,15-17} However, these reports do not provide a molecular mechanistic rationale for the use of PD-1 inhibitors specific to this patient population, nor do they provide support for the use of these agents for long-term disease management. We report stable disease for 2 years in response to pembrolizumab in a patient with XP and metastatic cutaneous SCC, along with molecular findings to support the use of PD-1 inhibitors in patients with XP. The case report was categorized as exempt by our institution's institutional review board, and consent was not obtained because all information included is presented in a deidentified manner.

CASE REPORT

The patient, a product of a consanguineous marriage, initially presented at age 1 year with a benign skin lesion on her forehead. In the first 2 years of life, she

developed additional premalignant lesions on her face and body, which recurred despite treatment with laser therapy. She was diagnosed with XP at age 2 years on the basis of clinical presentation and family history. Over the next several years, she developed multiple malignant cutaneous lesions involving her face and right conjunctiva, requiring iterative surgical resections. At age 7 years, she developed right-sided facial weakness and swelling. Magnetic resonance imaging of the brain demonstrated a 2.9 × 2.7 × 1.4 cm well-defined lesion arising from the body of the right sphenoid bone, involving the cavernous sinus, and encasing the right carotid artery; the lesion was concerning for metastatic SCC.

Two months later, the patient presented to Seattle Children's Hospital with severe facial pain and cough. Repeat imaging demonstrated an infiltrative mass involving the right parotid and masticator space with bony involvement of the right mandible, as well as infiltration through the pterygopalatine fossa into the right orbital apex, cavernous sinus, and right middle cranial fossa. Extensive perineural spread along the right inferior alveolar nerve and right third through sixth cranial nerves was observed, in addition to leptomeningeal spread into the right aspect of the posterior fossa (Figs 1A to 1D).

Biopsies of sites concerning for malignant skin lesions were performed, including separate left lower eyelid, right conjunctiva and cornea, and right preauricular masses; all were diagnostic of SCC. Biopsy of a right parotid lymph node revealed metastatic SCC. Tumor cells were macrodissected from the non-neoplastic lymphoid cells in the lymph node. Mutational analysis of tumor samples using the University of Washington Laboratory of Medicine UW-OncoPlex Cancer Gene Panel (University of Washington, Seattle, WA;)¹⁸ demonstrated ultramutated primary tumors and metastases (total mutation burden ranged from 53 to 460 mutations/Mb) with an excess of C>T and CC>TT lowfrequency mutations (Fig 2A), characteristic of UV damage in the setting of nucleotide excision repair deficiency (Catalogue of Somatic Mutations in Cancer signature 7). The non-neoplastic lymphoid tissues



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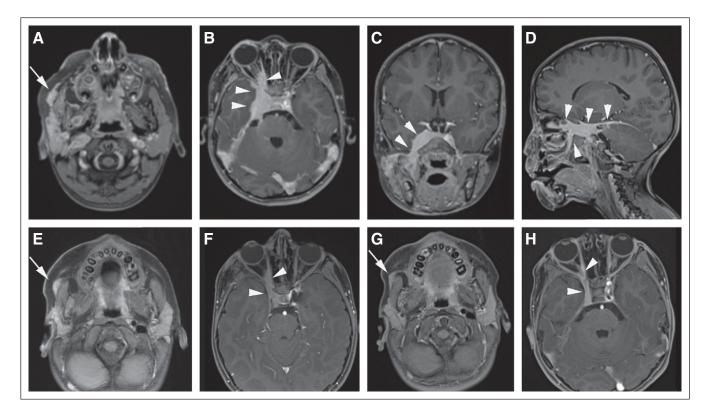


FIG 1. Perineural spread of squamous cell carcinoma (A to D) at time of diagnosis and (E to H) after therapy, shown by contrast-enhanced T1-weighted magnetic resonance imaging. (A) Axial image through face at level of parotid gland shows asymmetric nodular enhancement throughout right parotid gland, as well as more anterior nodular superficial enhancing tissue (arrow). (B) Axial, (C) coronal, and (D) sagittal images through head at level of cavernous sinus and right pterygopalatine fossa show extensive abnormal enhancing tissue within cavernous sinus, extending anteriorly into the right orbital apex, as well as posteriorly toward posterior fossa (arrowheads). (E and F) Five months after initiation of therapy, imaging shows dramatic reduction in tumor burden, both (E, arrow) in superficial tissues of face and (F, arrowheads) within cavernous sinus and orbital apex. (G and H) Thirteen months after initiation of therapy, disease burden had diminished further, both (G, arrow) in superficial tissues of the face and (H, arrowheads) within the cavernous sinus and orbital apex.

were also tested and did not show any unexpected mutations (Data Supplement). Both tumors showed a significant strand bias (P < .001), concordant with the transcription-coupled repair function of the nucleotide excision repair complex (Fig 2B). Intersection of the filtered somatic variants from the tumors revealed that there were two independent primary tumors (conjunctival and corneal), which did not share any variants, as well as two independent metastases to the right parotid lymph node.

Germline genetic testing found homozygous NM_ 004628.4 c.2116-1G>A in the *XPC* gene. There was no evidence of other well-described mechanisms of ultramutation, such as somatic *POLE* or *POLD1* exonuclease domain proofreading mutations, in any tumor tested. There was also no evidence of microsatellite instability (MSI) in any tumor (all tumors were MSI negative) using the microsatellite instability by next-generation sequencing method.²⁰

The case was reviewed at the Seattle Children's Hospital multidisciplinary tumor board, which recommended against larger resection, based on extent of disease and anticipated morbidity, and against systemic therapy with traditional chemotherapeutic agents, because they have not demonstrated efficacy in advanced SCC. On the basis of encouraging reported results in MSI-high malignancies to immune checkpoint blockade, pembrolizumab (2 mg/kg intravenously every 3 weeks) was initiated 1 month after diagnosis, using the recent US Food and Drug Administration indication for MSI-high malignancies to support insurance approval.

After five cycles of pembrolizumab, follow-up imaging demonstrated a considerable decrease in tumor bulk and resolution of leptomeningeal disease along the right pons and cerebellum (Figs 1E to 1H). The patient experienced resolution of the chronic cough and reported substantial improvement in the facial pain (initially the pain required scheduled opioid medications, but they have now been discontinued without pain). Presently, the patient has received pembrolizumab for 24 months, with stable imaging findings for more than 18 months and no clinically significant adverse effects.

Although the patient's oculocutaneous (conjunctival) lesions responded to therapy after incomplete resection, her right corneal tumor persisted and showed mild progression

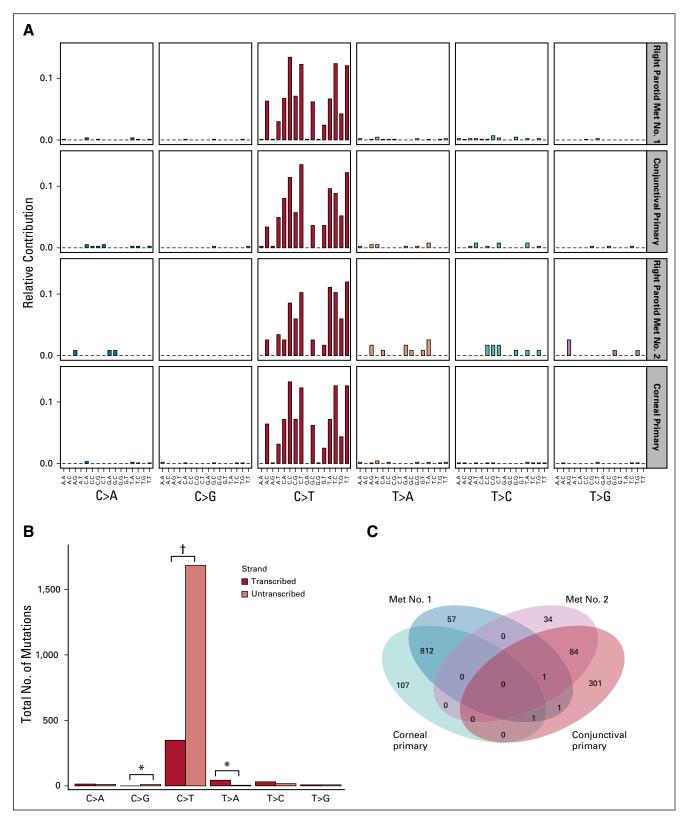


FIG 2. Mutation profile analysis of the corneal and conjunctival primary tumors, along with their parotid lymph node metastases (Met), was performed on identified somatic single nucleotide variants.¹⁹ (A) All four tumors show mutation patterns consistent with base excision repair deficiency (Catalogue of Somatic Mutations in Cancer mutation signature 7). (B) Analysis of mutation signatures based on the transcribed gene strand shows a strong bias of C>T mutations on the untranscribed strand (1,683 *v* 348 mutations on the transcribed strand), consistent with the transcription-coupled nature of the nucleotide excision repair pathway. (C) Comparison and set overlap of somatic variants identified in four sequenced samples reveals two unrelated primary tumors (corneal and conjunctival), each with unique metastases to the parotid lymph nodes. (*) P < .01. (†) P < .001.

on clinical exam. Mutational analyses demonstrated that the ocular lesions had different mutations but a similar mutational burden compared with her metastatic tumor (Data Supplement). Mutations implicated in PD-1 resistance, including *WNT*, were not identified in analysis of the patient's tumors.²¹⁻²³ Topical fluorouracil, which is efficacious in cutaneous SCC associated with XP, was initiated in the affected eye, and no additional tumor progression was noted after 1 month of local treatment.

DISCUSSION

We report the case of a pediatric patient with XP who demonstrated long-term partial response of advanced cutaneous SCC to pembrolizumab with development of no clinically significant adverse effects. Although a small number of prior reports have discussed the use of checkpoint blockade for advanced SCC in the setting of XP, this report adds:

- 1. The molecular justification of the use of PD-1 inhibitors specific to this patient population;
- 2. Support for the use of PD-1 inhibitors in long-term disease management of advanced SCC, and;
- 3. Acknowledges the potential limitation of PD-1 inhibitors for the treatment of SCC involving immune-privileged sites, such as the cornea.

XP represents a deficit in DNA nucleotide excision repair, resulting in sensitivity to UV radiation. Loss of XPC (or XPE) is consistent with deficient global genomic repair (GGR) but relatively preserved transcription-coupled repair (TCR); this contrasts with loss of XPA, XPB, or XPD, which results in a GGR-negative/TCR-negative phenotype.^{24,25} The TCR-negative/GGR-positive mutational signature of *XPC* is demonstrated in this patient with a greater burden of C>T mutations on the untranscribed strand (Fig 2B). The novel report of our patient's mutational signature enriches our understanding of XP and further supports the potential efficacy of immune checkpoint blockade with PD-1 inhibitors in the treatment of advanced SCC among patients

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with XP. Primarily, immune checkpoint inhibitors depend on neoantigen presentation via major histocompatibility complex 1. Theoretically, patients with an intact TCR, such as those with *XPC* mutations, would potentially have a less robust response to immune checkpoint inhibitors. Our experience disagrees with this, providing reassurance that this class of agents remains promising for this patient population. In addition, we were able to use molecular methods to demonstrate the coincidental development of two independent primary lesions with two paired metastatic lesions to better understand the origin of this patient's metastatic disease.

This report describes long-term sustained stable disease, including response of significant burden of disease in the CNS. Of the existing published reports using PD-1 inhibitors in patients with XP, the longest reported time to follow-up was 18 months,¹⁶ with other studies describing therapy for no more than 1 year.^{5,16,17} Our patient's sustained response supports the use of PD-1 inhibitors for long-term disease management in this setting. This is important because few options for alternative therapies exist in patients with advanced SCC that are promising for increasing progression-free survival. Moreover, PD-1 inhibitors have the potential to do this with minimal adverse effects, providing a quality-of-life benefit, which is an important consideration for individuals with advanced cancer.

Our patient's right corneal lesion demonstrated discordant poor response. The cornea is immune privileged²⁶ and does not have T-cell immunosurveillance, potentially limiting the ability of immune checkpoint blockade to treat malignancies in the cornea and other immune-privileged sites, such as the testis. This concept is particularly intriguing given the lack of response seen with immune checkpoint blockade in cisplatin-resistant testicular germ cell tumors.²⁷ In conclusion, our experience and molecular findings support the use of PD-1 inhibitors in advanced cutaneous SCC, especially in patients with XP, and highlights the need for additional research.

AUTHOR CONTRIBUTIONS

Conception and design: Angela Steineck, Jay F. Sarthy, Colin C. Pritchard, Andrew W. Stacey, Nicholas A. Vitanza, Bonnie Cole Financial support: Colin C. Pritchard Administrative support: Bonnie Cole Provision of study materials or patients: Teresa Chapman, Bonnie Cole Collection and assembly of data: Angela Steineck, Colin C. Pritchard, Teresa Chapman, Bonnie Cole Data analysis and interpretation: Angela Steineck, Niklas Krumm, Colin C. Pritchard, Teresa Chapman, Nicholas A. Vitanza, Bonnie Cole Manuscript writing: All authors Final approval of manuscript: All authors AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST The following represents disclosure information provided by authors of this manuscript. All relationships are considered compensated.

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APPENDIX

Molecular Methods

Tumor and germline samples were processed, sequenced, and analyzed using the University of Washington Laboratory Medicine UW-OncoPlex Cancer Gene Panel (University of Washington, Seattle, WA).¹⁸ Single nucleotide variants and indels in targeted regions were called from aligned BAM files using the Genome Analysis Toolkit (Broad Institute, Cambridge, MA) and the Variant Detection in Massively Parallel Sequencing Data—VarScan. Common artifacts and polymorphisms were filtered by limiting analyzed variants to those with low population frequency (not present in the Phase 3 1000 Genomes [http://phase3browser.1000genomes.org/index.html]; < 0.01%, 0.005%, and 0.1% frequency in the National Heart, Lung, and Blood Institute Exome Sequencing Project, Exome Aggregation Consortium, and an in-house database, respectively) and variant allele fraction greater than 1%. Germline variants were removed from all tumor samples. Mutation signatures and figures were created from selected variants using R and the MutationalPatterns package.¹⁹