Retina

Retinoblastoma Is Characterized by a Cold, CD8+ Cell Poor, PD-L1− Microenvironment, Which Turns Into Hot, CD8+ Cell Rich, PD-L1+ After Chemotherapy

Clelia Miracco,1 Paolo Toti,1 Maria Chiara Gelmi,2 Sara Aversa,1 Gennaro Baldino,3 Paolo Galluzzi,4 Sonia De Francesco,2 Federica Petrelli,1 Ester Sorrentino,1 Giuseppe Belmonte,1 Daniela Galimberti,5 Sandra Bracco,6 and Theodora Hadjistilianou2

1Department of Medicine, Surgery and Neuroscience, Pathological Anatomy Section, University Hospital of Siena, Siena, Italy
2Department of Medicine, Surgery and Neuroscience, Ophthalmology Unit, University Hospital of Siena, Siena, Italy
3Department of Health Promotion Sciences, Maternal and Infant Care, Internal Medicine and Medical Specialties (PROMISE), University of Palermo, Palermo, Italy
4Department of Medicine, Surgery and Neuroscience, Unit of Neuroimaging and Neurointervention, University Hospital of Siena, Siena, Italy
5Department of Maternal, Newborn and Child Health, Unit of Pediatrics, University Hospital of Siena, Siena, Italy
6Department of Medicine, Surgery and Neuroscience, Unit of Neuroimaging and Neurointervention, University Hospital of Siena, Siena, Italy

Correspondence: Maria Chiara Gelmi, Department of Medicine, Surgery and Neuroscience, Ophthalmology Unit, University Hospital of Siena, Siena, Italy; mariachiara.gelmi@student.unisi.it.

Received: August 5, 2020
Accepted: January 3, 2021
Published: February 4, 2021

Citation: Miracco C, Toti P, Gelmi MC, et al. Retinoblastoma is characterized by a cold, CD8+ cell poor, PD-L1− microenvironment, which turns into hot, CD8+ cell rich, PD-L1+ after chemotherapy. Invest Ophthalmol Vis Sci. 2021;62(2):6. https://doi.org/10.1167/iovs.62.2.6

**Purpose.** To investigate the impact of chemotherapy (CHT) on human retinoblastoma (RB) tumor microenvironment (TME).

**Cases and Methods.** Ninety-four RBs were studied, including 44 primary RBs treated by upfront surgery (Group 1) and 50 primary RBs enucleated after CHT (S-CHT), either intra-arterial (IAC; Group 2, 33 cases) or systemic (S-CHT; Group 3, 17 cases). Conventional and multiplexed immunohistochemistry were performed to make quantitative comparisons among the three groups, for the following parameters: tumor-infiltrating inflammatory cells (TI-ICs); programmed cell death protein 1 (PD-1) positive TI-ICs; Ki67 proliferation index; gliosis; PD-1 ligand (PD-L1) protein expression; vessel number. We also correlated these TME factors with the presence of histological high-risk factors (HHRF+) and RB anaplasia grade (AG).

**Results.** After CHT, a decrease in both RB burden and Ki67 positivity was observed. In parallel, most subsets of TI-ICs, PD-1+ TI-ICs, gliosis, and PD-L1 protein expression significantly increased (P < 0.001, P = 0.02, P < 0.001, respectively). Vessel number did not significantly vary. Age, HHRFs+ and AG were significantly different between primary and chemoreduced RBs (P < 0.001, P = 0.006, P = 0.001, respectively) and were correlated with most TME factors.

**Conclusions.** CHT modulates host antitumor immunity by reorienting the RB TME from anergic into an active, CD8+, PD-L1+ hot state. Furthermore, some clinicopathological characteristics of RB correlate with several factors of TME. Our study adds data in favor of the possibility of a new therapeutic scenario in human RB.

Keywords: retinoblastoma, tumor microenvironment, chemotherapy, PD-1/PD-L1, multiplexed immunohistochemistry

Therapy increased retinoblastoma (RB) survival up to over 95%, with a high rate of eye salvage in high-income countries.1,2 There is an array of therapy approaches, ranging from upfront surgery to local treatments.1 Chemotherapy (CHT) alone or coupled with other treatments is now the preferred conservative approach.3 Despite therapy, a number of RBs progress, prompting the search for new approaches.3

The study of tumor microenvironment (TME) has been providing knowledge for novel therapies in cancer.5 TME consists of a mix of cancerous and noncancerous components and their products, which play complex, bidirectional, immunostimulant, and immunosuppressive interactions, from which the immune response against cancer derives.4 A mechanism to escape the immune response in cancer is the activation of negative regulatory pathways (immune checkpoints [i-CPs]), which, under normal physiological conditions, maintain immune homeostasis.5 Interactions between suppressive i-CPs and their ligands inhibit the
response of effector immune cells, usually by inducing T-cell exhaustion, with a progressive loss of effector functions, and coexpression of inhibitory receptors. Both cancer cells and nontumor cells may overexpress i-CPs, thus limiting normal antitumor immune responses. The blockade of i-CPs is a novel immunotherapeutic approach to potentiate host immunological responses against neoplasms, already used for a number of cancers. Two members of the B7 family are among the most widely investigated i-CPs: programmed cell death receptor-1 (PD-1) and programmed cell death ligand-1 (PD-L1); PD-L1 inhibitors are already used for cancer therapy.

The effectiveness of i-CP blockade largely depends on the presence of inflammatory/immune cells within the tumor tissue and on the expression of the targeted i-CP by TME. Nowadays, the frequency of tumor-infiltrating lymphocytes and the expression levels of PD-L1 in cancer tissue are used as prognostic markers and as predictors of response to PD-L1/PD-1 inhibitor therapy in several cancer types.

The TME of RB is still sparsely explored. There are only few investigations on the impact of CHT on RB TME. In the present study, in a cohort of 94 patients who underwent enucleation for RB, we investigated the following elements at the tumor tissue level: the frequency of several subsets of T1-ICs, including lymphocytes, dendritic-like cells, macrophages and myeloid-derived suppressor-like granulocytic (G-MDS-like) cells, the RB proliferation rate, the extent of gliosis, the protein expression of PD-L1 and PD-1, and the number of vessels. Investigations were conducted by conventional and multiplexed immunohistochemistry. The latter allows the simultaneous detection of multiple TME antigens in tumor tissues and was validated by immunofluorescence.

The presence of histological high-risk factors (HHRFs) according to the International RB Staging Working Group guidelines and the degree of anaplasia according to Mendoza et al. (AG-M) were also assessed. Data were compared among RBs subdivided into three groups: group 1 (44 cases), with no previous treatment; group 2 (33 cases), treated with local CHT (IAC); and group 3 (17 cases), treated with systemic CHT (S-CHT) before enucleation.

Methods

Case Series (Patients, Samples and Research Ethics)

Archival, formalin-fixed, paraffin-embedded tissue samples from 143 consecutive RBs of 133 patients operated on for RB from 2010 to 2019 at the Ophthalmology Unit of the University Hospital of Siena were retrieved. Exclusion criteria were previous radiotherapy or treatments at other Institutions and tumor tissue not sufficient to perform our analyses or altered by severe vascular complications. The final case study consisted of 94 cases, which included 44 patients without any prior therapy (group 1), and 50 patients who underwent chemotherapy before enucleation, divided into 33 patients treated with IAC (group 2) and 17 patients treated with S-CHT (group 3). In all cases, written informed consent was obtained from parents or caregivers.

Histopathological Procedures

For each tumor, histology was reassessed on hematoxylin and eosin-stained slides by two pathologists (C.M., P.T.) blinded to clinical data, according to the latest American Joint Committee on Cancer 2018 pathologic classification and staging system. Tumor pT and the following features were reviewed: growth pattern (endophytic, exophytic, mixed, diffuse); histological grade (well, moderately, or poorly differentiated); tumor seeding (vitreous, suprachoroidal). The degree of anaplasia was also assessed in each case according to Mendoza et al. (AG-M): 1 (retinocytoma), 2 (mild anaplasia), 3 (moderate anaplasia), and 4 (severe anaplasia); the highest AG-M registered that occupied >10% of the tumor was assigned in each case. The presence of the following histological high-risk factors (HHRF) was also registered, according to the International Retinoblastoma Working Group: postlaminar optic nerve (ON) invasion, massive choroidal invasion, prelaminar or laminar ON invasion combined with nonmassive choroidal invasion, RB invasion of the anterior segment, extraocular diffusion.

In each case, the TME parameters to be studied were evaluated on immunostained sections.

Conventional Immunohistochemistry

Immunohistochemistry was performed as previously described, using the Ventana Benchmark ULTRA automatic devices (Ventana; Roche Diagnostics, Monza, Italy). For each case, we examined two to three tissue blocks, including standard pupil–optic nerve sections. Briefly, 3 μm-thick serial sections were deparaffinized, rehydrated and incubated at 37°C with the primary antibodies (listed in Table 1), according to manufacturers’ instructions. Subsequently, the appropriate secondary antibody was applied, and the sections were counterstained with Hematoxylin II (Ventana). We applied the UltraView Universal Detection kit (Ventana), using HRP multimer and either diaminobenzidine or new fuchsin as chromogens. Each reaction was run with appropriate positive and negative controls; for the latter the primary antibodies were omitted.

Multiplexed Immunohistochemistry

Multiplexed immunohistochemistry was performed on the platform Ventana Discovery by applying the recommended protocol. The multiple immunostains performed are shown in Table 2.

Immunofluorescence

To validate multiplexed immunohistochemistry, immunofluorescence was carried out in 10 representative cases of each group, as previously described.

Quantitative Evaluation of Immunostaining

Five to 15 high-power fields (HPF) were evaluated at magnification ×400 (one HPF = 0.16 mm²), avoiding necrotic...
and calcified areas. In some group 2 and 3 cases, five fields covered the entire lesional area. Immunopositivity was manually assessed through computer-assisted stereology. Briefly, TIFF images (resolution: $1160 \times 835$ pixels) were captured from each field by an optical system composed of a Zeiss Axiocam MRc5 mounted on a Zeiss Axioscope 40 microscope (AxioVision Rel. 4.41 software version; Zeiss, Oberkochen, Germany) and analyzed through the public domain ImageJ processing tool (imagej.nih.gov/ij; ImageJ software, version 1.50i).

Immunostained TI-ICs and PD-1+TI-ICs were counted at random, starting from areas with the highest density (“hot spot” areas). The proliferation index (PI) was the percentage of Ki67 positive nuclei, on all nuclei. GFAP+ areas were assessed as the percentage in the entire lesion. All PD-L1 positivity (PD-L1+ tumor areas and PD-L1+TI-ICs) was measured in each field according to literature recommendations\(^{29}\) and expressed as the percentage in the lesional area.

CD34 labeled vessels were counted in each HPF.

**Statistics**

The statistical analyses were carried out using IBM SPSS 25. First, Shapiro Wilk test was used to check whether the data were normally distributed, both in the total cohort and when dividing the cases by treatment group. Next, we compared the histopathological features in the three groups (group 1: no CHT, group 2: IAC, and group 3: S-CHT). We used the Kruskal Wallis test to compare continuous variables across the three groups. Spearman’s correlation coefficient was used to study the correlation between clinicopathological variables and TME components. We tested the correlation between TME components and the single HHRFs with Kruskal-Wallis test.

**RESULTS**

**Clinicopathological Features**

The main clinicopathological data of the final cohort of 94 RBs are shown in Table 3.

**Group 1 (Primary RBs; $n = 44$)**

Pathological stage was pT3 to pT4 in 59.1% of the cases. International Classification of Retinoblastoma (ICRB) groups D and E constituted 81.8% of the cases. At histology, most cases showed a diffuse proliferation of small blue cells, with frequent mitoses, admixed to necrosis and calcifications, without or with occasional Homer Wright or Flexner-Wintersteiner rosettes. Large, hyperchromatic, and pleomorphic nuclei were also observed in a number of cases. In two eyes, retinocytoma-like areas were seen.

A high (G3-G4) histological grade and a high (3-4) anaplasia grade were assigned to 77.3% and 63.6% of cases, respectively. One or more HHRFs were found in 28 (63.6%) cases.
Two patients died; in both cases, RB infiltrated the transected end of the optic nerve, leading to extraocular tumor spreading.

**Group 2 (IAC Chemoreduced RBs; \( n = 33 \))**

Pathological stage was pT3–4 in 15.15% of the cases. ICRB groups D and E constituted 57.6% of the cases. In most cases, gliotic areas and calcifications largely replaced RB tissue, in which rosettes were variably found. Retinocytoma-like areas were observed in 11 cases (33.3%). In two of which RB was virtually absent. Highly pleomorphic RB areas were not observed. A high (G3) histological grade and a high (3) anaplasia grade were assigned to 52.9% and 35.3% of cases, respectively. One or more HHRFs were found in seven (41.2%) cases. At the last follow-up, no patients died of the disease

**Retinoblastoma Microenvironment Features**

In group 1, in most cases, all TI-ICs subsets were sparse and found in perivascular region and nearby necrotic areas (Figs. 1A, 1B, 1G). Most of them were macrophages. Ki67+ nuclei was observed. Both PD-L1 and PD-1+ positivity increased in retinal areas closest to RB. In 9 cases (20.5%), a patchy, weak-to-moderate-to-strong PD-1 immunopositivity was observed in RB cells (Fig. 5C-D). In five cases, TI-ICs were easily observed, mostly within large GFAP+ and mCHI+ gliotic areas,
partly merging with retinocytoma-like areas. In these cases, KI67 positivity was low.

CD34 stained the endothelium of thin-walled, regularly-shaped vessels, usually surrounded by aggregates of viable RB cells.

In group 2, in 32 cases (96.96%), heterogeneously distributed TI-ICs were easily found, most frequently in gliotic areas (Fig. 1C). CD8+ lymphocytes usually coexpressed TIA-1 (Figs. 5A, 5B). PD-L1 colocalized with GFAP in glial cells (Figs. 6A–6E). TI-ICs were also found admixed with RB cells. One case had large areas of viable RB cells, few TI-ICs, and high KI67 proliferative index and showed limited GFAP+ and PD-L1+ areas. In eight cases (24.2%), a patchy, weak-to moderate-to strong PD-1 immunopositivity was observed in RB cells (Figs. 5A, 5B).

In group 3, there were numerous heterogeneously distributed TI-ICs (Figs. 1D, 1E, 1F, 1H), mainly in gliotic areas and mixed with RB cells. Coexpression of GFAP and PD-L1 was observed (Figs. 6F–6J). Three cases (17.6%) showed a heterogeneous, patchy, weak-to moderate-to strong immunopositivity to PD-1 in RB cells (Figs. 5E, 5F).

TI-ICs were also observed in normal ocular structures in all chemoreduced RBs, mainly within the choroid.

In both groups 2 and 3, KI67 positivity was heterogeneous, high in RB viable cells, and low in retinocytoma-like areas and in gliotic areas (Figs. 4C, 4D). In both groups 2 and 3, CD34-positive, thin-walled, regularly-shaped vessels were observed within RB tissue and gliotic areas.

In all groups, no coexpression of CD8 and PD-1 was found.

Statistics

The median and range of values for each parameter are reported in Table 4. Data were not normally distributed (see Supplementary Tables S1 and S2); therefore we used nonparametric testing for the subsequent analyses.

As shown in Table 4, patient age was significantly lower in group 1 than in group 2 but there was no significant difference between groups 1 and 3 nor between groups 2 and 3. The number of cells expressing CD4, CD8, granzyme B, TIA-1, CD1a/S100, CD68 and CD163 was significantly higher in group 2 and group 3 cases compared to group 1 cases, as were GFAP and PDL1 positivity, but there was no significant difference between the two groups that received chemotherapy (groups 2 and 3). The proliferation index KI67, on the contrary, was significantly higher in group 1 than in groups 2 and 3. The number of PD1+ cells was significantly higher in group 2 compared to group 1, but there was no significant difference between groups 1 and 3 nor between groups 2 and 3. CD11b+/CD14+/CD15+ cells were significantly less in group 2 compared to group 1, but no significant difference was found between groups 1 and 3 nor between groups 2 and 3. The number of cells expressing CD20 and FOXP3 and the number of CD34+ vessels did not
FIGURE 2. GFAP (green) and PD-L1 (red) double immunofluorescence in a group 1 RB showing regression. Nuclei are stained blue with DAPI. GFAP (green) and PD-L1 (red) positivity colocalize within a gliotic area (arrows). Perivascular glial cells (asterisks in the vessel lumen) and glial cells in the retina show colocalization of GFAP and PD-L1 as well. Nuclei (blue) of PD-L1-negative viable RB cells are recognizable within the gliotic area (arrows) and infiltrating the retina. Merge images in the box at the top (GFAP and PD-L1), on the right and in the bottom box (GFAP, PD-L1, and DAPI). Magnification $\times$ 200. Immunofluorescence: Fluorescein isothiocyanate, green; Rhodamine, red; DAPI, blue secondary fluorochrome–conjugated antibody (goat anti-rabbit Alexa Fluor 488 [green], goat anti-mouse Alexa Fluor 568 [red]).

show any significant difference among the groups. Figure 7 shows the distribution of the parameters across the three groups.

When considering clinicopathological factors, group 1 cases more frequently had HHRFs and a higher AG-M than group 2 and group 3 cases (Table 5).

The presence of HHRFs (Table 6) is directly correlated with CD11b+/CD14−/CD15+ ($P = 0.007$) and Ki67 ($P = 0.004$), that were higher in group 1, whereas it was inversely correlated with CD8+ ($P = 0.03$), granzyme B+ ($P = 0.04$), TIA-1+ (0.05), GFAP% ($P = 0.008$) and PD-L1% (0.01), that were lower in group 1. Similarly, a higher AG-M was directly correlated with FOXP3+ ($P < 0.001$), CD11b+/CD14−/CD15+ ($P = 0.03$), and Ki67% ($P < 0.001$), whereas it was inversely correlated with CD4+ ($P = 0.02$), CD8+ ($P < 0.001$), granzyme B+ ($P < 0.001$), TIA-1+ ($P < 0.001$), CD1a+/S100+ ($P < 0.001$), CD68+ ($P < 0.001$), CD163+ ($P < 0.001$), GFAP% ($P < 0.001$), PD-L1+ ($P = 0.03$), and PD-L1% ($P < 0.001$). Considering the HHRFs individually, none of them showed a statistically significant correlation with TME factors (data not shown).

**DISCUSSION**

Chemotherapy induces RB regression, and RBs may rarely regress spontaneously as well. Ophthalmoscopy and imaging give a reliable estimate of the histopathology and degree of regression.30–37 Upon regression, RB becomes smaller and shows calcifications. Changes in the TME of regressed RB are largely unknown.

In untreated RBs (group 1), we appreciated very few TI-ICs in most cases. Conversely, a large number of TI-ICs was observed in 49 of 50 chemoreduced RBs and in five group 1 cases that showed spontaneous regression.

The immune response and the number of TI-ICs within a tumor largely depend on its immunogenicity.4 RB is a poorly immunogenic neoplasm, which may justify its low frequency of TI-ICs.8,38 Immunogenicity is also associated with response to i-CP blockade.39 Immunologically “hot/inflamed,” “warm,” and “cold/non-inflamed” tumor histologic specimens based on tumor-infiltrating lymphocyte density and PD-L1 expression have been correlated to different therapy responses.6,7
Untreated RBs Differ From CHT-Treated RBs in the Frequency of TI-ICs

In regressed RB, the frequency of almost all TI-ICs increased significantly, suggesting a complex involvement of TI-ICs. A robust response of antitumor T cells emerged, mainly supported by CD4+, CD8+, granzyme-b+, and TIA-1+ lymphocytes and macrophages, which are the main subsets responsible for the control of tumor growth. Both CD4+ and CD8+ cells can release interferon γ (IFN-γ), a main determinant of tumor regression.40,41 We registered an increase of TIA-1+ cells that outnumbered CD8+ cells; probably partly because of an increase of TIA-1+ natural killer (NK) cells, that we did not evaluate.

CHT, besides directly killing cancer cells, triggers immunogenic cell death. Apoptosis is induced by therapy in RB.42 However, the CHT-induced extracellular vesicles released by damaged cells can be either proimmune or immunosuppressive, depending on their content and on the TME.43 Intriguingly, melphalan-derived vesicles can cause the release of IFNγ by NK cells.44 This might have been a contributory mechanism to the increase in effector cells that we demonstrated in group 2 patients treated with melphalan. In our study, multiplexed immunostaining for TIA-1, CD8, and PD-1 showed that the majority of the CD8+ cells were also TIA-1+, whereas they did not express PD-1, which is an indicator of CD8 cell exhaustion.7,45 This immune profile identifies active CD8+ lymphocytes, which likely retain their effector properties, although more investigations are mandatory to better profile their functionality.

S-100+CD1a+ dendritic-like cells were sparse in group 1 and increased significantly in chemoreduced RBs. After CHT, we observed a significant increase in CD68+ and CD163+ macrophages as well. M1 (proinflammatory/tumoricidal) and M2 (anti-inflammatory/protumorigenic) macrophages express a functional state and can switch between phenotypes, depending on the context.4 In humans, however, CD163 is still considered a marker of M2 macrophages, which are correlated with upregulated PD-L1 in cancer.46 Their re-education is the aim of novel immunotherapy, and the concomitant i-CP blockade was demonstrated to yield a synergistic effect.46
FIGURE 4. (A, B) Conventional immunohistochemistry for PD-L1: A representative case of group 1 RB, almost completely negative for PD-L1 (A). PD-L1 positivity is limited to few RB cells within necrotic areas (B, asterisk), and in perivascular areas. (C, D) Ki67 (red) and PD-L1 (brown) double immunohistochemistry in a group 3 chemoreduced RB. Note the heterogeneous frequency of Ki67+ nuclei, high in viable RB cells on the left (D) and very low within a PD-L1+ (white asterisk) gliotic area blending with a retinocytoma-like area (black asterisk), which also shows few Ki67+ nuclei (D). Magnification: A, C: ×1; B: ×200; D: ×400.

FIGURE 5. (A, B) Multiplexed immunohistochemistry for PD-1 (brown), CD8 (blue), and TIA-1 (red). Representative case of group 2 patients. (A) Inflammatory infiltrate (on the left) and an area of viable RB tissue (asterisk). (B) Detail showing brown-stained, PD-1+ RB cells on the right, and CD8+ blue-stained lymphocytes on the left; most CD8+ lymphocytes co-express TIA-1 (red, granular stain); red cytotoxic granules are also detectable admixed with RB cells. (C, D, E, F) Conventional immunohistochemistry for PD-1. (C) A group 1 RB expressing high PD-1; PD-1 positivity is also observable within the retina (asterisk). (D) Detail of PD-1 cytoplasmic positivity of RB cells. (E) A group 3 RB at scanning power; the arrow indicates an area of viable RB tissue showing PD-1 cytoplasmic positivity (F). Magnification: A: ×200; B, D, F: ×400; C: ×100; E: ×1. The red chromogen new fuchsin, the brown chromogen diaminobenzidine and the blue chromogen HighDef Blue were used.
FIGURE 6. (A, B, F, G) Multiplexed immunohistochemistry for synaptophysin (blue); GFAP (red), and PD-L1 (brown). (C–E, H–J) Immunofluorescence for PD-L1 (red) and GFAP (green) (A) Representative case of group 2 patients; viable RB tumor cells (blue) identified by positivity to synaptophysin, admixed with glial cells. (B) Detail of glial cells coexpressing GFAP (red) and PD-L1 (brown). (C–E) Immunofluorescence for PD-L1 (C, red) and GFAP (D, green) in a gliotic area of another case of group 2 RB. Merge image (E) shows extensive colocalization of PD-L1 and GFAP and DAPI-stained RB nuclei (blue). (F, G) Multiplexed immunohistochemistry for GFAP (red) and PD-L1 (brown) in a RB of group 3. The detail (G) shows coexpression of GFAP and PD-L1 within a gliotic area; the asterisk indicates viable RB cells virtually negative to PD-L1. (H–J) Immunofluorescence for PD-L1 (H, red) and GFAP (I, green) in the same case. In the merge image (J), GFAP colocalizes with PD-L1. Magnification: A,B,F,G: ×400; C–E, H–J: ×200.
CD34
PD-L1
PD-1
GFAP
CD11b
CD163
CD1a
CD20
FOXP3
TIA-1
Granzyme B

The inhibition of antitumor immunity in other cancers.4,48
gliosis.
which may contribute to the negative prognostic impact of

We observed that gliotic areas strongly expressed PD-L1,
and degree of anaplasia, bearing an impact on prognosis.
ated with some pathological determinants of metastatic risk
frequency was low and did not change after CHT.

al.18 reported an increased expression of PD-L1 and PD-

exert multiple immunosuppressive functions.4 Their iden-

Myeloid-derived suppressor cells (MDSCs), subdivided
into monocytic (Mo-MDSCs, CD11b+ CD14+ CD15+) and
granulocytic (G-MDSCs, CD11b+ CD14+CD15+) subsets, exert
multiple immunosuppressive functions.4 Their identifi-
cation by immunohistochemistry is complex.4 The term
MDSC-like is therefore recommended.4

We found few G-MDS-like cells in all groups; however,
their frequency decreased significantly in group 2.

CHT-Does Not Affect the Frequency of
FOXp3+ Tregs and CD20+ Lymphocytes

Tregs, reliably identified by FOXP3 staining,47 are crucial in
the inhibition of antitumor immunity in other cancers.4,48
They were sparse in the cold TME of group 1 RB, and did
not vary in regressed RBs; however, their positive correlation
with AG-M, suggests a possible role in RB as well.
The multiple functions of CD20+ lymphocytes within
TME are starting to be unraveled.49 In all our cases, their
frequency was low and did not change after CHT.

CHT-Treated RBs Differ From Untreated RBs in
the Extent of Gliosis, PD-1+ TI-ICs and PD-L1
Expression: RB Cells Express PD-1

In treated RBs, we observed a significantly higher gliosis
than in untreated cases. Gliosis was high in five sponta-
neously regressed group 1 RBs as well.

In a previous study, a poor prognostic impact was
associated to gliosis, because of its production of the
insulin-like growth factor protein–5,13 Recently, Singh et
al.48 reported an increased expression of PD-L1 and PD-
1 in stromal/immune cells and a decreased expression
of PD-L1 and an increased expression of PD-1 in RB
cells after chemoreduction.50 These factors were associ-
ated with some pathological determinants of metastatic risk
and degree of anaplasia, bearing an impact on prognosis.
We observed that gliotic areas strongly expressed PD-L1,
which may contribute to the negative prognostic impact of
gliosis.

These data indicate that PD-L1 and PD-1 may be suitable
candidates for immunotherapy in RB. Recently, the expres-
sion of B7H3, another member of the B7 family, showed
correlation with clinical and pathological data in RB.59 The
B7 family therefore deserves further study in RB.
The assessment of PD-L1 expression in cancer by
immunohistochemistry is standardized and is the most
common method to predict anti-PD-1/anti-PD-L1 therapeu-
tic response across different cancers.29,50–52

PD-1 is constitutively expressed by activated T lympho-
cytes and macrophages and by other TI-ICs after cytokine
stimuli.53 Binding of PD-1 to PD-L1 inhibits T-cell activation,
allowing immunosuppression and neoplastic growth.
Blockade of this interaction has yielded therapeutic benefits
in many patients.55 In our cases, the frequency of PD-1+ TI-
ICs was not very high, but it increased significantly in groups
2 and 3.

PD-L1 expression in cancer can be influenced by many
intracellular and extracellular signals.50 PD-L1 expression
may be induced by IFN-γ52; this mechanism, documented
also in a RB cell line,56 may have occurred in group 2
patients, who received melphalan therapy, which is known
to induce release of IFNγ.44

We did not observe colocalization of CD8 and PD-1; fur-
thermore, CD8+ cells largely exceeded the number of
PD-1+ TI-IC in all three groups.

As recently observed by Singh et al.,20 we found RB cells
expressing PD-1 to a variable extent, with a similar incidence
across the three groups (20.5% cases of group 1 and 20.8% in
all chemoreduced RBs).

Nowadays the targets of PD-1 inhibitors are lymphocytes
and not cancer cells; PD1+ tumor cells could be an inter-
esting future therapy candidate.

CHT Turns RB TME From Cold (Immune Type II)
To Hot (Immune Type I)

The composition, the functionality, and the spatial disposi-
tion of the immune infiltrate, which vary across different
cancer types, identify different subclasses of TME for

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Group 1</th>
<th>Group 2</th>
<th>Group 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>Median</td>
<td>Range</td>
<td>Median</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CD4+</td>
<td>24</td>
<td>2–88</td>
<td>1.9</td>
</tr>
<tr>
<td>CD8+</td>
<td>0.8</td>
<td>0.2–46.5</td>
<td>0.1</td>
</tr>
<tr>
<td>Granzyme B+</td>
<td>0.0</td>
<td>0–3.5</td>
<td>0.5</td>
</tr>
<tr>
<td>TIA-1+</td>
<td>0.5</td>
<td>0–3.6</td>
<td>1</td>
</tr>
<tr>
<td>FOXP3+</td>
<td>0.5</td>
<td>0–4.7</td>
<td>0.5</td>
</tr>
<tr>
<td>CD14+</td>
<td>0.4</td>
<td>0–4.7</td>
<td>0.4</td>
</tr>
<tr>
<td>CD68+</td>
<td>12.4</td>
<td>5.7–72.9</td>
<td>12.4</td>
</tr>
<tr>
<td>CD163+</td>
<td>8.4</td>
<td>5–108.3</td>
<td>8.4</td>
</tr>
<tr>
<td>CD11b+/CD14−/CD15+</td>
<td>2.2</td>
<td>0.3–12.4</td>
<td>2.2</td>
</tr>
<tr>
<td>Ki67+6%</td>
<td>10.5</td>
<td>3.1–47.5</td>
<td>10.5</td>
</tr>
<tr>
<td>GPAP+</td>
<td>1.2</td>
<td>0.3–20</td>
<td>1.2</td>
</tr>
<tr>
<td>PD-1+</td>
<td>0.0</td>
<td>0–28.3</td>
<td>0.0</td>
</tr>
<tr>
<td>CD34+</td>
<td>5.2</td>
<td>0.3–12.4</td>
<td>5.2</td>
</tr>
</tbody>
</table>

Group 1, no CHT; Group 2, IAC; Group 3, S-CHT.
ns, not significant.
Figure 7. Distribution values of CD4+, CD8+, Granzyme B+ and TIA-1+ lymphocytes, and percentage of GFAP+ and PD-L1+ areas across the three treatment groups.

Table 5. Distribution of Histopathological Factors Across Treatment Groups

<table>
<thead>
<tr>
<th>Histopathological Factors</th>
<th>Group 1 (n = 44)</th>
<th>Group 2 (n = 33)</th>
<th>Group 3 (n = 17)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HHRF*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Absent</td>
<td>16 (36)</td>
<td>24 (73)</td>
<td>10 (58)</td>
</tr>
<tr>
<td>Present</td>
<td>28 (64)</td>
<td>9 (27)</td>
<td>7 (41)</td>
</tr>
<tr>
<td>Anaplasia grade*</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Retinocytoma</td>
<td>0 (0)</td>
<td>2 (6)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Mild</td>
<td>16 (36)</td>
<td>24 (73)</td>
<td>11 (65)</td>
</tr>
<tr>
<td>Moderate</td>
<td>23 (52)</td>
<td>7 (21)</td>
<td>6 (35)</td>
</tr>
<tr>
<td>Severe</td>
<td>5 (11)</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
</tbody>
</table>

* Number (percentage)
CD34
PD-L1
PD-1
GFAP
Ki67
CD11b
RB,57 as observed also by us.58 Moreover, the combination of RB TME, from type II (cold) to type I (hot), suggests that CHT-induced type I immune signature (high CD8+); TIA-1+; PD-L1−) was accompanied by a reprogrammed functionally excluded TI-ICs with PD-L1 immunonegativity and a high AG-M.

In Group 1, the majority of cases (n = 39 [88.6%]) showed a cold TME (CD8+; PD-L1−), which was positively correlated with the presence of HHRFs and high AG-M.

Conversely, 49 of 50 (98%) chemoreduced RBs showed an active immune signature (high CD8+; TIA-1+; PD-L1+), which was negatively correlated with the presence of HHRFs and a high AG-M.

In our experience, RB regression, either spontaneous or induced by CHT, was accompanied by a reprogrammed RB TME, from type II (cold) to type I (hot), suggesting a novel immunotherapeutic scenario. Immunotherapy combined with CHT could allow less-intensive treatment regimens. Epigenetic promoter hypermethylation occurs in RB,55–57 as observed also by us.58 Moreover, the combination of hypomethylating and immunomodulatory agents is yielding promising results in cancer, as we observed in unresectable melanoma.59–61

**CONCLUSIONS**

The perspective of modulating the immune response in RB for therapeutic purposes is interesting. Immunotherapy requires knowledge of the TME components, their multifaceted functions and spatial distribution, for which multiplexed analyses at tumor tissue level are very informative. In our experience, all regressed RBs showed TME changes in a similar manner; correlative studies between next-generation imaging and TME could better profile cohorts of patients for novel treatments.

**Acknowledgments**

The authors thank Marzio Vestri for his technical support. We also acknowledge the contributions of ASROO, scientific society of Retinoblastoma and Ocular Oncology.

**References**


