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Emerging biomarkers for the combination of radiotherapy and immune checkpoint blockers

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Abstract

Over the past few years, multiple immune checkpoint blockers (ICBs) have achieved unprecedented clinical success and have been approved by regulatory agencies for the treatment of an increasing number of malignancies. However, only a limited fraction of patients responds to ICBs employed as a standalone intervention, calling for the development of combinatorial regimens. Radiation therapy (RT) stands out as a very promising candidate for this purpose. Indeed, RT mediates antineoplastic effects not only by cytotoxic and cytostatic mechanisms, but also by modulating immunological functions, both locally (within the irradiated field) and systemically. As combinatorial regimens involving RT and ICBs are being developed and clinically tested at an accelerating pace, it is paramount to identify biomarkers that reliably predict the likelihood of individual patients to respond. Here, we discuss emerging biomarkers that may potentially predict the response of cancer patients to RT plus ICBs.

Keywords

DNA damage response; mutational load; natural killer cells; PD-L1; type I interferon

Introduction

Over the past decade, cancer immunotherapy has gone all the way from a promising preclinical application to a clinical reality [1, 2]. In particular, immune checkpoint blockers (ICBs) have been shown to induce durable clinical responses in individuals affected by a variety tumors, resulting in the approval of six ICBs for use in cancer patients by the US Food and Drug Administration (FDA) and other regulatory agencies worldwide [3, 4].

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However, the percentage of patients obtaining clinical benefits from any ICBs employed as single immunotherapeutic interventions is relatively low (15–30%), calling for the development of novel combinatorial regimens. Combining distinct ICBs has been shown to ameliorate overall response rates in some oncological indications, but this is associated with increased toxicity [5, 6]. Similarly, chemotherapy and targeted anticancer agents can synergize with ICBs in some settings, but side effects can also be considerable [7]. Radiation therapy (RT) is a particularly promising candidate for combination with ICB, for at least three reasons [8]. First, RT has been universally used to treat patients for more than a century and its effectiveness is well established. Second, RT is an accessible and relatively economical procedure associated with limited and manageable side effects, reflecting the extensive knowledge about its use. Third, it is now clear that – besides mediating cytotoxic and cytostatic effects on malignant cells – RT has multipronged immunomodulatory effects. Such effects, which emerge locally (within the irradiated field) but may have systemic impact, can be harnessed to boost the therapeutic activity of ICBs [9] (Figure 1).

RT increases the antigenicity of malignant cells by promoting the upregulation of MHC class I molecules on the cell surface [10, 11], by favoring the expression of tumor-associated antigens [12], and (at least potentially) by enhancing genetic instability or reactivating endogenous retroviruses [13, 14]. Moreover, RT boosts the adjuvanticity of cancer cells by at least two mechanisms. On the one hand, cancer cells surviving irradiation expose increased amounts of (1) immunostimulatory ligands for killer cell lectin like receptor K1 (KLRK1; best known as NKG2D), hence favoring natural killer (NK) cell activation [15, 16]; (2) co-stimulatory molecules such as TNF receptor superfamily member 9 (TNFSF4; best known as OX40L) and TNFSF9 (best known as CD137 or 4-1BB) [17]; and (3) death receptors such as Fas cell surface death receptor (FAS), resulting in increased susceptibility to lysis by immune effector cells [18]. On the other hand, neoplastic cells succumbing to irradiation emit several danger-associated molecular patterns that favor the activation of a tumor-specific immune response [19]. Such an immunogenic cell death modality relies, amongst multiple factors, on the timely release of type I interferon (IFN) [20, 21], which enables clinically relevant abscopal responses [22, 23]. Finally, RT can directly affect stromal cells, endothelial cells as well as multiple components of the immunological tumor infiltrate [24]. A detailed description of the immunobiology of RT goes beyond the scope of the current review, and can be accessed in other publications [9, 24]. However, it is important to mention that cytosolic nucleic acid sensing has recently been shown to play a major role in the immunogenicity of RT as it connects the DNA damage response (DDR) to innate and adaptive immunity [21, 25–27]. Moreover, dose and fractionation seem to have a major impact on the ability of RT to drive immunological tumor rejection. For instance, hypofractionated RT appears to mediate superior immunostimulatory effects when compared to RT administered in single ablative doses, at least in part owing to robust type I IFN responses [21, 28]. Similarly, the effects of radiation on the vascular endothelium are dosedependent, with doses above 8 Gy resulting in endothelial apoptosis that can contribute to clinical responses [29] Conversely, endothelial activation, which enables tumor infiltration by immune cells, has been observed at low radiation doses (0.5–2 Gy) [30]. Thus, considerable attention should be given to radiation dose and schedule when combinatorial regimens are conceived.

It has been proposed that RT can be harnessed as an *in situ* vaccine to generate a systemic antitumor response that sensitizes ICB-resistant tumors to treatment [8]. Although several clinical trials are ongoing to investigate the potential synergy between RT and ICBs (as well as other forms of immunotherapy) [31, 32], the understanding of the molecular, cellular and systemic effects of these treatments when used in combination is still evolving. Similarly, accurate predictions of the likelihood of individual patients to respond to RT plus

immunotherapy remain elusive. Here, we discuss preclinical and clinical data on emerging biomarkers that could be prospectively evaluated for their potential to predict efficacy when RT is combined with ICBs or other forms of immunotherapy.

Predictive biomarkers of response to RT

Over the past century, accrued scientific understanding of the mechanisms underlying the effects of radiotherapy on cancer and normal tissues has resulted in well established protocols of treatment that both optimize tumor control and limit normal tissue toxicitities. While most fatal recurrences are systemic, some patients recur at the primary tumor site, in the absence of detectable systemic recurrence. These isolated "in field" recurrences have elicited extensive interest among radiation biologists.

Preclinical models have demonstrated that radioresistant neoplastic cells are indeed less susceptible to the induction of cellular senescence and regulated cell death (RCD) by RT than their radiosensitive counterparts. Similar to chemoresistance [33], radioresistance can be innate or acquired, and can originate from molecular alterations in a plethora of cellular processes involved in the biological response to radiation [34]. For a comprehensive discussion of biomarkers for predicting clinical responses to RT, we refer the reader to a special issue of *Seminars in Radiation Oncology* devoted to this topic [35]. Here, we will briefly discuss four main types of biomarkers that have been associated with predictive value for response to RT: (1) components of the DDR machinery, (2) genetic and (3) epigenetic signatures of radioresistance; and (4) microenvironmental biomarkers, focusing on factors that have been also shown to affect responses to imunotherapy.

DDR-related biomarkers

Although numerous DNA-damaging agents are routinely used in the clinical management of a variety of tumors, few biomarkers are available to identify potential responders to RT within patient populations and/or to guide decision making with respect to dose and administration schedule [35]. ATM serine/threonine kinase (ATM) plays a basic role in the DDR to double-strand breaks (DSBs) [36]. Levels of MRE11 homolog, double strand break repair nuclease (MRE11), a component of the heterotrimeric complex that initiates ATM signaling at DSBs caused by RT [37], regulate the initiation of DDR-driven apoptosis when DNA damage is irreparable [38]. Consistently, individuals with muscle-invasive bladder carcinoma expressing high levels of MRE11 exhibited superior cancer-specific survival following RT as compared to patients bearing MRE11^{low} tumors [39, 40]. Along similar lines, variations in the copy number of nibrin (*NBN*, which encodes another component of the MRE11-containing complex that recognizes DSBs) have been shown to influence the likelihood of response to RT. In particular, *NBN* copy gains were a reliable predictor of

biochemical relapse-free survival rates at 5 years among 139 localized prostate cancer patients treated with image-guided RT, while the same marker had no predictive value among men treated by radical prostatectomy [41]. Moreover, a combined assessment of the phosphorylation status of checkpoint kinase 1 (CHEK1), the expression level of tumor protein p53 (TP53; best known as p53), and their subcellular localization (CHEK1 and p53 are critical transducers of the DDR initiated by single-strand breaks) was associated with early local recurrence in a large cohort of >900 breast cancer patients receiving adjuvant RT [42]. Interestingly, markers of an ongoing DDR such as the phosphorylation of H2A histone family member X (H2AFX; best known as H2AX) have been detected in circulating tumor cells (CTCs) from non-small cell lung carcinoma (NSCLC) patients undergoing RT [43]. However, whether DDR in CTCs has any prognostic or predictive value remains to be elucidated. Furthermore, it has recently been proposed that the well-established link between human papillomavirus (HPV) positivity and improved responses to RT amongst head and neck squamous cell carcinoma patients [44–46] may reflect the ability of cyclin dependent kinase inhibitor 2A (CDKN2A) - which is upregulated upon HPV infection - to inhibit the DDR [47]. That said, the abundance of MRE11 had no predictive value in a cohort of patients with squamous cell carcinomas of the anus treated with RT in combination with chemotherapy and did not add to the prognostic value of p16 (a marker for HPV) and tumour-infiltrating lymphocyte scores [48]. Moreover, even though the molecular pathways linking RT-driven DNA damage to cellular senescence or RCD have been extensively characterized in preclinical models [49, 50] and at least in part confirmed in the clinical, the actual predictive value of other components of the DDR machinery for cancer patients remains unknown.

Genetic signatures

A signature encompassing 31 genes involved in cell cycle regulation, DNA replication, and cell-to-cell interaction identified by analyzing the radiosensitivity of the NCI-60 cancer cell panel [51] was associated with prognostic and predictive value in two distinct cohorts of 276 and 463 irradiated glioma patients, from the Gene Expression Omnibus (GEO) and The Cancer Genome Atlas (TCGA), respectively [52]. However, the actual predictive (rather than prognostic) value of this signature remains to be validated in prospective randomized clinical trials. An IFN-related DNA damage resistance signature (IRDS) involving the analysis of seven gene pairs has been proposed as a predictive biomarker for radiosensitivity, based on data from 295 breast cancer patients receiving adjuvant chemoradiation [53, 54]. Individual with IRDS⁺ lesions exhibited inferior locoregional control after adjuvant chemotherapy and RT as compared to patients bearing IRDS⁻ lesions [54]. Similar observations were obtained in cohorts of breast patients receiving either adjuvant chemotherapy or RT [54]. Conversely, IRDS had no prognostic value amongst patients undergoing endocrine therapy or no additional therapy [54]. Importantly, although this signature partially assesses the radiosensitivity of malignant cells (three of the seven genes are directly involved in the DDR), it also interrogates IFN pathways, which are intimately involved in anticancer immunity [55]. Finally, a gene-expression-based radiosensitivity index and the linear quadratic model have been harnessed to generate a genomic-adjusted radiation dose (GARD) based on 8271 tissue samples from the Total Cancer Care cohort [56]. In multivariable analysis, GARD was independently associated with disease outcome in five

distinct cohorts of breast (n=263 and n=77), lung (n=60) and pancreas (n=40) and glioblastoma (n=98) patients analyzed retrospectively [56]. Specifically, breast cancer patients with high GARD values exhibited significantly improved metastasis-free survival at 5-year follow-up when compared to patients with low GARD values [56]. Whether the IRDS or GARD has predictive value for patients prospectively treated with RT plus immunotherapy remains to be defined (see below).

Epigenetic signatures

microRNAs regulate a plethora of cellular processes potentially involved in radiosensitivity, including (but not limited to) cell growth and metabolism, differentiation, cell cycle control, autophagy, RCD and the DDR [57-60]. Preclinical investigation in this area unveiled the ability of multiple microRNAs including (but not limited to) miR-17-92 [61], miR-34 [62, 63], miR-145 [64, 65], miR-205 [66], miR-300 [67], miR-338-5p [68] to influence the radiosensitivity of malignant cells of various origin, in vitro and/or in vivo. For instance, low plasma circulating levels of miR-145 were significantly associated with poor differentiation, lymph node invasion and poor clinical outcome in a cohort of 120 cervical cancer patients [69]. A logistic regression model based on the levels of miR-9 and miR-200a generated on a training cohort of 60 cervical cancer patients receiving standard chemoradiation had robust predictive value when validated in a cohort of 42 similar patients [70]. Likewise, specific epigenetic profiles simultaneously assessing the expression of multiple (up to several dozens) different microRNA have been associated with improved responses to adjuvant chemoradiation in cohorts of individuals affected by glioblastoma [71] and colorectal carcinoma [72–74]. However, the actual predictive (over prognostic) value of these signatures cannot be discerned from most of these studies. In addition, standard-of-care regimens often combine chemotherapy with RT, making it impossible to isolate the effects of radiation.

Microenvironmental biomarkers

Multiple variables of the tumor microenvironment have been shown to influence the likelihood of cancer patients to respond to RT. Hypoxia is perhaps the best-characterized of these biomarkers [75]. Indicators of hypoxia such as the expression levels of hypoxia inducible factor 1 alpha subunit (HIF1A) or solute carrier family 2 member 1 (SLC2A1; best known as GLUT1) as well as pimonidazole reactivity [76] have been retrospectively associated with poor disease outcome in multiple cohorts of patients receiving RT [77-80]. Indeed, hypoxic malignant cells are known to exhibit reduced radiosensitivity, reflecting (at least in part) the fact that the damage inflicted to macromolecules by RT involves the formation of reactive oxygen species. Most importantly, chronic hypoxia leads to major changes in the metabolism and phenotype of cancer and stromal cells, promoting metastatic dissemination and immunosuppression [81, 82]. Some of the immunosuppressive effects of hypoxia are mediated by HIF1A-dependent transactivation of vascular endothelial growth factor A (VEGFA), which induces CD4⁺CD25⁺FOXP3⁺ regulatory T (T_{reg}) cells and myeloid-derived suppressor cells (MDSCs) in the tumor microenvironment [83]. Conversly, growing evidence indicates that a favorable immunological infiltrate, with high intratumoral levels of CD8⁺ cytotoxic T lymphocytes (CTLs) and/or limited infiltration by T_{reg} cells predicts clinical responses to multiple therapeutic interventions, including radiotherapy [19,

84, 85]. For instance, an abundant lymphocytic tumor infiltrate has been associated with improved disease outcome amongst patients with triple negative breast cancer treated in studies of adjuvant doxorubicin-based chemotherapy or carboplatin plus accelerated radiotherapy [86, 87].

The so-called immunoscore has been linked to superior disease outcome amongst 55 colorectal cancer patients receiving neoadjuvant chemoradiation [88], as well as in a cohort of 116 patients with brain metastases including 81 individuals receiving whole-brain RT [89]. However, no data is available on the potential predictive value of the immunoscore in patients prospectively allocated to RT alone. Presently, neither the degree of hypoxia nor the abundance of one or more tumor-infiltrating immune cell populations is routinely used in the clinics to inform decision-making.

In summary, although the preclinical literature on the radiobiological determinants of response to RT is abundant, the current individualization of RT mainly reflects subjective anatomical differences that inform the geometric and physical alignment of the radiation beams. Radiation field configuration, dose and fractionation often have empirically developed as a compromise between optimal local disease control and recoverable toxicity of irradiated normal tissue, with little inclusion of biological diversity across a specific tumor site, with the notable exception of HPV status for head and neck cancers [90], and 1p/19q co-deletion in glioma, which defines tumors with a favorable prognosis and improved responses to chemotherapy that do not need RT [91, 92].

Predictive biomarkers of response to ICBs

ICBs can be associated with significant toxicity, which in some cases calls for treatment discontinuation, and are considerably more expensive than most standard treatments [5, 93]. Moeover reponses to ICBs often develop slowly, and many patients with an initial reponse eventually progress. Thus, over the past few years extraordinary efforts have been devoted to the identification of predictive markers of response, some of which are already employed in clinical settings for decision making [94].

Tumor biomarkers

The expression of the immunosuppressive molecule CD274 (best known as PD-L1) on the surface of malignant cells has been investigated as a potential biomarker of responses to ICBs targeting PD-L1 itself or its receptor programmed cell death 1 (PDCD1; best known as PD-1) since the early development of these agents. Malignant cells from different origin (and associated stromal cells) express indeed high levels of PD-L1, which turns off effector T cells and NK cells in a PD-1-dependent manner [95]. Thus, high PD-L1 expression is often responsible for resistance to immunological tumor rejection. Loss of phosphatase and tensin homolog (*PTEN*) – one of the most common oncogenic events across all human neoplasms – has been shown to favor PD-L1 expression and hence resistance to ICBs [96]. Topalian *et al.* were the first to show a relationship between clinical responses to a PD-1-targeting ICB and PD-L1 expression levels assessed by immunohistochemistry (IHC) [97]. In particular, 9 out of 25 patients (36%) with PD-L1⁺ tumors responded to the anti-PD-1 agent nivolumab (which is currently approved for the treatment of multiple tumors) [4],

while 0 out of 17 patients with PD-L1⁻ tumors did so [97]. A number of clinical trials reported thereafter confirmed a trend for superior response rates to PD-1 blockers amongst patients with PD-L1⁺ tumors [98–101]. However, the thresholds employed in these studies to define PD-L1 positivity exhibited considerable degree of variation (ranging from 1% to 50% malignant cells with membranous PD-L1 staining). Moreover: (1) some patients with low or even absent PD-L1 expression appear to benefit from immunotherapy with ICBs [99]; and (2) PD-L1 expression levels vary over a wide dynamic range [102]. Thus, the dichotomous stratification of cancer patients based on PD-L1 expression levels may not be the most appropriate approach to predict clinical responses to PD-1-targeting ICBs. Irrespective of this possibility, one immunohistochemical test to assess PD-L1 expression in bioptic material (PD-L1 22C3 pharmDx, from Dako) is currently approved by FDA as a companion diagnostic to assign NSCLC patients to treatment with the anti-PD-1 agent pembrolizumab [103]. Three additional immunohistochemical assays are approved as complementary diagnostics to inform on risk versus benefit of treatment with nivolumab in patients with non-squamous NSCLC and melanoma (PD-L1 28-8 pharmDx, from Dako) or treatment with atezolizumab or durvalumab (two FDA-approved ICB targeting PD-L1) in patients with metastatic urothelial cancer (PD-L1 SP142 and SP263 respectively, from Roche) [104]. As nowadays no less than 5 ICBs targeting PD-1 or PD-L1 are licensed by FDA and equivalent regulatory agencies for use in cancer patients [4], additional assays testing PD-L1 expression are expected to be available soon.

Another extensively investigated biomarker of clinical responses to ICBs is the tumor mutational load (*i.e.*, the number of non-germline, non-synonymous mutations per exome) [105]. These mutations have the capacity to generate tumor neoantigens, hence considerably boosting the antigenicity of malignant cells [105]. Several studies have demonstrated that a high mutational load is generally associated with an improved sensitivity of cancer patients to immunotherapy with ICBs [106–109]. That said, an increased burden of non-synonymous mutations (which can be assessed by whole-exome DNA sequencing of neoplastic material versus peripheral blood mononuclear cells) augments the likelihood, but does not necessarily result in the accumulation, of neoantigens. Nonetheless, the upstream mechanisms responsible for an increase in mutational burden currently represent the most promising biomarker to predict clinical responses to ICBs [110]. In particular, defects in the molecular machinery that ensures DNA integrity and high-fidelity transmission confer exquisite sendsitivity to ICB therapy. Mismatch repair (MMR) status predicted the likelihood of patients with a range of tumors to respond to immune checkpoint blockade with pembrolizumab [111, 112], confirming that MMR deficient (MMR-D) tumors are more prone to accumulate mutations than their proficient (MMR-P) counterparts, especially the mutational profile commonly associated with microsatellite instability (MSI) [113]. In 2017, the FDA licensed the use of pembrolizumab for the treatment of MMR-D or MSI high (MSI-H) malignancies irrespective of tissue of origin [112], representing the first tissueagnostic approval in the history of the agency. Similarly, nivolumab has recently been approved for use in patients with MMR-D or MSI-H colorectal carcinoma [114]. Several diagnostic tests are currently available to determine MMR/MSI status from biopic material, mostly based on the PCR-assisted assessment of microsatellite markers or the immunohistochemical quantification of MMR-related proteins [115]. Importantly, some

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tumors display a relatively high mutational burden but are not MSI-H, suggesting that mechanisms other than MSI can compromise genomic stability [116]. It is currently unclear which of these two biomarkers have superior predictive value [117].

Of note, several other tumor biomarkers have been associated with poor clinical responses to ICBs [118]. These include (but may not be limited to): (1) mutations in beta-2-microglobulin (*B2M*), a critical component of the MHC class I system for antigen presentation [119]; (2) mutations in genes encoding several components of the interferon gamma receptor 1 (IFNGR1) signaling pathway [120, 121]; (3) activation of WNT signaling, which limits tumor infiltration by immune effectors cells, at least in melanoma [122]; and (4) activation of a multicomponent resistance pathway driven by low-intensity, chronic type I IFN signaling [123]. However, these biomarkers have mostly (if not only) been investigated in melanoma patients (reflecting the prevalence of melanoma studies in the clinical development of ICBs), and are not universally associated with disease outcome [112, 124], which explains why they are not (yet) used in clinical settings for decision-making.

Other biomarkers

The composition of the tumor microenvironment as well as the systemic configuration of the immune system also play an important role in the susceptibility of cancer patients to respond to immunotherapy with ICB. Several studies have demonstrated that elevated levels of tumor-infiltrating lymphocytes are associated with improved clinical responses to ICBs in patients affected by a variety of malignancies [84]. For instance, a study involving 46 melanoma patients treated with pembrolizumab documented higher numbers of CD8⁺, PD-1⁺ and PD-L1⁺ cells at the invasive tumor margin as well as in the tumor core in pretreatment samples from responders (as compared to non responders) [125]. As discussed above, an abundant infiltration with CD8⁺ CTLs and/or a limited infiltration with CD4⁺ CD25⁺ FOXP3⁺ T_{reg} cells have been attributed robust prognostic and predictive value in patients affected by a large panel of tumor types and treated with a wide array of therapeutic interventions [19, 84, 85], suggesting that these potential biomarkers are not specific for immunotherapy with ICBs. Likewise, genetic signatures indicative of tumor infiltration with effector (as opposed to suppressive) cells and activation of innate and adaptive immunity appear to convey prognostic, if not predictive, value in several oncological settings, including ICB-based immunotherapy [20, 102, 126]. The Immunoscore also represents a promising biomarker in some oncological settings, notably colorectal carcinoma [88, 127]. However, its prognostic versus predictive value remains to be defined, and so far there are no indications that it may specifically predict clinical responses to ICBs. Systemic parameters including the circulating levels of MDSCs have also been proposed as potential predictors of ICB efficacy in cancer patients [128]. The specific predictive value of such biomarkers, however, remains to be elucidated, and none of these factors is currently assessed in the clinic as part of the decision-making process for immunotherapy with ICBs.

Given the complexity of tumor-host interactions and the dynamic nature of most immunological biomarkers, it is not surprising that each of them has shown limited value when used individually [118]. Efforts are ongoing to develop integrative models that take

into account multiple parameters and features of the tumor and of the host, such as the so-called "cancer immunogram" [129], to reliably assist clinical decision making in the clinic.

Predictive biomarkers of response to RT plus ICBs

The potential predictive value of the biomarkers discussed above needs to be studied in patients receiving RT plus ICBs. Indeed, some of the biomarkers that are associated with improved clinical responses to RT or ICB-based immunotherapy may have limited predictive value in the context of combinatorial regimens. As an example, while high PD-L1 expression levels are robustly associated with the response of melanoma and NSCLC patients to nivolumab or pembrolizumab (see above), a benefit on progression-free survival was observed irrespective of baseline PD-L1 expression in NSCLC patients treated with chemoradiation followed by durvalumab versus placebo [130]. This result is consistent with the hypothesis that RT can induce PD-L1 expression in the tumor microenvironment, as demonstrated in preclinical settings [131]. It has also been suggested that PD-L1 expression levels at baseline might predict the response of metastatic melanoma patients to RT plus CTLA4-targeting ICBs, based on the PD-L1 positivity in 4 out of 9 non-responding and in 0 out of 2 responding patients [132], but this has not been confirmed. Here, we will focus our discussion on mechanism-based biomarkers that are emerging as candidates to specifically predict the response to RT plus ICBs (not necessarily to either of these treatments administered alone).

NKG2D ligands

NKG2D not only operates as a major NK-cell activatory receptor (NKAR), hence driving innate lymphoid immunity, but also stabilizes the immunological synapsis between CD8⁺ CTLs and their targets, hence supporting adaptive immunity [16]. Several DNA-damaging agents including RT promote the exposure of NKG2D ligands on the surface of malignant cells, hence rendering them potentially susceptible to NK cell-dependent lysis or improved recognition by CTLs [133]. However, cancer cells often express increased levels of metalloproteases that shed NKG2D ligands from the cell surface and create decoys with immunosuppressive activity [16]. Accordingly, high circulating levels of a soluble NKG2D ligands, including MHC class I polypeptide-related sequence A (MICA), MHC class I polypeptide-related sequence B (MICB), UL16 binding protein 1 (ULBP1) and UL16 binding protein 2 (ULBP2) have been attributed negative predictive value in melanoma patients treated with various ICBs including nivolumab, pembrolizumab and ipilimumab (which are currently approved for the treatment of melanoma patients) [134–137]. These observations suggest that soluble NKG2D ligands and antibodies that neutralize their activity [138, 139] may constitute easily accessible predictive biomarkers for patients receiving RT plus ICBs. Further investigation is warranted to properly assess this possibility.

Type I IFN responses

An abundant preclinical and clinical literature demonstrates that type I IFN release by neoplastic cells and dendritic cells (DCs) is paramount for the initiation of therapeutically relevant anticancer immune responses by chemotherapy, RT and immunotherapy [20, 21, 25, 140–143]. However, many tumors are resistant to ICBs because they are poorly infiltrated by

basic leucine zipper ATF-like transcription factor 3 (BATF3)-dependent DCs [122], a DC subset specialized in antigen cross-presentation to CD8⁺ T cells [144]. As it favors the release of type I IFN in the tumor microenvironment, RT has the potential to create a tumor microenvironment that is permissive to the recruitment and activation of BATF3-dependent DCs and CTLs [21, 142, 143]. Such an activity critically relies on the sequential activation of Mab-21 domain containing 1 (MB21D1; best known as cGAS) and transmembrane protein 173 (TMEM173; best known as STING) by tumor-derived double-stranded DNA (dsDNA) accessing the cytosolic compartment of cancer cells and/or DCs [21, 25, 26, 145]. In some circumstances, cGAS-STING signaling is impaired in cancer cells, generally as a consequence of epigenetic inactivation [146, 147], and this may impair the ability of radiation to enhance recruitment of BATF3-dependent DCs to poorly immunogenic tumors [148]. Thus, the expression levels of cGAS and STING at baseline represent a promising biomarker for the identification of patients who may achieve durable benefits from combinatorial regimens involving RT and ICBs. Of note, the DNA exonuclease three prime repair exonuclease 1 (TREX1) has been demonstrated to counteract the ability of RT to drive type I IFN secretion in cancer cells by degrading cytosolic dsDNA [21]. Importantly, TREX1 is upregulated by RT, but only at single doses above 12–18 Gy in most carcinoma cells, and this dose range is amenable to change across different malignancies [21]. This implies that TREX1 levels need to be measured in the tumor after RT to identify RT doses with optimal immunostimulatory effects. While this is not feasible in most patients, using bioptic material obtained at diagnosis to perform ex vivo irradiation and/or to establish patient-derived tumor xenografts (PDTXs) in immunodeficient mice (which can subsequently be tested for RT-driven TREX1 upregulation) stands out as a promising approach to guide the selection of an RT dose and schedule that are synergistic with ICBs [148].

These examples emphasize the need for well-designed biomarker-driven clinical trials to determine not only which patient and perhaps which lesion, in the metastatic setting, should be irradiated, but also how RT should be delivered to generate an *in situ* vaccine and increase responses to ICBs. At this stage in the development of combinations of RT and immunotherapy, interrogating the tissue is of paramount importance. Circulating biomarkers, including cytokines, exosomes and tumor-derived DNA [149] should be investigated in parallel and may, in time, be proven to provide safer and cheaper alternatives, at least in some situations. Oncological settings in which ICBs are poorly effective as standalone therapies, like breast carcinoma, may be best suited to this aim, especially in situations in which biopsies can be collected longitudinally. One example is the TONIC trial, recently presented at ESMO, in which patients with metastatic triple negative breast cancer were randomly assigned to one of five 2-week induction treatments: (1) RT given in 3 fractions of 8 Gy to one metastatic lesion, (2) low dose doxorubicin, (3) low dose cyclophosphamide, (4) cisplatin given two times, (5) no induction treatment, followed by nivolumab until progression. The trial is designed to evaluate 10 patients with paired pre and post-treatment biopsies in each arm in order to select the best induction treatment, giving consideration to both clinical response and degree of immunological tumor infiltration [150]. Similar trials should be conducted in patients with tumors amenable to serial biopsing in order to compare the efficacy of different RT regimens.

Concluding remarks

While local disease control by RT is generally achievable, occasional patients develop isolated recurrences and their prospective identification remains elusive. A century of radiation biology has identified several mechanisms that explain radioresistance, but approaches to identify patients at risk for such isolated recurrences (and hence prevent them) have generally failed in the clinic. With the renaissance of cancer immunotherapy, considerable efforts have been dedicated at the identification of predictive biomarkers of clinical responses to ICBs, with promising results. Indeed, two of these biomarkers (PD-L1 expression levels by malignant cells and MMR/MSI status) have already been implemented in the clinic to assist decision-making.

It is now clear that the response to RT is also dependent on its immunomodulatory effects (Figure 1), and upcoming efforts towards the identification of novel biomarkers will have to take this notion into attentive consideration. Since RT stands out as a promising partner for immunotherapy, especially for the treatment of neoplasms that exhibit limited immune infiltrate (so-called cold tumors) validated biomarkers that prospectively predict clinical responses to RT plus immunotherapy are warranted. Importantly, recent evidence about the mechanisms that regulate the immunogenicity of RT supports the notion that dose and fractionation may need to be optimized for each individual tumor [21]. The development of innovative methods such as the irradiation of bioptic specimens ex vivo or the establishment of PDTXs in immunodeficient mice may enable the identification of optimal RT dose and fractionation for each patient, hence overcoming the limitations of biomarkers developed on tumor type rather than on individual lesions. In this era of precision medicine, predictive biomarkers become essential to treatment decisions, but this critical research component is not sufficiently incorporated in most clinical trials. Nonetheless, recent advances in largescale data-rich biological analyses (so called "omics") and in functional imaging provide considrebale new opportunities for rapid progress in this field.

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Abbreviations

СТС	circulating tumor cell
CTL	cytotoxic T lymphocyte
DC	dendritic cell
DDR	DNA damage response
DSB	double-stand break

dsDNA	double-stranded DNA
FDA	Food and Drug Administration
ICB	immune checkpoint blocker
IFN	interferon
IHC	immunohistochemistry
IRDS	IFN-related DNA damage resistance signature
MMR	mismatch repair
MSI	microsatellite instability
NK	natural killer
NSCLC	non-small cell lung carcinoma
RCD	regulated cell death
RT	radiation therapy

Glossary

Abscopal response

Immunological response whereby the irradiation of a malignant lesion results in the regression or stabilization of a distant, non-irradiated lesion.

Adjuvanticity

Property of a specific molecule to enhance the immune response to an antigen.

Antigen cross-presentation

Ability of some antigen-presenting cells to present exogenous antigens via the route normally employed for endogenous antigens.

Antigenicity

Property of a chemical structure to be recognized as a foreign substance by the immune system.

Cellular senescence

Irreversible arrest of cell proliferation (growth) associated with specific morphological and secretory alterations, occurring in the context of specific stress responses.

Cytotoxic T lymphocyte (CTL)

Effector cell of the immune system that can mediate the lysis of target cells.

Danger-associated molecular pattern

Endogenous molecule that are normally invisible to the host immune system but, once emitted by stressed or dying cells, operate as endogenous adjuvants.

Dendritic cell (DC)

Professional antigen-presenting cells that play a key role to link innate and adaptive immunity.

Hypofractionation

The delivery of radiation therapy in a few fractions, each with a larger dose than standard 1.8 or 2 Gy.

Immune checkpoint blocker (ICB)

Monoclonal antibody that (re)instates anticancer immunosurveillance by inhibiting immunosuppressive receptors on CTLs and NK cells.

Immunological synapsis

Dynamic interface formed between an effector cell (T cell or NK cell) and an antigenpresenting cell (*e.g.*, dendritic cell) or a target cell (*e.g.*, tumor cell).

Immunoscore

Automated image analysis and quantification of effector and memory T cells at specific areas of neoplastic lesions.

Myeloid-derived suppressor cell (MDSC)

Member of a heterogeneous population of cells that are defined by their myeloid origin, immature state and ability to potently suppress T cell responses.

Natural killer (NK) cell

Innate lymphoid cell that function as both cytotoxic effector and regulator of immune responses.

Patient-derived tumor xenografts (PDTX)

Established from the transplantation of a fresh human tumor fragment from a cancer patient directly into a mouse, PDTX models usually preserve key features of a specific cancer.

Regulated cell death (RCD)

Type of cell death that occurs in the context of failing adaptation to stress and is controlled by a dedicated molecular machinery.

Regulatory T (T_{reg}) cell

T cell that prevents other immune cells (including CTLs) from attacking the host tissues, hence preventing autoimmune diseases.

Tumor-associated antigen

Antigen that are preferentially (but not uniquely) expressed by malignant cells.

Tumor neoantigen

Antigen encoded by tumor-specific mutated genes.

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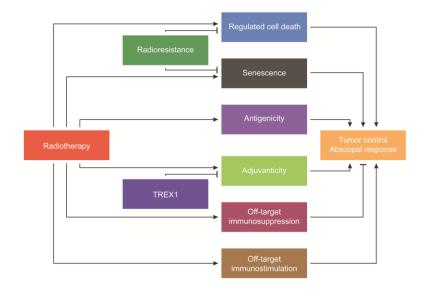


Figure 1. From radiotherapy to abscopal responses: the keys steps

Radiotherapy (RT) can mediate local tumor control and abscopal responses via three critical steps: (1) by inducing regulated cell death and/or senescence amongst malignant cells; (2) by increasing their antigenicity and/or adjuvanticity; and (3) by mediating local or systemic immunostimulatory effects that do not originate from malignant cells (off-target immunostimulation). Three major resistance mechanisms can counteract such effects and therefore compromise the therapeutic activity of RT: (1) the intrinsic radioresistance of malignant cells; (2) off-target immunosuppression; and (3) the induction of the DNA exonuclease three prime repair exonuclease 1 (TREX1).